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

(updated on 17/05/2023)

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

✉ clemence.reda@uni-rostock.de   •   🖥 https://clreda.github.io   •   ⌨ clreda

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   **(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, 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 repurosing 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 Wilczyńksi　　　　　**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 Ilsley　　　　　**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 migroglia 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   **French Ministry of Higher Education & Research**
PhD fellowship   *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   **French Ministry of Higher Education & Research**
Scholarship   *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

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

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

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

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

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](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](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](03172145)

Oral Communications at International Conferences

2023

C. Réda. Benchmarking collaborative filtering approaches to drug repurposing
e:Med Meeting 2023 on Systems Medicine (Berlin, Germany)   *10/10/2023*

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. **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*

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. **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, GitHub: `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, GitHub: `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, GitHub: `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
Large drug repurposing dataset with open-source generation
TRANSCRIPT
C. Réda
, Zenodo, DOI: 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" (conjointy 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); open-source software development.