Clémence Réda

PhD student in Genetics

☑ clemence.reda@inria.fr 'n clreda.github.io ♀ clreda

Education

2019 - present Doctorat, Université de Paris, Inserm UMR 1141 & CNRS UMR 9189

PhD in Genetics: Combination of gene regulatory networks and sequential machine learning for drug repurposing, supervised by Pr. Andrée Delahaye-Duriez & Dr. Émilie Kaufmann.

2018 – 2019 **M2 Master Vision, Apprentissage (MVA)**, École Normale Supérieure* (ENS) Paris-Saclay, (ex-École Normale Supérieure de Cachan)

Master's degree in Machine Learning. (summa cum laude, equiv. GPA: 4.0, no ranking)

2017 – 2018 Année de Recherche Prédoctorale à l'Étranger (ARPE), ENS Paris-Saclay

Ten-month long research internship at the Faculty of Mathematics, Informatics and Mechanics (MIM UW) of the University of Warsaw (Poland) included in the curriculum of ENS Paris-Saclay. Proof-of-concept on the explicit inclusion of biological interactions in gene regulatory networks and its impact on inference and simulation of transcriptomic regulation, in research team **Regulomics** supervised by Dr. Bartek Wilczyńksi. (Final grade (equiv. GPA): 4.0, no ranking)

- 2016 2017 M1 Master Parisien en Recherche en Informatique (MPRI), ENS Paris-Saclay Master's degree in Computer Sciences. (summa cum laude, equiv. GPA: 4.0, rank: 3/25)
- 2015 2016 **L3 Licence informatique fondamentale ENS Cachan**, École Normale Supérieure de Cachan Bachelor's degree in Computer Sciences. (cum laude, equiv. GPA: 4.0, rank: 10/26)

Previous Work Experiences

Research internships

2019 Teams Integrative Genomics (PROTECT UMR 1141) & SCOOL/CRISTAL (UMR 9189), Supervision (4 months) by Pr. Andrée Delahaye-Duriez and Dr. Émilie Kaufmann, Paris & Villeneuve d'Ascq, France 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.

2017 Team Genomics and Regulatory Systems Unit, Okinawa Institute of Science and Technology (5 months) (OIST), Supervision by Dr. Nicholas Luscombe and Dr. Garth Ilsley, Onna-son, Japon 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).

2016 Centre de Bioinformatique de Bordeaux (CBiB), Supervision by Dr. Macha Nikolski and le Dr. Mathieu (2 months) Raffinot, Bordeaux, France

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.

Teaching & Mentoring Experiences

2020 – 2021 **Doctorant Contractuel avec Mission d'Enseignement (DCME) (Teaching Assistant)**, *Biostatistics*, (64 hours a year) *programming and bioinformatics*, Université de Paris, UFR Sciences de la Vie

Supervision of a Masters's degree internship, Joint supervision of a Masters intern on the analysis of (6 months) targeted single-cell RNA sequencing data of inflammatory microglia in development, Inserm

2019 – 2020 Supervision of a Masters's degree project, Proposal of a project on drug repurposing based on (2 months) collaborative filtering, and joint supervision of a Masters student in the course **Graphs in Machine** Learning in masters **MVA** (2020), ENS Paris-Saclay

^{*} École Normale Supérieures are selective French schools for research and teaching.

Grants

- 2019 Research program for project REPOS, Inserm-CNRS "Digital health challenge" AAP 2019 (1 year)
- 2019 2022PhD scholarship, Contrat Doctoral Spécifique aux Normaliens (CDSN) 2019, ENS.X19RDTME-SACLAY19-22 (3 years)

Research

Papers

- Dealing With Misspecification In Fixed-Confidence Linear Top-m Identification, C. Réda, A. Tirinzoni 2021 & R. Degenne, [research, accepted], Proceedings of the 35^{th} Conference on Neural Information Processing Systems (NeurIPS 2021), HAL: 03409205. Impact factor: 33.5
 - **Top-***m* **identification for linear bandits**, *C. Réda*, *É. Kaufmann & A. Delahaye-Duriez*, [research], Proceedings of the 24^{th} International Conference on Artificial Intelligence and Statistics 2021 (AISTATS 2021), 130, HAL: 03172145. Impact factor: 9.9
- Machine learning applications in drug development, C. Réda, É. Kaufmann & A. Delahaye-Duriez, [re-2020 view], Computational and Structural Biotechnology Journal, 18, 241-252, DOI: 10.1016/j.csbj.2019.12.006. Impact factor: 6.0
 - Automated inference of gene regulatory networks using explicit regulatory modules, <u>C. Réda</u> & B. Wilczyński, [research], Journal of Theoretical Biology, 486, DOI: 10.1016/j.jtbi.2019.110091. Impact factor : 2.3
- 2019 Identification de cibles thérapeutiques et repositionnement de médicaments par analyses de réseaux géniques, A. Delahaye-Duriez, C. Réda & P. Gressens, [review], Médecine/Sciences, 35(6-7), 515-518, DOI : 10.1051/medsci/2019108. Impact factor : 0.7

Talks

- February 2022 DSABNS 2022, C. Réda. Gene network oriented drug discovery: automated inference of Boolean networks for drug target prediction (talk)
- NeurIPS 2021, C. Réda. Dealing With Misspecification In Fixed-Confidence Linear Top-m Identification December 2021 (poster)
 - April 2021 **AISTATS 2021**, *C. Réda*. Top-*m* identification for linear bandits (poster)
 - October 2020 Journées de recherche respiratoire (J2R) 2020, C. Réda. Transcriptome of neurons in a model of Congenital Central Hypoventilation Syndrome (poster). Conference has been cancelled due to the pandemic
 - Journées Ouvertes de Biologie, Informatique et Mathématique (JOBIM) 2020, C. Réda. Automated July 2020 inference of gene regulatory networks using explicit regulatory modules (oral)
 - Workshop 6, European Conference on Computational Biology (ECCB) 2018, C. Réda. Automated Sept. 2018 inference of gene regulatory networks using explicit regulatory modules (oral)
 - June 2018 BioInformatics in Toruń (BIT) 2018, C. Réda. Automated inference of gene regulatory networks using explicit regulatory modules (oral)

Commitment to popularization of sciences and law making

Popularization of sciences

- December 2016 -
 - Published on Tryalgo [in French]: series of blog posts on known algorithms with concrete applications, Sept. 2018 aimed at high school and college students (approx. 2,400 unique monthly users; two of these posts constitute the Top-2 most visited pages.
 - Published on Binaire (blog on Computer Science affiliated with the newspaper Le Monde) and The October2016 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

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

Language proficiency

French C2 Native speaker. English C1 TOEFL score (in 2016): 643/677.

Intermediate level, studied at school for seven years. B1

Spanish