Carlos **Ronchi**

Mathematician · Computational biologist

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Summary

Mathematician doing a PhD in molecular life sciences in a breast cancer lab at the Federal Polytechnic School of Lausanne (EPFL) in Switzerland. Developed **statistical algorithms** for **biomarker** discovery with transcriptomics data in breast cancer. Experienced in **transcriptomic analysis**, including single cell and bulk RNA-seq and microarray. I am dedicated and detail oriented, using recent tools for reports and pipelines using reproducible standards, such as **quarto** markdown, **docker** and **shiny apps**. Developed novel **biostatistical algorithms** and pipelines to analyse growth measurement data from in vivo and high-throughput experiments using **bayesian inference**. Experienced in **communicating** with bioscientists regarding their projects and helping them tackling their questions. Previously worked with **deep learning** and **artificial intelligence** in problems related to protein stability and computer vision.

Education

École Polytechnique Fédérale de Lausanne - EPFL   *Lausanne, VD, Switzerland*

PhD in Molecular Life Sciences   *Sep. 2020 - August 2024*

- Supervisor: Cathrin Brisken
- Fellow of Marie Curie actions (MSCA) - Horizon 2020

University of São Paulo - USP   *São Carlos, SP, Brazil*

M.Sc. in Mathematics   *Aug. 2017 - Nov. 2019*

- Supervisor: Marcio Gameiro; FAPESP fellow; GPA: 3.8/4.0

Rutgers University   *Piscataway, New Jersey, USA*

Visiting Research Student   *Jan. 2019 - Jun. 2019*

- Supervisor: Konstantin Mischaikow; BEPE FAPESP Excellence Scholarship

Federal University of Paraná - UFPR   *Curitiba, PR, Brazil*

B.Sc. in Mathematics   *Apr. 2013 - Jul. 2017*

- Awarded an excellence scholarship to spend 1.5 years in Germany. One year spent at RFW-Universität Bonn, Germany
- GPA: 4/4

Research Experience

PhD student at EPFL   *Lausanne, Switzerland*

Marie Curie fellow (MSCA - Horizon 2020)   *Sep. 2020 - Current*

- Developed a novel platform (EMBER) for biomarker discovery and breast cancer diagnosis using bulk RNA-seq and microarray. Manuscript under review
- Developed several R packages for biostatistics and bioinformatic analysis in the lab (biogrowleR), increasing the productivity of team members and standardizing several statistical protocols. Manuscript in preparation
- Used Bayesian Inference in novel ways to extract insights from data generated in the lab, leading to better interpretation of the results
- Developed several analysis pipelines for transcriptomics data that is shared in the group and used by non-bioinformaticians as well
- Experienced in communicating with bioscientists. Paying attention to their needs and helping them in clarifying their questions with biostatistics and computational biology
- Supervised and mentored master students in individual projects
- Went to multiple conferences in different countries to present my research
- Lead teaching assistant of genomics and bioinformatics in 2022 and 2023, a class with over 100 students. Organized exercise sessions, R tutorials and tutored several students in individual projects
- Started and organized bi-weekly seminar with experts on cancer prevention

Research intern at AstraZeneca   *Cambridge, UK*

funded by MSCA - Horizon 2020   *Oct. 2022 - Dec. 2022*

- Worked in a project to extract insights in real-world data
- Presented my research for multiple scientists in both the bioscience and bioinformatics department
- Introduced novel ways to interpret their drug pipeline discovery platform results by using bayesian inference

Research assistant at Brisken's lab at School of Life Sciences - EPFL *Lausanne, Switzerland*

FUNDED BY ÉCOLE POLYTECHNIQUE FÉDÉRALE DE LAUSANNE (EPFL) *Jan. 2020 - August 2020*

- Improved current packaging standards in the laboratory and introduced software best practices (ttmap)

Master's student *São Carlos, Brazil*

FUNDED BY FAPESP *Aug. 2017 - Nov. 2020*

- Developed novel ways to predict protein stability by applying persistent homology, tools from topological data analysis (TDA) and deep learning
- Combined machine learning and persistent homology to improve the accuracy in image classification problems
- Implemented TDA algorihtms in Julia (MapperMDS.jl, PersistenceImage.jl), allowing researchers to speed up their computations by using a faster language
- Developed web-based tools to visualize the results of optimal cycle extraction from persistent homology, helping researchers understand their results (3dPD)
- Collaboration with material science researchers to understand the optimal Hansen Solubility Parameters of organic semiconductors (HSP.jl)
- Awarded the best poster presentation among all master students in the mathematics department at ICMC - USP 2018

Undergradute researcher *Curitiba, Brazil*

FUNDED BY PROGRAMA DE ATRAÇÃO DE JOVENS TALENTOS (CSF-PAJT) *Jul. 2016 - Jul. 2017*

- Applied Convolutional Neural Networks (CNNs) to predict LaTeX characters, improving the accuracy of existing algorithms

IT and Data Science

Programming languges

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- R, python, Julia
- bash, docker, Slurm
- LaTeX

ember

HTTPS://CHRONCHI.GITHUB.IO/EMBER/

- Novel breast cancer diagnosis tool for biomarker discovery and treatment decision

biogrowleR

HTTPS://UPBRI.GITLAB.IO/BIOGROWLER/

- Tutorial, pipelines and randomization algorithms for longitudinal in vivo and and in vitro experiments in R

ttmap

HTTPS://GITLAB.COM/UPBRI/TTMAP

- Implementation of Two-Tier Mapper in R, a topological tool to analyse RNA-Seq data

ProteinPersistent.jl

HTTPS://GITHUB.COM/CHRONCHI/PROTEINPERSISTENT.JL

- Julia package that provides functions to obtain the persistent homology of a protein using the python package ripser

Languages

Portuguese (Native), English (excellent command/C1), German (good command/B2), French (good command/B2)

Hobbies

· Table tennis: captain of my team in the Swiss inter-cantonal championship

· Soccer

· Hiking