Publications

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1 Methodological papers

In Journals

[1] Christophe Ambroise, Alia Dehman, Pierre Neuvial, Guillem Rigaill, and Nathalie Vialaneix. “Adjacency-constrained hierarchical clustering of a band similarity matrix with application to Genomics.” In: **Algorithms for Molecular Biology** (2019).

[2] Alain Celisse, Guillemette Marot, Morgane Pierre-Jean, and Guillem Rigaill. “New efficient algorithms for multiple change-point detection with reproducing kernels”. In: **Computational Statistics & Data Analysis** 128 (2018), pp. 200–220.

[3] Paul Fearnhead and Guillem Rigaill. “Changepoint detection in the presence of outliers”. In: **Journal of the American Statistical Association** (2018), pp. 1–15.

[4] Julien Chiquet, Yves Grandvalet, and Guillem Rigaill. “On coding effects in regularized categorical regression”. In: **Statistical Modelling** 16.3 (2016), pp. 228–237.

[5] Robert Maidstone, Toby Hocking, Guillem Rigaill, and Paul Fearnhead. “On optimal multiple changepoint algorithms for large data”. In: **Statistics and Computing** (2016), pp. 1–15.

[6] Julien Chiquet, Pierre Gutierrez, and Guillem Rigaill. “Fast tree inference with weighted fusion penalties”. In: **Journal of Computationnal and Graphical Statistics** (2015).

[7] Guillem Rigaill. “A pruned dynamic programming algorithm to recover the best segmentations with 1 to K_max change-points.” In: **Journal de la Société Française de Statistique** 156.4 (2015), pp. 150–175.

[8] Alice Cleynen, The Minh Luong, Guillem Rigaill, and Gregory Nuel. “Fast estimation of the Integrated Completed Likelihood criterion for change-point detection problems with applications to Next-Generation Sequencing data”. In: **Signal Processing** 98 (2014), pp. 233–242.

[9] Alice Cleynen, Michel Koskas, Emilie Lebarbier, Guillem Rigaill, and Stéphane Robin. “Segmentor3IsBack: an R package for the fast and exact segmentation of Seq-data.” In: **Algorithms for Molecular Biology** 9 (2014), p. 6.

[10] Guillem Rigaill, Sandrine Balzergue, Véronique Brunaud, Eddy Blondet, Andrea Rau, Odile Rogier, José Caius, Cathy Maugis-Rabusseau, Ludivine Soubigou-Taconnat, Sébastien Aubourg, Lurin Claire, Martin-Magniette Marie-Laure, and Delannoy Etienne. “Synthetic data sets for the identification of key ingredients for RNA-seq differential analysis”. In: **Briefings in bioinformatics** (2016).

[11] Morgane Pierre-Jean, Guillem Rigaill, and Pierre Neuvial. “Performance evaluation of DNA copy number segmentation methods”. In: **Briefings in bioinformatics** (2014), bbu026.

[12] Guillem Rigaill, Sidney Cadot, Roelof JC Kluin, Zheng Xue, Rene Bernards, Ian J Majewski, and Lodewyk FA Wessels. “A regression model for estimating DNA copy number applied to capture sequencing data”. In: **Bioinformatics** 28.18 (2012), pp. 2357–2365.

[13] Guillem Rigaill, Émilie Lebarbier, and Stephane Robin. “Exact posterior distributions and model selection criteria for multiple change-point detection problems”. In: **Statistics and Computing** 22.4 (2012), pp. 917–929.

[14] Franck Picard, Emilie Lebarbier, Mark Hoebeke, Guillem Rigaill, Baba Thiam, and Stéphane Robin. “Joint segmentation, calling, and normalization of multiple CGH profiles”. In: **Biostatistics** (2011).

[15] Guillem Rigaill, Philippe Hupé, Anna Almeida, Philippe La Rosa, Jean-Philippe Meyniel, Charles Decraene, and Emmanuel Barillot. “ITALICS: an algorithm for normalization and DNA copy number calling for Affymetrix SNP arrays”. In: **Bioinformatics** 24.6 (2008), pp. 768–774.

In Proceedings

[16] Toby Dylan Hocking, Guillem Rigaill, and Guillaume Bourque. “PeakSeg: constrained optimal segmentation and supervised penalty learning for peak detection in count data”. In: **Proceedings of The 32nd International Conference on Machine Learning**. 2015, pp. 324–332.

[17] Guillem Rigaill, Toby Hocking, Jean-Philippe Vert, and Francis Bach. “Learning sparse penalties for change-point detection using max margin interval regression”. In: **Proceedings of The 30th International Conference on Machine Learning**. 2013, pp. 172–180.

[18] Guillem Rigaill, Emilie Lebarbier, and Stéphane Robin. “Exact posterior distributions over the segmentation space and model selection for multiple change-point detection problems”. In: **Proceedings of COMPSTAT’2010**. Springer, 2010, pp. 557–564.

2 Applied papers

In Bioinformatics

[19] Bastien Malbert, Guillem Rigaill, Veronique Brunaud, Claire Lurin, and Etienne Delannoy. “Bioinformatic Analysis of Chloroplast Gene Expression and RNA Posttranscriptional Maturations Using RNA Sequencing”. In: **Plastids**. Springer, 2018, pp. 279–294.

[20] Rim Zaag, Jean Philippe Tamby, Cécile Guichard, Zakia Tariq, Guillem Rigaill, Etienne Delannoy, Jean-Pierre Renou, Sandrine Balzergue, Tristan Mary-Huard, Sébastien Aubourg, ML Martin-Magniette, and V Brunaud. “GEM2Net: from gene expression modeling to-omics networks, a new CATdb module to investigate Arabidopsis thaliana genes involved in stress response”. In: **Nucleic acids research** (2014), gku1155.

[21] Toby D Hocking, Valentina Boeva, Guillem Rigaill, Gudrun Schleiermacher, Isabelle Janoueix-Lerosey, Olivier Delattre, Wilfrid Richer, Franck Bourdeaut, Miyuki Suguro, Masao Seto, and F Bach. “SegAnnDB: interactive Web-based genomic segmentation”. In: **Bioinformatics** 30.11 (2014), pp. 1539–1546.

[22] Jorma J de Ronde, Guillem Rigaill, Sven Rottenberg, Sjoerd Rodenhuis, and Lodewyk FA Wessels. “Identifying subgroup markers in heterogeneous populations”. In: **Nucleic acids research** (2013), gkt845.

[23] Tatiana Popova, Elodie Manié, Dominique Stoppa-Lyonnet, Guillem Rigaill, Emmanuel Barillot, and Marc-Henri Stern. “Genome Alteration Print (GAP): a tool to visualize and mine complex cancer genomic profiles obtained by SNP arrays”. In: **Genome Biology** 10.11 (2009), R128–R128.

In Biology

[24] Marc-André Lemay, Davoud Torkamaneh, Guillem Rigaill, Brian Boyle, Adrian O Stec, Robert M Stupar, and François Belzile. “Screening populations for copy number variation using genotyping-by-sequencing: a proof of concept using soybean fast neutron mutants”. In: **BMC genomics** 20.1 (2019), pp. 1–16.

[25] Sylvie Maubant, Brisson Tahtouh Tania, Amélie, Virginie Maire, Fariba Némati, Bruno Tesson, Mengliang Ye, Guillem Rigaill, Maïté Noizet, Aurélie Dumont, David Gentien, Marty-Prouvost Bérengère, de Koning Leanne, Sardar Faisal Mahmood, Didier Decaudin, Francisco Cruzalegui, Tucker Gordon C, Sergio Roman-Roman, and Thierry. Dubois. “LRP5 regulates the expression of STK40, a new potential target in triple-negative breast cancers”. In: **Oncotarget** (2018).

[26] Virginie Maire, Faisal Mahmood, Guillem Rigaill, Mengliang Ye, Amélie Brisson, Fariba Némati, David Gentien, Gordon C Tucker, Sergio Roman-Roman, and Thierry Dubois. “LRP8 is overexpressed in estrogen-negative breast cancers and a potential target for these tumors”. In: **Cancer medicine** (2018).

[27] Elise Albert, Renaud Duboscq, Muriel Latreille, Sylvain Santoni, Matthieu Beukers, Jean-Paul Bouchet, Fréderique Bitton, Justine Gricourt, Charles Poncet, Véronique Gautier, José M Jiménez-Gómez, Guillem Rigaill, and Mathilde. Causse. “Allele specific expression and genetic determinants of transcriptomic variations in response to mild water deficit in tomato”. In: **The Plant Journal** (2018).

[28] Andrew Lloyd, Aurélien Blary, Delphine Charif, Catherine Charpentier, Joseph Tran, Sandrine Balzergue, Etienne Delannoy, Guillem Rigaill, and Eric Jenczewski. “Homoeologous exchanges cause extensive dosage-dependent gene expression changes in an allopolyploid crop”. In: **New Phytologist** (2018).

[29] Jean-Tristan Brandenburg, Tristan Mary-Huard, Guillem Rigaill, Sarah J Hearne, Hélène Corti, Johann Joets, Clémentine Vitte, Alain Charcosset, Stéphane D Nicolas, and Maud I Tenaillon. “Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts”. In: **PLoS genetics** 13.3 (2017), e1006666.

[30] Damien Guillaumot, Mauricio Lopez-Obando, Kevin Baudry, Alexandra Avon, Guillem Rigaill, Andéol Falcon de Longevialle, Benjamin Broche, Mizuki Takenaka, Richard Berthomé, Geert De Jaeger, et al. “Two interacting PPR proteins are major Arabidopsis editing factors in plastid and mitochondria”. In: **Proceedings of the National Academy of Sciences** 114.33 (2017), pp. 8877–8882.

[31] Anne-Sophie Dumas, Ludivine Taconnat, Evangelos Barbas, Guillem Rigaill, Olivier Catrice, Delphine Bernard, Abdelilah Benamar, David Macherel, Abdelhak El Amrani, and Richard Berthomé. “Unraveling the early molecular and physiological mechanisms involved in response to phenanthrene exposure”. In: **BMC genomics** 17.1 (2016), p. 818.

[32] Céline Baldeyron, Amélie Brisson, Bruno Tesson, Fariba Némati, Stéphane Koundrioukoff, Elie Saliba, Leanne De Koning, Elise Martel, Mengliang Ye, Guillem Rigaill, D Meseure, A Nicolas, D Gentien, D Decaudin, M Debatisse, S Depil, F Cruzalegui, A Pierré, S Roman-Roman, GC Tucker, and T Dubois. “TIPIN depletion leads to apoptosis in breast cancer cells”. In: **Molecular oncology** (2015).

[33] Sylvie Maubant, Bruno Tesson, Virginie Maire, Mengliang Ye, Guillem Rigaill, David Gentien, Francisco Cruzalegui, Gordon C Tucker, Sergio Roman-Roman, and Thierry Dubois. “Transcriptome analysis of Wnt3a-treated triple-negative breast cancer cells”. In: **PloS one** 10.4 (2015), e0122333.

[34] Virginie Maire, Fariba Némati, Marion Richardson, Anne Vincent-Salomon, Bruno Tesson, Guillem Rigaill, Eléonore Gravier, Bérengère Marty-Prouvost, Leanne De Koning, Guillaume Lang, D Gentien, A Dumont, E Barillot, E Marangoni, D Decaudin, S Roman-Roman, A Pierré, F Cruzalegui, S Depil, GC Tucker, and T. Dubois. “Polo-like kinase 1: a potential therapeutic option in combination with conventional chemotherapy for the management of patients with triple-negative breast cancer”. In: **Cancer research** 73.2 (2013), pp. 813–823.

[35] Anne Vincent-Salomon, Vanessa Benhamo, Eléonore Gravier, Guillem Rigaill, Nadège Gruel, Stéphane Robin, Yann de Rycke, Odette Mariani, Gaëlle Pierron, David Gentien, F Reyal, P Cottu, A Fourquet, R Rouzier, X Sastre-Garau, and O. Delattre. “Genomic instability: a stronger prognostic marker than proliferation for early stage luminal breast carcinomas”. In: **PloS one** 8.10 (2013).

[36] Virginie Maire, Céline Baldeyron, Marion Richardson, Bruno Tesson, Anne Vincent-Salomon, Eléonore Gravier, Bérengère Marty-Prouvost, Leanne De Koning, Guillem Rigaill, Aurélie Dumont, D Gentien, E Barillot, S Roman-Roman, S Depil, F Cruzalegui, A Pierré, GC Tucker, and T. Dubois. “TTK/hMPS1 is an attractive therapeutic target for triple-negative breast cancer”. In: **Plos One** 8.5 (2013).

[37] Aurore Toullec, Damien Gerald, Gilles Despouy, Brigitte Bourachot, Melissa Cardon, Sylvain Lefort, Marion Richardson, Guillem Rigaill, Maria-Carla Parrini, Carlo Lucchesi, D Bellanger, MH Stern, T Dubois, X Sastre-Garau, O Delattre, A Vincent-Salomon, and F. Mechta-Grigoriou. “Oxidative stress promotes myofibroblast differentiation and tumour spreading”. In: **EMBO molecular medicine** 2.6 (2010), pp. 211–230.

[38] Floria Lizárraga, Renaud Poincloux, Maryse Romao, Guillaume Montagnac, Gaëlle Le Dez, Isabelle Bonne, Guillem Rigaill, Graça Raposo, and Philippe Chavrier. “Diaphanous-related formins are required for invadopodia formation and invasion of breast tumor cells”. In: **Cancer research** 69.7 (2009), pp. 2792–2800.

[39] Bérengère Marty, Virginie Maire, Eléonore Gravier, Guillem Rigaill, Anne Vincent-Salomon, Marion Kappler, Ingrid Lebigot, Fathia Djelti, Audrey Tourdès, Pierre Gestraud, P Hupé, E Barillot, F Cruzalegui, GC Tucker, MH Stern, JP Thiery, JA Hickman, and T. Dubois. “Frequent PTEN genomic alterations and activated phosphatidylinositol 3-kinase pathway in basal-like breast cancer cells”. In: **Breast Cancer Res** 10.6 (2008), R101.

[40] Marc A Bollet, Nicolas Servant, Pierre Neuvial, Charles Decraene, Ingrid Lebigot, Jean-Philippe Meyniel, Yann De Rycke, Alexia Savignoni, Guillem Rigaill, Philippe Hupé, A Fourquet, B Sigal-Zafrani, E Barillot, and JP. Thiery. “High-resolution mapping of DNA breakpoints to define true recurrences among ipsilateral breast cancers”. In: **Journal of the National Cancer Institute** 100.1 (2008), pp. 48–58.

3 Pre-prints and papers in preparation

Pre-publications

[41] Toby Dylan Hocking, Guillem Rigaill, Paul Fearnhead, and Guillaume Bourque. “Generalized Functional Pruning Optimal Partitioning (GFPOP) for Constrained Changepoint Detection in Genomic Data”. In: **arXiv preprint arXiv:1810.00117** (2018).

[42] Toby Dylan Hocking, Guillem Rigaill, Paul Fearnhead, and Guillaume Bourque. “A log-linear time algorithm for constrained changepoint detection”. In: **arXiv preprint arXiv:1703.03352** (2017).

[43] Guillem Rigaill. “Pruned dynamic programming for optimal multiple change-point detection”. In: **arXiv preprint arXiv:1004.088** (2010).

[44] Vanesa S Garcia de la Torre, Clarisse Majorel-Loulergue, Dubiel A Gonzalez, Ludivine Soubigou-Taconnat, Guillem Rigaill, Yohan Pillon, Louise Barreau, Sebastien Thomine, Bruno Fogliani, Valerie Burtet-Sarramegna, et al. “Wide cross-species RNA-Seq comparison reveals a highly conserved role for Ferroportins in nickel hyperaccumulation in plants”. In: **bioRxiv** (2018), p. 420729.

In preparation

[45] Vincent Runge, Toby Dylan Hocking, Gaetano Romano, Fatemeh Afgah, Paul Fearnhead, and Guillem Rigaill. “gfpop : an R Package for Univariate Graph-constrained Changepoint Detection”. In: (?).

[46] Audrey Hulot, Julien Chiquet, Florence Jaffrézic, and Guillem Rigaill. “Fast tree aggregation for consensus hierarchical clustering”. In: (?).

4 Softwares

Packages R

[48] Guillem Rigaill, Toby Hocking, Robert Maidstone, and Paul Fearnhead. Fpop. `https://cran.r-project.org/web/packages/fpop/index.html`. R package for segmentation using optimal partionning and function pruning. 2018.

[49] Paul Fearnhead and Guillem Rigaill. robseg. `https://github.com/guillemr/robust-fpop`. R package for changepoint detection in the presence of outliers. 2017.

[50] Julien Chiquet, Valentin Dervieux, and Guillem Rigaill. AriCode. `https://CRAN.R-project.org/package=aricode`. aricode: a package for efficient computations ofstandard clustering comparison measures. 2018.

[51] Audrey Hulot, Julien Chiquet, and Guillem Rigaill. MergeTree. `https://CRAN.R-project.org/package=mergeTress`. mergeTrees: Aggregating Trees. 2018.

[52] Pierre. Gutierrez, Guillem Rigaill, and Julien Chiquet. Fused-Anova. `https://r-forge.r-project.org/projects/fusedanova/`. This package adjusts a penalized ANOVA model with Fused-LASSO penality. 2013.

[53] Toby Hocking and Guillem Rigaill. PeakSegDP. `https://github.com/tdhock/PeakSegDP`. Peak detection via Constrained Optimal Segmentation (Dynamic Programming algorithm). 2014.

[54] Alice Cleynen, Emilie Lebarbier, Michel Koskas, Guillem Rigaill, and Stéphane Robin. Segmentor3IsBack. `https://CRAN.R-project.org/package=Segmentor3IsBack`. R package for the segmentation of RNAseq profiles. 2014.

[55] M Pierre-Jean, Pierre Neuvial, and G Rigaill. jointSeg. `https://CRAN.R-project.org/package=jointSeg`. jointseg: Joint Segmentation of Multivariate (Copy Number) Signals. 2015.

[56] P Picard, M Hoebeke, E Lebarbier, V Miele, G Rigaill, and S Robin. cghseg. `http://cran.r-project.org/web/packages/cghseg/index.html`. cghseg is an R package dedicated to the analysis of CGH profiles using segmentation models. 2011.

5 Talks

Invited

[57] Changepoint detection in the presence of outliers and constraints. GDR Stat et Santé. Conservatoire national des Arts et Métiers (CNAM), Paris, 2019.

[58] A statistical method to detect abrupt changes in trees. Workshop Change Point Detection: Limit Theorems, Algorithms, and Applications in Life Sciences. Alfried Krupp Wissenschaftskolleg, Greifswald, 2019.

[59] Changepoint detection in the presence of outliers. Statistical Scalability Workshop 2018. Windemere, UK, 2018.

[60] On exact multiple changepoint algorithms. Optimal partitioning and functional pruning. Time Dynamic Change Point Models and its Applications. Institut für Mathematische Stochastik der Universität Göttingen, 2014.

[61] On exact multiple changepoint algorithms. Optimal partitioning and functional pruning. Inference for Change-Point and Related Processes. Isaac Newton Institute. Cambridge, 2014.

[62] Partitionnement optimal et élagage fonctionnel pour la détection de ruptures multiples. 46èmes Journées de Statistique. Session "New challenges for new data". Rennes, 2014.

Submitted

[63] A fast homotopy algorithm for a large class of weighted classification problems. Proceedings of the MLCB NIPS'14 workshop. Montreal, 2014.

[64] A fast homotopy algorithm for a large class of weighted classification problems. SMPGD: Statistical Methods for Post-Genomic Data workshop. Paris, 2014.

[65] Segmentor3IsBack: an R package for the fast and exact segmentation of Seq-data. The R User Conference, useR! Albacete, 2013.

[66] Exact posterior distributions and model selection criteria for multiple change-point detection problems. Recent Advances in Changepoint Analysis. University of Warwick, 2012.

[67] A statistical approach to estimate copy number from capture sequencing data. STATSEQ. Verona, 2012.

[68] An exact algorithm for estimating the read depth of NGS profiles using irregular histograms. STATSEQ. Toulouse, 2011.

[69] An Exact Algorithm for the Segmentation of NGS Profiles using Compression. JOBIM : Journées Ouvertes en Biologie, Informatique et Mathématiques. Paris, 2011.

[70] Exact and fast segmentation of large SNP/CGH profiles. SMPGD: Statistical Methods for Post-Genomic Data workshop. Marseille, 2010.

[71] DNA Copy number analysis. Defining a probability for the segmentation space. SMPGD: Statistical Methods for Post-Genomic Data workshop. Paris, 2009.

[72] GINCOS: a method to normalize Affymetrix GeneChip Human Mapping 50K Set. JOBIM : Journées Ouvertes en Biologie, Informatique et Mathématiques. Marseille, 2007.