Computational Oncology
Memorial Sloan Kettering Cancer Center
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https://elsab.github.io/
Born September 14th, 1988
Two children

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 **ASH Abstract Achievement Award**.

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 Synposium*. Invited talk.

12/2021 Molecular International Prognosis Scoring System for Myelodysplastic Syndromes. *2021 ASH Annual Meeting*. Selected talk.

11/2021 A clinical-molecular and personalized risk scoring system for patients with myelodysplastic syndromes. *EMBL Cancer Genomics Conference*. 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 Bioconductor 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.