Elsa Bernard

Curriculum Vitae

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Born September 14th, 1988
One child

Education

2012-2016 **PhD in Bioinformatics**, *PSL Research University*, Paris, France.
- Description: Deciphering splicing with sparse regression techniques in the era of high-throughput RNA sequencing.
- Supervisor: Jean-Philippe Vert.

2012 **Master of Science in Probability and Statistics**, *University Paris 7*, Paris, France.
- Obtained with the highest honors.

2008-2012 **Bachelor of Science in Geosciences**, *Ecole Normale Supérieure*, Paris, France.

2006-2008 **University-preparatory school**, *Lycée Lakanal*, Sceaux, France.
- Intensive scientific preparation for entrance exams for top French universities.

Work Experiences

2016-present **Postdoctoral researcher**, *Papaemmanuil lab*, MSKCC, New York, USA.
- Prognosis and disease evolution in myelodysplastic syndromes.
- Mentor: Elli Papaemmanuil.

2012-2016 **PhD student in Bioinformatics**, *CBIO*, Mines ParisTech, Paris, France.

2011 **Research assistant in Statistics**, *LSCE*, CEA, Saclay, France (9 months).

2009 **Research assistant in Geosciences**, *CAOS*, NYU, New York, USA (6 months).

Awards

2017 Recipient of the **Francois Wallace Monahan Fellowship**.

2016 **Excellent Shotgun Communication Award** at the 1st International Caparica Conference in Splicing (Portugal).

2013 **Second place at the DREAM 8 NHIES-NCATS-UNC Toxicogenetics challenge** (international bioinformatic competition on predicting in vitro cytotoxicity based on genomic profiles of cell lines exposed to chemical compounds), with E. Scornet, Y. Jiao, V. Stoven, T. Walter and J.-P. Vert.

Other Research Activities

Reviewer for journals Nucleic Acide Research, Bioinformatics, BMC Bioinformatics, Annals of Applied Statistics, GENE.

Teaching Practical session of "Kernel methods in computational biology" at Mines ParisTech, 2013-2014 (6 hours). Tutorial on "Differential expression analysis with RNA-seq data" at Institut Curie, 2015 (3 hours).

Supervision	Master's degree internship of Ingrid Vallée from Paris Descartes University. Subject: study of BRCA1 splice variants with targeted RNA-sequencing.
Software	Bioconductor R package FlipFlop for estimation of isoforms from RNA-seq data. `http://cbio.ensmp.fr/flipflop`
Scientific visit	Huber lab at EMBL Heidelberg, working on predicting in vitro drug responses on CLL patients, May 2015.

Skills

Programming	R, MATLAB, BASH, knowledge in HTML, C/C++ and PYTHON
Software	LaTeX, SVN, Inkscape
Languages	French mother tongue, fluent in English.

International Conference Communications

09/2016	A time- and cost-effective clinical diagnosis tool to quantify abnormal splicing from targeted single-gene RNA-seq. *Splicing 2016 conference.*
12/2014	A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. *NIPS 14 workshop on computational biology.*
09/2014	Fast isoform detection from RNA-Seq data with network flow techniques. *ECCB 14 RADIANT workshop.*
11/2013	Kernel bilinear regression for toxicogenetics. *RECOMB 13 conference on regulatory and systems genomics, with DREAM challenges.*
07/2013	FlipFlop: Fast Lasso based Isoform Prediction as a FLOw Problem. *ECCB 13 HitSeq workshop.*
12/2012	Efficient sparse method for RNA isoforms identification and quantification from RNA-seq data with network flows. *NIPS 12 workshop on computational biology.*

Publications

○ J.-L. Plouhinec, S. Medina-Ruiz, C. Borday, **E. Bernard**, J.-P. Vert, M. Eisen, R. Harland and A.-H. Monsoro-Burq. A molecular atlas of the developing ectoderm defines neural, neural crest, placode and non-neural progenitor identity in vertebrates. *PLOS Biology*, 2017 (in press).

○ **E. Bernard**, Y. Jiao, E. Scornet, V. Stoven, T. Walter and J.-P. Vert. Kernel multitask regression for toxicogenetics. *Moleculars Informatics*, 2017 (in press).

○ **E. Bernard**, L. Jacob, J. Mairal, E. Viara and J.-P. Vert. A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. *BMC Bioinformatics*, i16:262, 2015.

○ **E. Bernard**, L. Jacob, J. Mairal and J.-P. Vert. Efficient RNA isoform identification and quantification from RNA-seq data with network flows. *Bioinformatics*, 30(17):2447-2455, 2014.

○ **E. Bernard**, P. Naveau, M. Vrac and O. Mestre. Clustering of maxima: spatial dependencies among heavy rainfall in france. *Journal of Climate*, 26, 7929-7937, 2013.

- K.S. Smith and **E. Bernard**. Geostrophic turbulence near rapid changes in stratification. *Physics of Fluids*, 25, 046601, 2013.