

Title	Author	Journal/Conf.	Publisher	Number	Page	Year
EUCALYPT: efficient tree reconciliation enumerator	Beatrice Donati, Christian Baudet, Blerina Sinaimeri, Pierluigi Crescenzi, Marie-France Sagot	Algorithms for Molecular Biology	BioMed Central	10 (1)	11	2015
Mitochondrial respiration and genomic analysis provide insight into the influence of the symbiotic bacterium on host trypanosomatid oxygen consumption	Allan Cezar de Azevedo Martins, Ana Carolina Loyola Machado, Cecilia Coimbra Klein, Luciane Prioli Ciapina, Luiz Gonzaga Paula de Almeida, Ana Tereza R. de Vasconcelos, Marie-France Sagot, Wanderley de Souza, Marcelo Einicker-Lamas, Antonio Galina, Maria Cristina Machado Motta	Parasitology	Cambridge University Press (CUP)	142 (2)	352-362	2015
MEDUSA: A multi-draft based scaffolder	Emanuele Bosi, Beatrice Donati, Marco Galardini, Sara Brunetti, Marie-France Sagot, Pietro Lió, Pierluigi Crescenzi, Renato Fani, Marco Fondi	Bioinformatics	Oxford University Press (OUP)			2015
Genome reduction and potential metabolic complementation of the dual endosymbionts in the whitefly <i>Bemisia tabaci</i>	Qiong Rao, Pierre-Antoine Rollat-Farnier, Dan-Tong Zhu, Diego Santos-Garcia, Francisco J Silva, Andrés Moya, Amparo Latorre, Cecilia C Klein, Fabrice Vavre, Marie-France Sagot, Shu-Sheng Liu, Laurence Mouton, Xiao-Wei Wang	BMC Genomics	BioMed Central	16	226	2015
Two Host Clades, Two Bacterial Arsenals: Evolution through Gene Losses in Facultative Endosymbionts	Pierre-Antoine Rollat-Farnier, Diego Santos-Garcia, Qiong Rao, Marie-France Sagot, Francisco J Silva, Hélène Henri, Einat Zchori-Fein, Amparo Latorre, Andrés Moya, Valérie Barbe, Shu-Sheng Liu, Xiao-Wei Wang, Fabrice Vavre, Laurence Mouton	Genome Biology and Evolution	Oxford University Press (OUP)	7 (3)	839-855	2015
Cophylogeny Reconstruction via an Approximate Bayesian Computation	Christian Baudet, Beatrice Donati, Blerina Sinaimeri, Pierluigi Crescenzi, Christian Gautier, Catherine Matias, Marie-France Sagot	Systematic Biology	Oxford University Press (OUP)	64 (3)	416-431	2015
MIRINHO: An efficient and general plant and animal pre-miRNA predictor for genomic and deep sequencing data	Susan Higashi, Cyril Fournier, Christian Gautier, Christine Gaspin, Marie-France Sagot	BMC Bioinformatics	BioMed Central	In press		2015
RIME: Repeat identification	Maria Federico, Pierre Peterlongo, Nadia Pisanti, Marie-France Sagot	Discrete Applied Mathematics	Elsevier	163 (3)	275-286	2014
Telling metabolic stories to explore metabolomics data: A case study on the yeast response to cadmium exposure	Paulo Vieira Milreu, Cecilia Coimbra Klein, Ludovic Cottret, Vicente Acuña, Etienne Birmelé, Michele Borassi, Christophe Junot, Alberto Marchetti-Spaccamela, Andrea Marino, Leen Stougie, Fabien Jourdan, Pierluigi Crescenzi, Vincent Lacroix, Marie-France Sagot	Bioinformatics	Oxford University Press (OUP)	30 (1)	61-70	2014
The genome of <i>Cardinium cBtQ1</i> provides insights into genome reduction, symbiont motility, and its settlement in <i>Bemisia tabaci</i>	Diego Santos-Garcia, Pierre-Antoine Rollat-Farnier, Francisco Beitia, Einat Zchori-Fein, Fabrice Vavre, Laurence Mouton, Andrés Moya, Amparo Latorre, Francisco J Silva	Genome Biology and Evolution	Oxford University Press (OUP)	6 (4)	1013-1030	2014
Using cascading Bloom filters to improve the memory usage for de Bruijn graphs	Kamil Salikhov, Gustavo Sacomoto, Gregory Kucherov	Algorithms for Molecular Biology	BioMed Central	9 (1)	2	2014

On the genetic architecture of cytoplasmic incompatibility: inference from phenotypic data	Igor Nor, Jan Engelstädtér, Olivier Duron, Max Reuter, Marie-France Sagot, Sylvain Charlat	The American Naturalist	University of Chicago Press	182 (1)	15-24	2014
Biosynthesis of vitamins and cofactors in bacterium-harbouring trypanosomatids depends on the symbiotic association as revealed by genomic analyses	Cecilia C Klein, João M P Alves, Myrna G Serrano, Gregory A Buck Ana Tereza R. Vasconcelos, Marie-France Sagot, Marta M G Teixeira, Erney P Camargo, Maria Cristina M Motta	PLoS One	PLOS	8 (11)	79786	2014
Short and long-term genome stability analysis of prokaryotic genomes	Matteo Brilli, Pietro Liò, Vincent Lacroix, Marie-France Sagot	BMC Genomics	BioMed Central	14 (1)	309	2013
Endosymbiosis in trypanosomatids: the genomic cooperation between bacterium and host in the synthesis of essential amino acids is heavily influenced by multiple horizontal gene transfers	João Alves, Cecilia Klein, Flávia Da Silva, André Costa-Martins, Myrna Serrano, Gregory Buck, Ana Tereza R. Vasconcelos, Marie-France Sagot, Marta Teixeira, Maria Cristina Motta, Erney Camargo	BMC Evolutionary Biology	BioMed Central	13 (1)	190	2013
Predicting the proteins of <i>Angomonas deanei</i> , <i>Strigomonas culicis</i> and their respective endosymbionts reveals new aspects of the trypanosomatidae family	Maria Cristina Machado Motta, Allan Cezar de Azevedo Martins, Silvana Sant'Anna De Souza, Carolina Moura Costa Catta-Preta, Rosane Silva, Cecilia Coimbra Klein, Luiz Gonzaga Paula De Almeida, Oberdan De Lima Cunha, Luciane Prioli Ciapina, Marcelo Brocchi, Ana Cristina Colabardini, Bruna De Araujo Lima, Carlos Renato Machado, Célia Maria De Almeida Soares, Christian Macagnan Probst, Claudia Beatriz Afonso De Menezes, Claudia Elizabeth Thompson, Daniella Castanheira Bartholomeu, Daniela Fiori Gradia, Daniela Parada Pavoni, Edmundo C Grisard, Fabiana Fantinatti-Garboggi, Fabricio Klerynton Marchini, Gabriela Flávia Rodrigues-Luiz, Glauber Wagner, Gustavo Henrique Goldman, Juliana Lopes Rangel Fietto, Maria Carolina Elias, Maria Helena S Goldman, Marie-France Sagot, Maristela Pereira, Patrícia H Stoco, Rondon Pessoa De Mendonça-Neto, Santuza Maria Ribeiro Teixeira, Tales Eduardo Ferreira Maciel, Tiago Antônio De Oliveira Mendes, Turán P Ürményi, Wanderley De Souza, Sergio Schenkman Ana Tereza R. Vasconcelos	PLoS One	PLOS	8 (4)	60209	2013
Navigating the unexplored seascape of pre-miRNA candidates in single-genome approaches	Nuno Mendes, Steffen Heyne, Ana T. Freitas, Marie-France Sagot, Rolf Backofen	Bioinformatics	Oxford University Press (OUP)	28 (23)	3034-3041	2012
Structural and dynamical analysis of biological networks	Cecilia Klein, Andrea Marino, Marie-France Sagot, Paulo Vieira Milreu, Matteo Brilli	Briefings in Functional Genomics and Proteomics	Structural and dynamical analysis of biological networks	14	309	2012
RHEA – A manually curated resource of	Rafael Alcantara Kristian B. Axelsen, Anne Morgat,	Nucleic Acids Research	Oxford University	40	D754-60	2012

biochemical reactions	Eugení Belda, Elisabeth Coudert, Alan Bridge, Hong Cao, Paula de Matos, Marcus Ennis, Steve Turner, Gareth Owen, Lydie Bougueret, Ioannis Xenarios, Christoph Steinbeck		Press (OUP)			
KiSSPLICE: de-novo calling alternative splicing events from RNA-seq data	Gustavo A.T. Sacomoto, Janice Kielbassa, Rayan Chikhi, Raluca Uricaru, Pavlos Antoniou, Marie-France Sagot, Pierre Peterlongo, Vincent Lacroix	BMC Bioinformatics	BioMed Central	13 (Suppl 6)	S5	2012
Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts	Milana Frenkel-Morgenstern, Vincent Lacroix, Iakes Ezkurdia, Yishai Levin, Alexandra Gabashvili, Jaime Prilusky, Angela del Pozo, Michael Tress, Rory Johnson, Roderic Guigo, Alfonso Valencia	Genome Research	Cold Spring Harbor Laboratory Press	22 (7)	1231-42	2012
Exploration of the core metabolism of symbiotic bacteria	Cecilia C. Klein, Ludovic Cottret, Janice Kielbassa, Hubert Charles, Christian Gautier, Ana Tereza R. Vasconcelos, Vincent Lacroix, Marie-France Sagot	BMC Genomics	BioMed Central	13 (1)	438	2012
Mod/Resc Parsimony Inference: Theory and application	Igor Nor, Danny Hermelin, Sylvain Charlat, Jan Engelstadter, Max Reuter, Olivier Duron, Marie-France Sagot	Information and Computation	Elsevier	213	23-32	2012
Telling stories: Enumerating maximal directed acyclic graphs with a constrained set of sources and targets	Vicente Acuña, Etienne Birmelé, Ludovic Cottret, Pierluigi Crescenzi, Fabien Jourdan, Vincent Lacroix, Alberto Marchetti-Spaccamela ,Andrea Marino, Paulo Vieira Milreu, Marie-France Sagot, Leen Stougie	Theoretical Computer Science	Elsevier	457	1-9	2012
Sampling Solution Traces for the Problem of Sorting Permutations by Signed Reversals	Christian Baudet, Zanoni Dias, Marie-France Sagot	Algorithms for Molecular Biology	BioMed Central	7 (1)	18	2012
CHITARS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data	Milana Frenkel-Morgenstern, Alessandro Gorovovski, Vincent Lacroix, Mark Rogers, Kristina Ibañez, Cesar Boullosa, Eduardo Andres Leon, Asa Ben-Hur, Alfonso Valencia	Nucleic Acids Research	Oxford University Press (OUP)	41	142-151	2012
Bacterial syntenies: an exact approach with gene quorum	Yves-Pol Deniéou, Marie-France Sagot, Frédéric Boyer and Alain Viari	BMC Bioinformatics	BioMed Central	12	193	2011
<i>Wolbachia</i> detection: an assessment of standard PCR Protocols	Patricia M. Simões, Gladys Mialdea, Daphné Reiss, Marie-France Sagot, Sylvain Charlat	Molecular Ecology Resources	John Wiley	11 (3)	567-572	2011
UNIPATHWAY: a resource for the exploration and annotation of metabolic pathways	Anne Morgat, Eric Coissac, Elisabeth Coudert, Kristian B. Axelsen, Guillaume Keller, Amos Bairoch, Alan Bridge, Lydie Bougueret, Ioannis Xenarios, Alain Viari	Nucleic Acids Research	Oxford University Press (OUP)	40	761-769	2011
Close 3D proximity of evolutionary breakpoints argues for the notion of spatial synteny	Amélie S. Véron, Claire Lemaitre, Christian Gautier, Vincent Lacroix and Marie-France Sagot	BMC Genomics	BioMed Central	12 (1)	303	2011
CYCADS: an annotation database system to ease the development and update of BioCyc databases	Augusto F. Vellozo, Amélie S. Veron, Patrice Baa-Puyoulet, Jaime Huerta-Cepas, Ludovic Cottret, Gérard Febvay, Federica Calevro, Yvan Rahbé,	Database	Oxford University Press (OUP)		bar008	2011

	Angela E. Douglas, Toni Gabaldon, Marie-France Sagot, Hubert Charles, Stefano Colella					
CASSIS: detection of genomic rearrangement breakpoints	Christian Baudet, Claire Lemaitre, Zanoni Dias, Christian Gautier, Eric Tannier, Marie-France Sagot	Bioinformatics	Oxford University Press (OUP)	26 (15)	1897-8	2010
Graph-Based Analysis of the Metabolic Exchanges between Two Co-Resident Intracellular Symbionts, <i>Baumannia cicadellinicola</i> and <i>Sulcia muelleri</i> , with their Insect Host, <i>Homalodisca coagulata</i>	Ludovic Cottret, Paulo Vieira Milreu, Vicente Acuña, Alberto Marchetti-Spaccamela, Leen Stougie, Hubert Charles, Marie-France Sagot	PLoS Computational Biology	PLOS		289-301	2010
Computing an Evolutionary Ordering is Hard	Laurent Bulteau, Gustavo Sacomoto, Blerina Sinaimeri	Electronic Notes in Discrete Mathematics	VIII Latin-American Algorithms, Graphs and Optimization Symposium (LAGOS)			2015
Amortized $\tilde{O}(V)$ -Delay Algorithm for Listing Chordless Cycles in Undirected Graphs	Rui Ferreira, Roberto Grossi, Romeo Rizzi, Gustavo Sacomoto, Marie-France Sagot	Lecture Notes in Computer Science, Springer	22th Annual European Symposium on Algorithms (ESA)	8737	418-429	2014
Efficiently listing bounded length st-paths	Romeo Rizzi, Gustavo Sacomoto, Marie-France Sagot.	Lecture Notes in Computer Science, Springer	Twenty-Fifth International Workshop on Combinatorial Algorithms (IWOCA 2014)	in press		2014
Length and Symmetry on the Sorting by Weighted Inversions Problem	Christian Baudet, Ulisses Dias, Zanoni Dias	Advances in Bioinformatics and Computational Biology	9th Brazilian Symposium on Bioinformatics (BSB)	8826	99-106	2014
Navigating in a Sea of Repeats in RNA-seq without Drowning	Gustavo Sacomoto, Blerina Sinaimeri, Camille Marchet, Vincent Miele, Marie-France Sagot, Vincent Lacroix	Lecture Notes in Computer Science, Springer	Proceedings of 14th Workshop on Algorithms in Bioinformatics (WABI)	8701	82-96	2014
Greedy Randomized Search Procedure to Sort Genomes using Symmetric, Almost-Symmetric and Unitary Inversions	Ulisses Dias, Christian Baudet, Zanoni Dias	ACM Proceedings	4th ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB)		181-190	2013
A polynomial delay algorithm for the enumeration of bubbles with length constraints in directed graphs and its application to the detection of alternative splicing in RNA-seq data	Gustavo Akio Tominaga Sacomoto, Vincent Lacroix, Marie-France Sagot	Lecture Notes in Computer Science, Springer	Workshop on Algorithms in Bioinformatics (WABI)	8126	99-111	2013
Telling stories fast	Michele Borassi, Pierluigi Crescenzi, Vincent Lacroix, Andrea Marino, Marie-France Sagot, Paulo Vieira Milreu	Lecture Notes in Computer Science, Springer	2th International Symposium Experimental Algorithms (SEA)	7933	200-211	2013

Optimal Listing of Cycles and st-Paths in Undirected Graphs	Etienne Birmelé, Rui Ferreira, Roberto Grossi, Andrea Marino, Nadia Pisanti, Romeo Rizzi, Gustavo Sacomoto	ACM Proceedings	24th Annual ACM-SIAM Symposium on Discrete Algorithms (SODA)			2013
Efficient bubble enumeration in directed graphs events from RNA-seq data	Etienne Birmelé, Pierluigi Crescenzi, Rui Ferreira, Roberto Grossi, Vincent Lacroix, Andrea Marino, Nadia Pisanti, Gustavo Sacomoto, Marie-France Sagot	Lecture Notes in Computer Science, Springer	International Symposium on String Processing and Information Retrieval (SPIRE)	7608	118-129	2012
Minimum Ratio Cover of Matrix Columns by Extreme Rays of Its Induced Cone	Alexandre S. Freire, Vicente Acuña, Pierluigi Crescenzi, Carlos E. Ferreira, Vincent Lacroix, Paulo V. Milreu, Eduardo Moreno, Marie-France Sagot	Lecture Notes in Computer Science, Springer	International Symposium on Combinatorial Optimization (ISCO)	7422	165-177	2012
Enumerating Chemical Organisations in Consistent Metabolic Networks: Complexity and Algorithms	Paulo V. Milreu, Vicente Acuna, Etienne Birmelé, Pierluigi Crescenzi, Alberto Marchetti-Spaccamela, Marie-France Sagot, Leen Stougie, Vincent Lacroix	Lecture Notes in Computer Science, Springer	Workshop on Algorithms in Bioinformatics (WABI)	6293	226-237	2010
Mod/Resc Parsimony Inference	Igor Nor, Danny Hermelin, Sylvain Charlat, Jan Engelstadter, Max Reuter, Olivier Duron, Marie-France Sagot	Lecture Notes in Computer Science, Springer	Symposium on Combinatorial Pattern Matching (CPM)	6129	202-213	2010