Liste complète des publications

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Publications[1]

Articles dans des revues avec comité de lecture

Articles en cours de relecture

- M. Giacofci, S. Lambert-Lacroix, F. Picard Minimax wavelet estimation for multisample heteroscedastic non-parametric regression, *soumis à Scandinavian Journal of Statistics*, 2015, `arxiv 1511.04556`
- G. Durif, F. Picard, S. Lambert-Lacroix, Adaptive Sparse PLS for Logistic Regression with Application to High Dimensional Classification, *soumis à Computational Statistics and Data Analysis*, 2015, `arxiv 1502.05933`
- H.L. Lopez-Maestre, L. Brinza, C. Marchet, S. Bastien, M. Boutigny, D. Monnin, A. El Filali, C.M. Carareto, C. Viera, F. Picard, N. Kremer, F. Vavre, M.-F. Sagot, V. Lacroix, De novo identification, differential analysis and functional annotation of SNPs from RNASeq data in non-model species, *soumis à Nucleic Acid Research*, 2015, `biorxiv 035238`
- A. Muyle, J. Kafer, N. Zemp, S. Mousset, F. Picard, G. Marais, A probabilistic method for identifying sex-linked genes using RNA-Seq derived genotyping data, *soumis à Bioinformatics*, 2015 `biorxiv 023358`

Publications en statistique (13)

- S. Ivanoff, F. Picard, V. Rivoirard Adaptive Lasso and group-Lasso for functional Poisson regression, *Journal of Machine Learning Research*, *accepté*, 2015
- E. Bonafede, F. Picard, S. Robin, C. Viroli Modeling overdispersion heterogeneity in differential analysis using mixtures, *Biometrics*, *accepté*, 2015
- Viallon V., Lambert-Lacroix S., Hoefling H. and Picard F. On the robustness of the generalized fused lasso to prior specification, *Statistics and Computing* **2014** vol. pp.1-17
- Miele V., Picard F., Dray S. Spatially constrained clustering of ecological networks, *Methods in Ecology and Evolution* **2014** vol. pp.1-9
- Giacofci M., Lambert-Lacroix S., Marot G., Picard F. Wavelet-based clustering for mixed-effects functional models in high dimension. *Biometrics*, **2013**, vol. 69, pp. 31-40.
- Picard F., Schbath S., Lebarbier E., Neuvial P., Chiquet J., Statistiques et Génome, *La gazette des Mathématiciens* 130, 1-32, **2011**.
- Picard F., Lebarbier, M. Hoebeke, Rigaill, G., Thiam, B. and Robin, S., Joint segmentation, calling and normalization of multiple CGH profiles. *Biostatistics* 12(3):413-28, **2011**
- Picard, F. Lebarbier, E., Budinska, E. and Robin, S., Joint segmentation of multivariate Gaussian processes using mixed linear models. *S. Comp. Stat. & Data Analysis* 55,1160-1170, **2011**
- Zanghi H., Picard F., Miele V., Ambroise C., Strategies for online inference of model-based clustering in large and growing networks. *Ann. Applied Stat.* **2010** 4(2)687-714,
- Picard F., Daudin J-J., Koskas M., Schbath S., Robin, S., Assessing the exceptionality of network motifs. *Journal of Computational Biology* **2008**, 15:1-20 .

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[1] Les étudiants et post-docs que j'ai encadrés apparaissent en orange

- Daudin J.-J., Picard F., Robin S., A mixture model for random graphs. *Statistics and computing* **2008**, 18:173-183.
- Picard F., Robin S., Lebarbier E., Daudin J-J., A segmentation/clustering model for the analysis of array CGH data, *Biometrics* **2007** 63:758-766..
- Picard F., Robin S., Lavielle M., Vaisse C., Daudin J-J., A statistical approach for array CGH data analysis, *BMC BioInformatics* **2005** Feb 11;6(1):27.

Publication en bioinformatique (6)

- G. Rigaill, V. Miele, and F. Picard. Fast and parallel algorithm for population-based segmentation of copy-number profiles, *Computational Intelligence Methods for Bioinformatics and Biostatistics*, Springer **2014** vol 79 pp. 248-258
- Modolo L., Picard F., Lerat E. A new genome-wide method to track horizontally transferred sequences: application to Drosophila, *Genome Biology and Evolution* **2014** vol. 6 pp.416-32
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- Picard F., Cadoret J.-C., Audit B., Arneodo A., Alberti A., Battail C., Duret L., Prioleau M.-N.,The spatiotemporal program of DNA replication is associated with specific combinations of chromatin marks in human cells, *PLoS Genetics* **2014** vol. 10
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Communications

Conférences Invitées (14)

- Adaptive Lasso and group-Lasso for functional Poisson regression, *8th International Conference of the ERCIM WG on Computational and Methodological Statistics*, Londres, Décembre 2015
- Introduction to the statistical analysis of omics data in high dimension, *LyonSysBio*, Lyon, Novembre 2015
- A.-L.Valton, F. Picard, P. Alberti, C. Saintomé, J.-F. Riou, and M.-N. Prioleau, G4 motifs are necessary but not sufficient for replication initiation in vertebrates, *Eukaryotic DNA replication & Genome maintenance*, Cold Spring Harbor, Septembre 2015

- Adaptive Generalized Fused-Lasso: Asymptotic Properties and Applications, *59th World Statistics Congres*, Hong-Kong, Aout **2013**.
- Fast and parallel Algorithm for Population-Based Segmentation of Copy-Number Profiles, *CIBB 2013, Tenth International Meeting on Computational Intelligence, Methods for Bioinformatics and Biostatistics*, Nice, France, Juin **2013**.
- Curve Clustering and Functional Mixed Models. Modeling, variable selection and application to Genomics, *7èmes Journées de Statistique Fonctionnelle et Opérationnelle*, Montpellier, France, Juin **2012**
- Wavelet-based clustering for mixed-effects functional models, (oratrice: M. Giacofci), *1st Conference of the International Society for NonParametric Statistics*, Chalkidiki, Grèce, Juin **2012**
- Using scan statistics for peak detection in NGS data, *3rd Bioinformatics Workshop Canceropôles CLARA-PACA*, Lyon, September **2011**
- Modèles de détection de ruptures et applications avec le logiciel R, *Journée Palettes R INED-SFdS-MNHN*, Paris, April **2011**
- Statistical assessment of chromosomal aberrations at the cohort level. *International Biometric Conference*, Florianopolis, Brazil, December **2010**
- Online Inference of Network Mixtures, *Statistical Methods for the Analysis of Network Data in Practice*, Dublin, Ireland, June **2009**
- Revisiting human replication origin data. *Statistical advances in Genome-scale Data Analysis - Workshop*, Ascona, Suisse, Mai **2009**
- La statistique en génomique, une question de place, *Journées Génotoul, Génopole Toulouse Midi-Pyrénées.* Toulouse, France, Décembre **2008**.
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- Rigaill, R. Miele, V., Picard, F., Fast and parallel Algorithm for Population-Based Segmentation of Copy-Number Profiles, *CIBB 2013, Tenth International Meeting on Computational Intelligence, Methods for Bioinformatics and Biostatistics*, Nice, France, Juin **2013**.
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- Picard F. Uncovering structure in biological networks, *Journées Ouvertes de Mathématique Informatique et Biology*, Bordeaux, France, Jul. **2006**.
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Posters (4)

- L. Modolo, E. Lerat, F. Picard, Zero-Inflated Gaussian Hidden Markov Models for Multiple Testing under Genomic Dependencies, *Statistical Methods for Post Genomic Data analysis*, Amsterdam, Pays-Bas, **2013**.
- A. Muyle, F. Picard, G. Marais, SEX-DETector : A model-based method for detecting sex chromosomes and studying sex determination in non-model organisms using NGS data. *Roscoff conference Jacques Monod : Recent advances on the evolution of sex and genetics systems*, Roscoff, France, **2013**.
-Picard F. Joint Segmentation of multiple aCGH profiles, *Statistics for Biomolecular Data Integration and Modeling - Workshop*, Ascona, Switzerland, **2007**.
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