

Elsa Bernard

Curriculum Vitae

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📄 <https://elsab.github.io/>
Born September 14th, 1988
One child

Education

- 2012-2016 **PhD in Bioinformatics**, *PSL Research University*, Paris, France.
 - 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.

Work Experiences

- 2016-present **Postdoctoral researcher**, *Papaemmanuil lab*, MSKCC, New York, USA.
 - Classification, 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 bioinformatics contest on predicting 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.

Student Supervision

- 2019 Philippe Pinel. Engineering student at *Mines ParisTech*.
Molecular classification of MDS patients.
- 2018 Pierre Guilmin. Engineering student at *Mines ParisTech*.
Supervised learning for somatic variant classification.
- 2017 Yoann Pradat. Engineering student at *Mines ParisTech*.
Integration of clinical and molecular data for prognosis models in AML.
- 2014 Ingrid Vallée. Master student at *Paris Descartes University*.
Study of BRCA1 splice variants with targeted RNA-sequencing.

Other Research Activities

- Reviewer for journals Nucleic Acids Research, Bioinformatics, BMC Bioinformatics, Annals of Applied Statistics, Frontiers in Genetics.
- Software Bioconductor R package FlipFlop for estimation of isoforms from RNA-seq data.
<http://cbio.enscm.fr/flipflop>
- Scientific visit Huber lab, EMBL Heidelberg, May 2015. Predicting in vitro drug responses on CLL cell lines.

Skills

- Programming R, PYTHON, BASH.
- Reproducibility notebooks (JUPYTER, R MARKDOWN), version-control (SVN, GIT).
- Languages French mother tongue, fluent in English.

Selected Communications

- 12/2018 Update of Mutational Impact on Diagnostic and Prognostic Evaluation of MDS. *ASH MDS Foundation Symposium*.
- 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*, 15(10):e2004045, 2017.
- **E. Bernard**, Y. Jiao, E. Scornet, V. Stoven, T. Walter and J.-P. Vert. Kernel multitask regression for toxicogenetics. *Molecular Informatics*, 36(10), 2017.
- **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.