

Elsa Bernard

Education

- 2012-2016** **PhD in Bioinformatics**, *Mines ParisTech/Institut Curie*, Paris, France.
Supervisor: Dr. Jean-Philippe Vert.
Dissertation: Deciphering splicing with sparse regression techniques from high-throughput RNA sequencing.
- 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**, *École Normale Supérieure*, Paris, France.

Work Experience

- 2021–** **Research Associate**, *Computational Oncology*, MSKCC, New York, USA.
- 2016-2021** **Research Fellow**, *Computational Oncology*, MSKCC, New York, USA.
Laboratory of Dr. Elli Papaemmanuil.
Classification, prognosis and clonal evolution of myelodysplastic syndromes.
- 2012-2016** **PhD Student in Bioinformatics**, *CBIO*, Mines ParisTech/Institut Curie, Paris, France.
- 2011** **Research Assistant in Statistics**, *LSCE*, CEA, Saclay, France.
- 2009** **Research Assistant in Geosciences**, *CAOS*, NYU, New York, USA.

Awards & Honors

- 2021 **Forbeck Scholar Awardee**.
- 2021 **MSK Society Scholar Prize**.
- 2020 **Top 10 MSK Cancer Science Breakthroughs of 2020**.
- 2019 **ASH Abstract Achievement Award**.
- 2016 **Excellent Shotgun Communication Award** at the 1st International Conference in Splicing.

Fellowships & Grants

- 2020 **EvansMDS Young Investigator Award**.
- 2017 Recipient of the **Francois Wallace Monahan Fellowship**.
- 2012 **PhD Scholarship**, *Ecole Normale Supérieure*.

Student Supervision

- 2020 [Emile Cohen](#). Master student at *École des Ponts ParisTech*.
Pan-cancer evaluation of *TP53* alterations.
- 2020 [Lily Monnier](#). Master student at *CentraleSupélec*.
Development of prognosis models for MDS.
- 2019 [Araxe Sarian](#). Master student at *Mines ParisTech*.
Allelic state of *TP53* mutations in MDS and AML.
- 2019 [Philippe Pinel](#). Master student at *Mines ParisTech*.
Molecular classification of MDS patients.

- 2018 [Pierre Guilmin](#). Master student at *Mines ParisTech*.
Supervised learning for somatic variant classification.
- 2017 [Yoann Pradat](#). Master student at *Mines ParisTech*.
Integration of clinical and molecular data for AML prognosis modelling.
- 2014 [Ingrid Vallée](#). Master student at *Paris Descartes University*.
Study of BRCA1 splice variants with targeted RNA-sequencing.

Other Research Activities

- Peer Review Blood, Leukemia Research, Nucleic Acids Research, Bioinformatics, BMC Bioinformatics, Annals of Applied Statistics, Frontiers in Genetics.
- Challenge 2013 NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge (2nd place). 2020 CTD-squared BeatAML DREAM Challenge (4th place).
- Conference Program Committee, International Society for Computational Biology ISMB/ECCB, 2017-2019.
- Visit Huber Group, EMBL Heidelberg, May 2015. Predicting in vitro drug responses on CLL cell lines.

Selected Communications

- 12/2021 While the WHO classification of MDS has helped MDS patients, we should now move to a genetically-inspired classification. *2021 ASH MDS Symposium*. [Invited talk](#).
- 12/2021 Molecular International Prognosis Scoring System for Myelodysplastic Syndromes. *2021 ASH Annual Meeting*. [Selected talk](#).
- 06/2021 TP53 in myeloid disease: implication of allelic state for genome stability and disease evolution. *2021 EHA Annual Meeting*. [Invited talk](#).
- 12/2020 Population genomics and personalized prognosis in myelodysplastic syndromes. *European Bio-conductor Meeting 2020*. [Invited keynote](#).
- 12/2019 Implication of *TP53* allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes. *2019 ASH Annual Meeting*. [Selected talk](#).
- 12/2018 Mutational impact on diagnostic and prognostic evaluation of myelodysplastic syndromes. *2018 ASH MDS Symposium*. [Invited talk](#).
- 09/2016 A time- and cost-effective clinical diagnosis tool to quantify abnormal splicing from targeted single-gene RNA-seq. *Splicing 2016 conference*. [Selected talk](#).
- 12/2014 A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. *NIPS 14 workshop on computational biology*. [Selected talk](#).
- 11/2013 Kernel bilinear regression for toxicogenetics. *RECOMB/ISCB 13 conference with DREAM challenges*. [Invited talk](#).
- 12/2012 Efficient sparse method for RNA isoforms identification and quantification from RNA-seq data with network flows. *NIPS 12 workshop on computational biology*. [Selected talk](#).

Publications

- EM Beauchamp, M Leventhal, **E Bernard** et al. *ZBTB33* is mutated in clonal hematopoiesis and myelodysplastic syndromes and impacts RNA Splicing. *Blood Cancer Discov*, 2(5), 500–517, 2021.
- T Gao, R Ptashkin, KL Bolton, ..., **E Bernard**, ..., SM Devlin, E Papaemmanuil. Interplay between chromosomal alterations and gene mutations shapes the evolutionary trajectory of clonal hematopoiesis. *Nat Commun*, 12, 338, 2021.
- KL Bolton, RN Ptashkin, T Gao, ..., **E Bernard**, ..., A Zehir, E Papaemmanuil. Cancer therapy shapes the fitness landscape of clonal hematopoiesis. *Nat Genet*, 52, 1219–1226, 2020.

- **E Bernard**, Y Nannya, RP Hasserjian et al. Implications of *TP53* allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes. *Nat Med*, 26, 1549–1556, 2020.
- EH Rustad, K Misund, **E Bernard** et al. Stability and uniqueness of clonal immunoglobulin CDR3 sequences for MRD tracking in multiple myeloma. *Am J Hematol*, 94:1364-1373, 2019.
- E Lamprianidou, E Zoulia, **E Bernard** et al. Multifaceted modes of action of azacytidine: a riddle wrapped up in an enigma. *Leuk. Lymphoma*, 60:13, 3277-3281, 2019.
- A Kazachenka, GR Young, . . . , **E Bernard**, E Papaemmanuil, I Kotsianidis, G Kassiotis. Epigenetic therapy of myelodysplastic syndromes connects to cellular differentiation independently of endogenous retroelement derepression. *Genome Med*, 11, 86, 2019.
- J-L Plouhinec, S Medina-Ruiz, C Borday, **E Bernard** et al. A molecular atlas of the developing ectoderm defines neural, neural crest, placode and nonneural progenitor identity in vertebrates. *PLOS Biol*, 15(10):e2004045, 2017.
- **E Bernard**, Y Jiao, E Scornet, V Stoven, T Walter, J-P Vert. Kernel multitask regression for toxicogenetics. *Mol Inform*, 36, 1700053, 2017.
- F Eduati, LM Mangravite, . . . , **E Bernard**, . . . , Y Xie, J Saez-Rodriguez. Prediction of human population responses to toxic compounds by a collaborative competition. *Nat Biotechnol*, 33, 933-940, 2015.
- **E Bernard**, L Jacob, J Mairal, E Viara, J-P Vert. A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. *BMC Bioinformatics*, 16, 262, 2015.
- **E Bernard**, L Jacob, J Mairal, 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, O Mestre. Clustering of maxima: spatial dependencies among heavy rainfall in france. *Journal of Climate*, 26(20), 7929-7937, 2013.
- KS Smith and **E Bernard**. Geostrophic turbulence near rapid changes in stratification. *Physics of Fluids*, 25, 046601, 2013.