

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

(08/05/2023)

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

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Biography & Major Achievements

The researcher's research journey led her to consider several aspects of drug development and repurposing, and got her acclimated to working in an interdisciplinary environment. In particular, her PhD was about the integration of a model of gene regulation into a drug repurposing pipeline, in order to properly assess the efficacy of a drug. In order to deal with the intrinsically stochastic regulatory mechanisms, she has designed a recommender system with multi-armed bandit algorithms which can deal with this stochasticity to estimate the most promising drug candidates in a sample-efficient way:

1. The researcher has worked on a method to automatically build disease-specific regulatory networks. This method allowed to retrieve in a transparent and reproducible way a cell-line-specific network from open-access databases. This method was applied to brain cell lines, on a subset of genes strongly coexpressed with epileptic phenotypes. She introduced for the first time a method which incorporates regulatory cascades and disease-specific transcriptomic information to detect master regulators, which can be targeted for better understanding the mechanisms behind the disease. This work led to a publication in the proceedings of the 20th *International Conference on Computational Methods in Systems Biology (CMSB 2022)*.
2. Multi-armed bandit algorithms were introduced by the researcher for the first time for drug repurposing, by tackling the problem of the identification of the N best arms/treatments in a set of K ones, using the known side information about these arms. In practice, this information is set of the drug signatures built upon transcriptomic data from the LINCS L1000 database. She introduced and studied a generic family of algorithms which solve this identification problem, that encompasses all prior adaptive sampling-based algorithms in the literature. Her co-authors and herself were able to study theoretically and empirically the effect of the model structure, especially linear models, on the performance of the algorithms. This work was published in the proceedings of the 24th *International Conference on Artificial Intelligence and Statistics (AISTATS 2021)*. This problem was tackled for non-linear models in a subsequent work published at the *Advances in Neural Information Processing System Conference (NeurIPS 2021)*, one of the most prestigious conferences in machine learning) with other co-authors.
3. She has contributed to the design of a framework integrating non-coding elements in gene regulatory networks. These non-coding elements were shown both theoretically and empirically to effectively structure and constraint the regulatory dynamics across the network, and increase the interpretability and understanding the regulatory mechanisms that lead to a specific transcriptomic phenotype. The corresponding work was published in the *Journal of Theoretical Biology* in 2020.

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

M2 Master Vision, Apprentissage (MVA)

(ex-École Normale Supérieure de Cachan)

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, in collaboration with [Dr. Jill-Jênn Vie from the Soda team at Inria Saclay, Paris, France](#).

Skills Collaborative Filtering · Python (Programming Language) · 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) & SCOOL (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) & SCOOL (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](#)).

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

Master internship | Dr. Nicholas Luscombe & Dr. Garth Ilesley **Onna-son, Japon**
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 (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 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.

Contrat Doctoral Spécifique aux Normaliens (CDSN) 2019

PhD fellowship

French Ministry of Higher Education & Research

2019–2022 (3 years)

Around 122 fellowships (less than 50% of the candidates) are granted yearly through a selective process based on scholastic records, recommendation letters, and the project proposal.

Élève fonctionnaire stagiaire de l'ENS Cachan

Scholarship

French Ministry of Higher Education & Research

2017,2018 (2 years)

Intern civil servant student at ENS de Cachan (Second concours: oral admission test in Computer Sciences, rank: 2, 4 positions every year at national level). Caesura for personal convenience from 01/09/2017 to 31/08/2018.

Research

Peer-Reviewed Scientific Journals

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

2022

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. Prioritization of Candidate Genes Through Boolean Networks

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

10/02/2022

2021

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

NeurIPS@Paris 2021 (Paris, France)

08/12/2021

2020

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

2018

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. 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

Commitment to Popularization of Sciences and Law Making

Popularization of Sciences.....

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 Training

Language Proficiency.....

French: C2 *Native speaker.*

English: C1 *TOEFL score (in 2016): 643/677.*

Spanish: B2 *Intermediate level, studied at school for seven years.*

Skills.....

Programming: Bash, Python, Ocaml, R, HTML/CSS, LaTeX, Jekyll (Ruby)

Training. Communication in talks and posters (including graphics and design using PowerPoint); mentoring; collaboration with mathematicians, computer scientists, bioinformaticians, biologists and medical practitioners; problem-solving abilities (in programming, in mathematics); adaptability to new disciplines (metagenomics, sequencing data processing, use of computing clusters, functional genomics, multi-armed bandit algorithms); familiarity with FAIR principles (training course "*Les principes FAIR appliqués à la bioinformatique*" from 31/08/2020 to 02/09/2020 in Paris, France).