

Judith Abécassis

Machine learning, health and biology

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Education

- 2016 - 2020 **PhD in Bioinformatics**, Mines Paristech and Institut Curie, *Statistical methods for deciphering intra-tumor heterogeneity: challenges and opportunities for cancer clinical management*, supervised by Jean-Philippe Vert and Fabien Reyal.
defended on March 9th 2020
- 2014 – 2015 **Master Degree in Machine Learning and Computer Vision**, École Normale Supérieure de Cachan, with honors.
- 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

- 2021 – **Postdoctoral researcher, Machine learning**, INRIA, Saclay.
Causal inference for mental health
- 2020 – 2021 **Research engineer**, Institut Curie.
Multi-Omics analyses on cancer samples
- 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 Reyal.
Subclonal reconstruction to better assess tumoral heterogeneity, and its implication in breast cancer prognosis and treatment.
- August 2013 – **Intern Data scientist – tinyclues**.
June 2014 supervised by David Bessis and Artem Kozhevnikov.
- 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

- 2017 – **Mentor for data scientist students**, OpenClassrooms.
Professionnal training on real-life data science projects in Python.
- 2018 – 2019 **Scientific consultant on the Data Science path**, OpenClassrooms.
Developement and improvement of projects, selection of relevant skills.
- 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 Programming project course in Python
- Sept 2014 – **Teaching assistant in computer science – BCPST 1st year, Lycée Henri IV.**
March 2016 Introduction to programming in Python
- 2012 **Teaching assistant in computer science – BCPST 2nd year, Lycée Henri IV.**
Programming project course in Matlab

Langues

- Anglais fluent
Allemand intermediate

Computer science skills

- Languages Python (Numpy, scipy, scikit-learn, seaborn), Matlab, R, bash, SQL – knowledge C, PHP, HTML

Main 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 Reyal, 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 Reyal, Jean-Philippe Vert, 2021, Nature Communications, <https://doi.org/10.1038/s41467-021-24992-y>

Evolution of synchronous bilateral breast cancers upon neoadjuvant chemotherapy provide insights into interactions between host, tumor and immunity

Anne-Sophie Hamy, Judith Abécassis, Lauren Darrigues, Cecile Laurent, Francois Zaccarini, Benjamin Sadacca, Myriam Delomenie, Enora Laas, Odette Mariani, Than Lam, Beatriz Grandal, Wilfrid Richer, Marick Lae, Ivan Bieche, Sophie Vacher, Jean-Yves Pierga, Celine Vallot, Judicael Hotton, Joshua Waterfall, Fabien Reyal, *in preparation*

Evaluation of mediation analysis methods in a variety of contexts

Judith Abécassis, Julie Josse, Bertrand Thirion, 2021, *cclear*, *under review*

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 Reyal, 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 Reyal, 2017, Scientific reports, <https://doi.org/10.1038/s41598-017-14770-6>

No impact of smoking status on breast cancer tumor infiltrating lymphocytes, response to neoadjuvant chemotherapy and prognosis

Vanille Simon, Lucie Laot, Enora Laas, Sonia Rozette, Julien Guerin, Thomas Balezeau, Marion Nicolas, Jean-Yves Pierga, Florence Coussy, Marick Laé, Diane De Croze, Beatriz Grandal, Judith Abecassis, Elise Dumas, Florence Lerebours, Fabien Reyal, Anne-Sophie Hamy, 2020, Cancers, <https://doi.org/10.3390/cancers12102943>

Conferences

- 2019 **ISMB (Basel, Switzerland).**

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