

Judith Abécassis

PhD Candidate

Machine learning applied to cancer genomics

39 rue de l'Eglise
75015 Paris – France

☎ 06 73 49 70 47

✉ judithabk6@gmail.com

25 Juillet 1991

Current education (2016 -)

PhD student in Bioinformatics *Mines Paristech/ Institut Curie*

supervised by Jean-Philippe Vert and Fabien Reyat

"Statistical methods for deciphering intra-tumor heterogeneity: challenges and opportunities for cancer clinical management."

Past education

2014 – 2015 **Master Degree in Machine Learning and Computer Vision**, *École Normale Supérieure de Cachan*, with honors.

2014 – 2014 **Complementary computer science courses**, *École Normale Supérieure de Paris et Université Pierre et Marie Curie (Paris VI)*.

2012 – 2013 **1st year Master Degree in Biology**, *École Normale Supérieure de Paris et Université Pierre et Marie Curie (Paris VI)*.
Spécialité Biologie cellulaire et moléculaire (génétique, génomique, évolution et bioinformatique).

2011 – 2012 **Bachelor Degree in Biology**, *École Normale Supérieure de Paris et Université Pierre et Marie Curie (Paris VI)*.

2009 – 2011 **Classe Préparatoire BCPST**, *Lycée Henri IV (Paris)*.
Biology, Chemistry, Physics et Geoscience.
Succeeded in all competitive exams (AgroParisTech et ENS).

Professional experience

April – June 2016 **Participation to the international program "Algorithmic Challenges in Genomics"**, *Simons Institute of University of Berkeley, California, USA*.

2015-2016 **Master 2 and final year at ENS internship**, *Mines ParisTech and Institut Curie*, supervised by Jean-Philippe Vert and Fabien Reyat.
Subclonal reconstruction to better assess tumoral heterogeneity, and its implication in breast cancer prognosis and treatment.

August 2013 – June 2014 **Intern Data scientist – tinyclues**, supervised by David Bessis and Artem Kozhevnikov.
Main assignments:

- exploratory analyses on new data types,
- development of applications to meet non-standard client needs,
- optimization of machine learning algorithms' performance in existing applications,
- setting up of quality control procedures on client-facing applications,
- setting up of a pipeline to automate parametrization steps in new client setup.

2013 **Six-month internship (Master 1)**, *Max Planck Institute for molecular Genetics*, Evolutionary Genomics group, supervised by Peter Arndt.
Analysis of clonally related antibody sequences.

2012 **Two-month internship (Bachelor)**, *Institut de Biologie de l'ENS (IBENS, Paris)*, DYOGEN Team supervised by Hugues Roest Crollius.
Study of the influence of some genomic parameters on the occurrence of evolutive breakpoints.

Teaching experience

2018 – **Scientific consultant on the Data Science path**, *OpenClassrooms*.
Development and improvement of projects, selection of relevant skills.

- 2017 – **Mentor for data scientist students**, *OpenClassrooms*.
 Professionnal training on real-life data science projects in Python.
- 2016 – 2019 **Teaching assistant**, *Mines Paristech*.
 Developement of materials, and tutorials for the courses "Introduction to machine learning",
 "Large scale machine learning", and "Introduction to Genomics and Bioinformatics"
- Sept 2015– **Teaching assistant in computer science – BCPST 2nd year**, *Lycée Henri IV*
 March 2016 (*Paris*).
 Programming project course in Python
- Sept 2014 – **Teaching assistant in computer science – BCPST 1st year**, *Lycée Henri IV*
 March 2016 (*Paris*).
 Introduction to programming in Python
- 2012 **Teaching assistant in computer science – BCPST 2nd year**, *Lycée Henri IV*
 (*Paris*).
 Programming project course in Matlab

Languages

Anglais **fluent**
 Allemand **intermediate**

Computer science skills

Languages Python, Matlab, R, bash – knowledge C, PHP, HTML
 Scientific Numpy, scipy, scikit-learn, seaborn
 programming
 in Python
 Databases MySQL
 OS Windows, Linux, Mac OS

First-author Publications

Assessing reliability of intra-tumor heterogeneity estimates from single sample whole exome sequencing data

Judith Abécassis, Anne-Sophie Hamy, Cécile Laurent, Benjamin Sadacca, Hélène Bonsang-Kitzis, Fabien Reyat, Jean-Philippe Vert, 2019, Plos One, <https://doi.org/10.1371/journal.pone.0224143>

Clonesig: Joint Inference of intra-tumor heterogeneity and signature deconvolution in tumor bulk sequencing data

Judith Abécassis, Fabien Reyat, Jean-Philippe Vert, 2019, BiorXiv, <https://doi.org/10.1101/825778>

Other Publications

The 3D organization of chromatin explains evolutionary fragile genomic regions

Camille Berthelot, Matthieu Muffato, Judith Abécassis, Hugues Roest Crollius, 2015, Cell reports, <https://doi.org/10.1016/j.celrep.2015.02.046>

A Stromal Immune Module Correlated with the Response to Neoadjuvant Chemotherapy, Prognosis and Lymphocyte Infiltration in HER2-Positive Breast Carcinoma Is Inversely Correlated with Hormonal Pathways

Anne-Sophie Hamy, Hélène Bonsang-Kitzis, Marick Lae, Matahi Moarii, Benjamin Sadacca, Alice Pinheiro, Marion Galliot, Judith Abécassis, Cecile Laurent, Fabien Reyat, 2016, PloS one, <https://doi.org/10.1371/journal.pone.0167397>

New insight for pharmacogenomics studies from the transcriptional analysis of two large-scale cancer cell line panels

Benjamin Sadacca, Anne-Sophie Hamy, Cécile Laurent, Pierre Gestraud, Hélène Bonsang-Kitzis, Alice Pinheiro, Judith Abécassis, Pierre Neuvial, Fabien Reyat, 2017, Scientific reports, <https://doi.org/10.1038/s41598-017-14770-6>

Conferences

- 2019 **ISMB (Basel, Switzerlandd)**.
 Clonesig: Joint Inference of intra-tumor heterogeneity and signature deconvolution in tumor bulk sequencing data