

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

(updated on 02/07/2024)

Systembiologie und Bioinformatik Rostock, Ulmenstraße 69, 18059 Rostock, Germany

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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<sup>†</sup> (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)

<sup>†</sup> *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 and Awards as Principal Recipient****Accessit from the Societe Savante Francophone d'Apprentissage Machine****SSFAM***PhD award (award list)*

2024

**Marie Skłodowska-Curie Postdoctoral Fellowship 2022****Horizon 2020***Postdoctoral grant*

2023–2025 (2 years)

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

**Research****Preprints****Joint Embedding-Classifer Learning for Interpretable Collaborative Filtering**

C. Réda, J.-J. Vie, O. Wolkenhauer

, Under review, HAL: [04625183](https://hal.archives-ouvertes.fr/hal-04625183)**Comprehensive evaluation of collaborative filtering in drug repurposing**

C. Réda, J.-J. Vie, O. Wolkenhauer

, Under review, HAL: [04626970](https://hal.archives-ouvertes.fr/hal-04626970)**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 Identification**

M. Jourdan &amp; 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 36<sup>th</sup> 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 20<sup>th</sup> 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 35<sup>th</sup> 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 24<sup>th</sup> 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

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

07/12/2022

### C. Réda. Prioritization of Candidate Genes Through Boolean Networks

20<sup>th</sup> 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 (...)

13<sup>th</sup> 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

## Poster Presentations at International Conferences

### C. Réda. JELLI: an interpretable embedding-learning recommender system for drug repurposing

JOBIM 2024 (Toulouse, France)

06/2024

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| <b>C. Réda. Towards a large-scale benchmark of collaborative filtering in drug repurposing</b><br><i>SMPGD 2024 (Paris, France)</i>  | 02/2024 |
| <b>C. Réda. Drug repurposing in breast cancer by combining bandit algorithms and Boolean networks (...)</b><br><i>ISMB/ECCB 2023 (Lyon France)</i>   | 07/2023 |
| <b>C. Réda. Prioritization of Candidate Genes Through Influence Maximization</b><br><i>Journées Ouvertes de Biologie, Informatique et Mathématique (JOBIM 2022, Rennes, France)</i>  | 07/2022 |
| <b>C. Réda. Dealing With Misspecification In Fixed-Confidence Linear Top-m Identification</b><br><i>35<sup>th</sup> International Conference on Advances in Neural Information Processing Systems (NeurIPS 2022, held virtually)</i> | 12/2021 |
| <b>C. Réda. Top-m identification for linear bandits</b><br><i>24<sup>th</sup> International Conference on Artificial Intelligence and Statistics (AISTATS 2021, held virtually)</i>  | 04/2021 |

## Open-Source Softwares & Datasets

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### Softwares

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#### 2024

##### Joint Embedding-classifier Learning for improved Interpretability (JELI)

C. Réda

, Zenodo, DOI: [10.5281/zenodo.12193722](https://doi.org/10.5281/zenodo.12193722), GitHub: [recess-eu-project/JELI](https://github.com/recess-eu-project/JELI)

Python package implementing an explicitly interpretable collaborative filtering

#### 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

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#### 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

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### Popularization of Sciences

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**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” (jointly 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

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**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).