

Année de publication : 2015

Elsa Bernard, Laurent Jacob, Julien Mairal, Eric Viara, Jean-Philippe Vert (2015 Aug 20)

A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples.

BMC bioinformatics : 262 : [DOI : 10.1186/s12859-015-0695-9](https://doi.org/10.1186/s12859-015-0695-9)

Résumé

Detecting and quantifying isoforms from RNA-seq data is an important but challenging task. The problem is often ill-posed, particularly at low coverage. One promising direction is to exploit several samples simultaneously.

Alice Schoenauer Sebag, Sandra Plancade, Céline Raulet-Tomkiewicz, Robert Barouki, Jean-Philippe Vert, Thomas Walter (2015 Jun 15)

A generic methodological framework for studying single cell motility in high-throughput time-lapse data.

Bioinformatics (Oxford, England) : i320-8 : [DOI : 10.1093/bioinformatics/btv225](https://doi.org/10.1093/bioinformatics/btv225)

Résumé

Motility is a fundamental cellular attribute, which plays a major part in processes ranging from embryonic development to metastasis. Traditionally, single cell motility is often studied by live cell imaging. Yet, such studies were so far limited to low throughput. To systematically study cell motility at a large scale, we need robust methods to quantify cell trajectories in live cell imaging data.

Nelle Varoquaux, Ivan Liachko, Ferhat Ay, Joshua N Burton, Jay Shendure, Maitreya J Dunham, Jean-Philippe Vert, William S Noble (2015 May 6)

Accurate identification of centromere locations in yeast genomes using Hi-C.

Nucleic acids research : 5331-9 : [DOI : 10.1093/nar/gkv424](https://doi.org/10.1093/nar/gkv424)

Résumé

Centromeres are essential for proper chromosome segregation. Despite extensive research, centromere locations in yeast genomes remain difficult to infer, and in most species they are still unknown. Recently, the chromatin conformation capture assay, Hi-C, has been re-purposed for diverse applications, including de novo genome assembly, deconvolution of metagenomic samples and inference of centromere locations. We describe a method, Centurion, that jointly infers the locations of all centromeres in a single genome from Hi-C data by exploiting the centromeres' tendency to cluster in three-dimensional space. We first demonstrate the accuracy of Centurion in identifying known centromere locations from high coverage Hi-C data of budding yeast and a human malaria parasite. We then use Centurion

Apprentissage statistique et modélisation des systèmes biologiques

to infer centromere locations in 14 yeast species. Across all microbes that we consider, Centurion predicts 89% of centromeres within 5 kb of their known locations. We also demonstrate the robustness of the approach in datasets with low sequencing depth. Finally, we predict centromere coordinates for six yeast species that currently lack centromere annotations. These results show that Centurion can be used for centromere identification for diverse species of yeast and possibly other microorganisms.

Ferhat Ay, Thanh H Vu, Michael J Zeitz, Nelle Varoquaux, Jan E Carette, Jean-Philippe Vert, Andrew R Hoffman, William S Noble (2015 Apr 19)

Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C.

BMC genomics : 121 : [DOI : 10.1186/s12864-015-1236-7](https://doi.org/10.1186/s12864-015-1236-7)

Résumé

Several recently developed experimental methods, each an extension of the chromatin conformation capture (3C) assay, have enabled the genome-wide profiling of chromatin contacts between pairs of genomic loci in 3D. Especially in complex eukaryotes, data generated by these methods, coupled with other genome-wide datasets, demonstrated that non-random chromatin folding correlates strongly with cellular processes such as gene expression and DNA replication.

Jiao Y., Vert J.P. (2015 Jan 1)

The Kendall and Mallows Kernels for Permutations

Proceedings of The 32nd International Conference on Machine Learning : 1935-1944

Résumé

Machairas V., Faessel M., Cárdenas-Peña D., Chabardes T., Walter T., Decencière E. (2015 Jan 1)

Waterpixels

IEEE Transactions on Image Processing : 24 : 3707-3716

Résumé

Scornet E., Biau G., Vert J.P., thers (2015 Jan 1)

Consistency of random forests

The Annals of Statistics : 43 : 1716-1741

Résumé

Grimm D.G., Azencott C.A., Aicheler F., Gieraths U., MacArthur D.G., Samocha K.E., Cooper D.N., Stenson P.D., Daly M.J., Smoller J.W., thers (2015 Jan 1)

The evaluation of tools used to predict the impact of missense variants is hindered by two types of circularity

Human mutation : 36 : 513-523

Résumé

Shervashidze N., Bach F. (2015 Jan 1)

Learning the structure for structured sparsity

IEEE Transactions on Signal Processing : 63 : 4894-4902

Résumé

Moarii M., Reyal F., Vert J.P. (2015 Jan 1)

Integrative DNA methylation and gene expression analysis to assess the universality of the CpG island methylator phenotype

Human genomics : 9 : 1

Résumé

Servant N., Varoquaux N., Lajoie B.R., Viara E., Chen C.J., Vert J.P., Heard E., Dekker J., Barillot E. (2015 Jan 1)

HiC-Pro: an optimized and flexible pipeline for Hi-C data processing

Genome biology : 16 : 1

Résumé

Ay F., Bunnik E.M., Varoquaux N., Vert J.P., Noble W.S., Le Roch K.G. (2015 Jan 1)

Multiple dimensions of epigenetic gene regulation in the malaria parasite *Plasmodium falciparum*

BioEssays : 37 : 182-194

Résumé

Veta M., Van Diest P.J., Willems S.M., Wang H., Madabhushi A., Cruz-Roa A., Gonzalez F., Larsen A.B., Vestergaard J.S., Dahl A.B., thers (2015 Jan 1)

Assessment of algorithms for mitosis detection in breast cancer histopathology

images

Medical image analysis : 20 : 237-248

Résumé

Eduati F., Mangravite L.M., Wang T., Tang H., Bare J.C., Huang R., Norman T., Kellen M., Menden M.P., Yang J., thers (2015 Jan 1)

Prediction of human population responses to toxic compounds by a collaborative competition

Nature biotechnology

Résumé

Machairas V., Decencièrè E., Walter T. (2015 Jan 1)

Spatial Repulsion Between Markers Improves Watershed Performance

International Symposium on Mathematical Morphology and Its Applications to Signal and Image Processing : 194-202

Résumé