

Clémence Réda | Marie Skłodowska-Curie Postdoctoral Fellow @ Universität Rostock

(updated on 21/02/2024)

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Education

Université Paris Cité, Inserm UMR 1141 & CNRS UMR 9189

PhD in Genetics

09/2019 – 09/2022

Doctorate Degree in Science. Title: **Combination of gene regulatory networks and sequential machine learning for drug repurposing**, supervised by [Pr. Andrée Delahaye-Duriez](#) (Inserm UMR 1141) & [Dr. Émilie Kaufmann](#) (CNRS UMR 9189).

Viva: 09/09/2022.

École Normale Supérieure[†] (ENS) Paris-Saclay

(ex-École Normale Supérieure de Cachan)

M2 Master Vision, Apprentissage (MVA)

09/2018 – 09/2019

Master's degree in Machine Learning. (*summa cum laude*, Grade: 16.17/20, no ranking)

ENS Paris-Saclay

M1 Master Parisien en Recherche en Informatique (MPRI)

09/2016 – 09/2017

Master's degree in Computer Sciences. (*summa cum laude*, Grade: 16.72/20, rank: 3/25)

École Normale Supérieure de Cachan

L3 Licence informatique fondamentale ENS Cachan

09/2015 – 09/2016

Bachelor's degree in Computer Sciences. (*cum laude*, Grade: 14.64/20, rank: 10/26)

[†] *École Normale Supérieures are selective French schools for research and teaching.*

Professional Experience

Research Positions

Marie Skłodowska-Curie Postdoctoral Fellow | [Pr. Olaf Wolkenhauer](#)

Rostock, Germany

Universität Rostock (SBI Rostock)

05/2023–present

Development of the RECeSS project, focusing on the development of new, improved techniques for drug development based on collaborative filtering approaches.

Skills Collaborative Filtering · Python (Programming Language) · Applied Machine Learning

Marie Skłodowska-Curie Postdoctoral Fellow (secondment) | [Dr. Jill-Jênn Vie](#)

Saclay, France

Inria Saclay (SODA team)

07/2023–10/2023

Development of the RECeSS project, focusing on the development of new, improved techniques for drug development based on collaborative filtering approaches.

Skills Collaborative Filtering · Benchmarking · Applied Machine Learning

Postdoctoral position | [Pr. Andrée Delahaye-Duriez](#)

Paris, France

Neurodiderot (UMR 1141)

09/2022–03/2023

Development and implementation of the NORDic pipeline for Boolean networks, Prefiguration of the multiomics workflow for the [RHU FAME](#) project led by [Pr. Élie Azoulay](#).

Skills Systems Biology · Programming · Interdisciplinary Research · Bioinformatics

PhD position | [Pr. Andrée Delahaye-Duriez](#) & [Dr. Émilie Kaufmann](#)

Paris, France

Neurodiderot (UMR 1141) & SCOOOL (UMR 9189)

09/2019–09/2022 (36 months)

Combination of gene regulatory networks and sequential machine learning for drug repurposing.

Skills Systems Biology · Multi-Armed Bandits · Interdisciplinary Research · Bioinformatics

Master internship | [Pr. Andrée Delahaye-Duriez](#) & [Dr. Émilie Kaufmann](#)

Paris, France

Neurodiderot (UMR 1141) & SCOOOL (UMR 9189)

03/2019–08/2019 (4 months)

Design of a drug repurposing method through a bandit algorithm combined with the prediction of transcriptomic states by a gene regulatory network. Application to the prediction of new anti-epileptics.

Skills Interdisciplinary Collaboration · Interdisciplinary Research · Statistical Learning · Project Design · Bioinformatics

Predoctoral internship | [Dr. Bartek Wilczyński](#)**Warsaw, Poland****Regulomics team (MIM UW)**

10/2017–07/2018 (10 months)

Proof-of-concept on the explicit inclusion of biological interactions in gene regulatory networks and its impact on inference and simulation of transcriptomic regulation. Led to a publication in *Journal of Theoretical Biology* (DOI : [10.1016/j.jtbi.2019.110091](https://doi.org/10.1016/j.jtbi.2019.110091)).

Skills Network Analysis · Epigenetics · Python (Programming Language) · Systems Biology · Scientific Presentation

Master internship | [Dr. Nicholas Luscombe](#) & [Dr. Garth Ilseley](#)**Onna-son, Japan****Genomics and Regulatory Systems Unit (OIST)**

02/2017–07/2017 (5 months)

Design and implementation of a single-cell RNA sequencing clustering method taking into account intergene expression dependencies using a probabilistic model ; implementation in R Shiny of a web application for the visualisation and preliminary analysis of single-cell RNA sequencing data. Application to transcriptomic data analysis in *Ciona intestinalis*.

Skills Benchmarking · R Shiny · Unsupervised Learning · Data Visualization · Python (Programming Language)

Bachelor internship | [Dr. Macha Nikolski](#) & [Dr. Mathieu Raffinot](#)**Bordeaux, France****Centre de Bioinformatique de Bordeaux (Université de Bordeaux)**

05/2016–07/2016 (2 months)

Design and implementation of compared analyses of taxonomic trees built from metagenomic data. Application to the analysis of data from intestinal guts of children afflicted with cystic fibrosis at Hôpital Pellegrin in Bordeaux.

Skills Metagenomics · Phylogenetics · Supervised Learning · Unsupervised Learning · Python (Programming Language)

Teaching & Mentoring Experiences**Biostatistics, programming and bioinformatics****Université Paris Cité***Doctorant Contractuel avec Mission d'Enseignement (DCME) (Teaching Assistant)*

09/2020–09/2021 (64 hours)

References: [Dr. Anne Badel](#) & [Pr. Olivier Taboureau](#)**Supervision of a Master-equiv. internship****SBI Rostock***Joint supervision of Rahul Bordoloi with [Pr. Olaf Wolkenhauer](#)*

09/2023–present

Development of a linear discriminant algorithm on multivariate temporal data.

Supervision of a Master internship**Inserm Neurodiderot***Joint supervision of Adrien Dufour with [Pr. Andrée Delahaye-Duriez](#)*

02/2020–07/2020 (6 months)

Identification of functional families of microglia cells from targeted single-cell RNA sequencing data of inflammatory microglia at a developmental stage.

Supervision of a Masters's degree project**ENS Paris-Saclay***Joint supervision of Ariane Alix with [Dr. Émilie Kaufmann](#)*

11/2019–01/2020 (2 months)

Proposal of a project on the adaptation of a published drug-target prediction method to drug repurposing using collaborative filtering in the course *Graphs in Machine Learning* taught by [Dr. Michał Valko](#) in Master Vision Apprentissage (MVA 2020).

Funding as Principal Recipient**Marie Skłodowska-Curie Postdoctoral Fellowship 2022****Horizon 2020***Postdoctoral grant*

2023–2025 (2 years)

[RECeSS project](#), Project ID: 101102016.

Research**Preprints****Multivariate Functional Linear Discriminant Analysis for the Classification of Short Time Series with Missing Data**R. Bordoloi, [C. Réda](#), O. Trautmann, S. Bej, O. Wolkenhauer

, *Under review*, DOI: [10.48550/arXiv.2402.13103](https://doi.org/10.48550/arXiv.2402.13103)

An Anytime Algorithm for Good Arm IdentificationM. Jourdan & [C. Réda](#)

, *Under review*, DOI: [10.48550/arXiv.2310.10359](https://doi.org/10.48550/arXiv.2310.10359)

Peer-Reviewed Scientific Journals**2024****stanscofi and benchcofi: a new standard for drug repurposing by collaborative filtering**[C. Réda](#), J.-J. Vie, O. Wolkenhauer

, *Journal of Open Source Software*, 9(93):5973, DOI: [10.21105/joss.05973](https://doi.org/10.21105/joss.05973)

2023**NORDic: a Network-Oriented package for the Repurposing of Drugs**[C. Réda](#) & A. Delahaye-Duriez

, *Journal of Open Source Software*, 8(90):5532, DOI: [10.21105/joss.05532](https://doi.org/10.21105/joss.05532)

2021

Machine learning applications in drug development

C. Réda, É. Kaufmann & A. Delahaye-Duriez

, *Computational and Structural Biotechnology Journal*, 18:241-252, DOI: [10.1016/j.csbj.2019.12.006](https://doi.org/10.1016/j.csbj.2019.12.006)

2020

Automated inference of gene regulatory networks using explicit regulatory modules

C. Réda & B. Wilczyński

, *Journal of Theoretical Biology*, 486:110091, DOI: [10.1016/j.jtbi.2019.110091](https://doi.org/10.1016/j.jtbi.2019.110091)

2019

Identification de cibles thérapeutiques et repositionnement de médicaments par analyses de réseaux géniques

A. Delahaye-Duriez, C. Réda & P. Gressens

, *Médecine/Sciences*, 35:515-518, DOI: [10.1051/medsci/2019108](https://doi.org/10.1051/medsci/2019108)

Peer-Reviewed Conference Proceedings.....

2022

Near-optimal Collaborative Learning in Bandits

C. Réda, S. Vakili, É. Kaufmann

, *Proceedings of the 36th Conference on Advances in Neural Information Processing Systems (NeurIPS 2022)*

HAL: [03825099](https://hal.archives-ouvertes.fr/hal-03825099) [[Selected as Oral](#)]

Prioritization of Candidate Genes Through Boolean Networks

C. Réda, A. Delahaye-Duriez

, *Proceedings of the 20th International Conference on Computational Methods in Systems Biology (CMSB 2022)*

Springer:89-121 [[Best Student Paper Award](#)]

2021

Dealing With Misspecification In Fixed-Confidence Linear Top-m Identification

C. Réda, A. Tirinzoni & R. Degenne

, *Proceedings of the 35th Conference on Neural Information Processing Systems (NeurIPS 2021)*, 34, HAL: [03409205](https://hal.archives-ouvertes.fr/hal-03409205)

Top-m identification for linear bandits

C. Réda, É. Kaufmann & A. Delahaye-Duriez

, *Proceedings of the 24th International Conference on Artificial Intelligence and Statistics (AISTATS 2021)*, 130

HAL: [03172145](https://hal.archives-ouvertes.fr/hal-03172145)

Oral Communications at International Conferences.....

C. Réda. Benchmarking collaborative filtering approaches to drug repurposing

e:Med Meeting 2023 on Systems Medicine (Berlin, Germany)

10/10/2023

C. Réda. Near-optimal Collaborative Learning in Bandits

35th International Conference on Advances in Neural Information Processing Systems (New Orleans, USA)

07/12/2022

C. Réda. Prioritization of Candidate Genes Through Boolean Networks

20th International Conference on Computational Methods in Systems Biology (Bucharest, Romania)

14/09/2022

C. Réda. Gene network oriented drug discovery: automated inference of Boolean networks (...)

13th Conference on Dynamical Systems Applied to Biology and Natural Sciences (held virtually)

10/02/2022

C. Réda. Dealing With Misspecification In Fixed-Confidence Linear Top-m Identification

NeurIPS@Paris 2021 (Paris, France)

08/12/2021

C. Réda. Automated inference of gene regulatory networks using explicit regulatory modules

Journées Ouvertes de Biologie, Informatique et Mathématique (JOBIM) 2020 (held virtually)

02/07/2020

C. Réda. Automated inference of gene regulatory networks using explicit regulatory modules

Workshop 6 of the 17th European Conference on Computational Biology (ECCB 2018, Athens, Greece)

08/09/2018

C. Réda. Automated inference of gene regulatory networks using explicit regulatory modules

Bioinformatics in Toruń (BIT 2018, Toruń, Poland)

28/06/2018

Poster Presentations at International Conferences.....

C. Réda. Towards a large-scale benchmark of collaborative filtering in drug repurposing

SMPGD 2024 (Paris, France)

02/2024

C. Réda. Drug repurposing in breast cancer by combining bandit algorithms and Boolean networks (...)

ISMB/ECCB 2023 (Lyon France)

07/2023

C. Réda. Prioritization of Candidate Genes Through Influence Maximization

Journées Ouvertes de Biologie, Informatique et Mathématique (JOBIM 2022, Rennes, France)

07/2022

C. Réda. Dealing With Misspecification In Fixed-Confidence Linear Top-m Identification

35th *International Conference on Advances in Neural Information Processing Systems (NeurIPS 2022, held virtually)* 12/2021

C. Réda. Top-m identification for linear bandits

24th *International Conference on Artificial Intelligence and Statistics (AISTATS 2021, held virtually)*

04/2021

Open-Source Softwares & Datasets

Softwares

2023

BENCHmark for drug Screening with COLlaborative FIltering (**benchscofi**)

C. Réda

, *Zenodo*, DOI: [10.5281/zenodo.8241505](https://doi.org/10.5281/zenodo.8241505), *GitHub*: [recess-eu-project/benchscofi](https://github.com/recess-eu-project/benchscofi)

Python package implementing algorithms and methods from the state-of-the-art in drug repurposing with collaborative filtering

STANdard for drug Screening by COLlaborative FIltering (**stanscofi**)

C. Réda

, *Zenodo*, DOI: [10.5281/zenodo.8038847](https://doi.org/10.5281/zenodo.8038847), *GitHub*: [recess-eu-project/stanscofi](https://github.com/recess-eu-project/stanscofi)

Python package for the automation of the training and validation of drug repurposing with machine learning

Network Oriented Repurposing of Drugs (NORDic)

C. Réda

, *Zenodo*, DOI: [10.5281/zenodo.7239047](https://doi.org/10.5281/zenodo.7239047), *GitHub*: [clreda/NORDic](https://github.com/clreda/NORDic)

Python package for the inference, analysis of Boolean networks & application to drug repurposing

Datasets

2023

PREDICT

C. Réda

, *Zenodo*, DOI: [10.5281/zenodo.7982964](https://doi.org/10.5281/zenodo.7982964)

Large drug repurposing dataset [with open-source generation](#)

TRANSCRIPT

C. Réda

, *Zenodo*, DOI: [10.5281/zenodo.7982969](https://doi.org/10.5281/zenodo.7982969)

Drug repurposing dataset on transcriptomic data [with open-source generation](#)

Commitment to Popularization of Sciences and Law Making

Popularization of Sciences

05/2023–present: Created and published on [RECeSS project blog](#): progress reports on the [RECeSS project](#) and introductory blog posts on drug repurposing and collaborative filtering.

12/2016–09/2018: Published on [Tryalgo](#) [in French] : series of blog posts on known algorithms with concrete applications, aimed at high school and college students (approx. 2,400 unique monthly users ; two of these posts constitute the Top-2 most visited pages).

10/2016: Published on [Binaire](#) (blog on Computer Science affiliated with French newspaper *Le Monde*) and [The Conversation](#) [in French] : “A.P.B. : La vie après le bac” (conjointly written with [Serge Abiteboul](#)). Explanation of the algorithm of Gale-Shapley which has been in use in a previous version of the French national web application for high school students’ applications to college

Popularization of Law-Making

12/2016–09/2018: Published on [Réfléchir.fr](#) [in French] : series of blog posts on laws passed since 2017 in France: explanation of their content and their consequences (534 followers on February, 24 2021).

Miscellaneous

2023–present: Selection as postdoc female mentoree by **Universität Rostock** to develop her professional career: access to seminars and personalized mentoring (see the [list of selected candidates](#)).