

# Carlos Ronchi

MATHEMATICIAN · COMPUTATIONAL BIOLOGIST

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## Summary

Mathematician doing a PhD in molecular life sciences in a wet lab at 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. Generated 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. Experienced in communicating to 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

PHD IN MOLECULAR LIFE SCIENCES

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

Lausanne, VD, Switzerland

Sep. 2020 - expected August 2024

### University of São Paulo - USP

M.Sc. IN MATHEMATICS

- Supervisor: Marcio Gameiro; FAPESP fellow; GPA: 3.83/4.00

São Carlos, SP, Brazil

Aug. 2017 - Nov. 2019

### Rutgers University

VISITING RESEARCH STUDENT

- Supervisor: Konstantin Mischaikow; BEPE FAPESP Scholarship

Piscataway, New Jersey, USA

Jan. 2019 - Jun. 2019

### Federal University of Paraná - UFPR

B.Sc. IN MATHEMATICS

- Excellence scholarship to spend 1.5 years in Germany. One year spent at RFW-Universität Bonn, Germany
- GPA: 94/100

Curitiba, PR, Brazil

Apr. 2013 - Jul. 2017

## Research Experience

### PhD student at EPFL

MARIE CURIE FELLOW (MSCA - HORIZON 2020)

- Developed a novel platform (EMBER) for biomarker discovery in breast cancer using bulk RNA-seq and microarray
- Developed several R packages for biostatistics and bioinformatic analysis in the lab (biogrowler), increasing the productivity of team members and standardizing several protocols
- 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 (biogrowler)

Lausanne, Switzerland

Sep. 2020 - Current

### Research intern at AstraZeneca

FUNDED BY MSCA - HORIZON 2020

- Academic placement to learn and understand the research process in pharmaceutical companies. 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

Cambridge, UK

Nov. 2022 - Nov. 2022

### Research assistant at Brisken's lab at School of Life Sciences - EPFL

FUNDED BY ÉCOLE POLYTECHNIQUE FÉDÉRALE DE LAUSANNE (EPFL)

- Improved current packaging standards in the laboratory and introduced software best practices on the way (ttmap)
- Studied statistical methods and how they are applied to answer breast cancer related questions

Lausanne, Switzerland

Jan. 2020 - August 2020

### Master's student

FUNDED BY FUNDAÇÃO DE AMPARO À PESQUISA DO ESTADO DE SÃO PAULO

- 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 algorithms 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)

São Carlos, Brazil

Aug. 2017 - Nov. 2020

## Undergraduate researcher

FUNDED BY PROGRAMA DE ATRAÇÃO DE JOVENS TALENTOS (CSF-PAJT)

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

Curitiba, Brazil

Jul. 2016 - Jul. 2017

## Teaching and Outreach

### EPFL

PHD STUDENT/RESEARCH OUTREACH AND SUPERVISION

- Supervised and mentored lab immersion projects for two master's students
- One of the student's project led to a short paper to be published
- Communicated my research in multiple conferences and visits to different labs in both academia and industry

Lausanne, Switzerland

Sep. 2020 - Now

### EPFL

PHD STUDENT/TEACHING ASSISTANT

- Teaching assistant of genomics and bioinformatics for over 100 students in 2022 and 2023. Organized exercise sessions and students projects for the final assignments. Supervised more 10 students in the final project where they had to reproduce figures from several papers.
- Started and organize bi-weekly seminars with experts on cancer prevention. The main audience is a group of european researchers and PhD students working under the same Marie Curie grant, a highly prestigious grant awarded by EU.
- Started and organized a monthly bioinformatics journal club for newly started PhD students from the network above.
- Teaching assistant of numerical analysis, a course with over 150 students.

Lausanne, Switzerland

Sep. 2020 - current

### PET - Educational Project

CORE MEMBER, FUNDED BY NATIONAL GOVERNMENT

- Developed teaching resources to teach high level mathematics to 100 high school students during one week. The topics were *Number Theory and Cryptography*; *Euclidean and Non-Euclidean geometries*.
- Organized an one week long academic session for math students, with courses and invited lectures.
- Teaching assistant of analytic geometry for over 20 students in a semester

Curitiba, Brazil

Aug. 2013 - Jul. 2014, Mar. - Jun. 2016

## Skills

### Programming and HPC Languages

R, python, Julia, LaTeX, bash, SQL, docker, Slurm  
Portuguese (Native), English (excellent command), German (good command), French (good command)

## Papers

### 2023

- Ronchi, C., & Haider, S., & Briskin C. **EMBER creates a unified space for independent breast cancer transcriptomic datasets enabling precision oncology** *In review*.
- Ronchi, C., & Ambrosini G. & Briskin C. **biogrowler: Extracting insights from growth measurement data.** *In preparation*.
- Ronchi, C., & Briskin, C. (2023). **Targeting the Progesterone Receptor in Breast Cancer: Mind the Short Form!** In Clinical Cancer Research (pp. OF1-OF2). American Association for Cancer Research (AACR). <https://doi.org/10.1158/1078-0432.ccr-22-3374>

## Projects

### ember

[HTTPS://CHRONCHI.GITHUB.IO/EMBER/](https://chronchi.github.io/ember/)

- An R package that implements the method described in the accompanying paper (In review).
- Integration of bulk RNA-seq and microarray datasets for individual samples. Suitable for biomarker discovery and cross dataset comparison.

### biogrowler

[HTTPS://UPBRI.GITLAB.IO/BIOGROWLER/](https://upbri.gitlab.io/biogrowler/)

- An R package that provides tutorials and auxiliary functions on how to analyse growth measurement data.
- Package was taught in workshops and has been used by other life scientist.

### ttmap

[HTTPS://GITLAB.COM/UPBRI/TTMAP](https://gitlab.com/upbri/ttmap)

- R package implementing Two-Tier Mapper, a topological tool to analyse RNA-Seq data.
- Developed a R package with a more user-friendly interface and API.
- Supervised a master's student that added tests and a shiny app interface to the package.

## ProteinPersistent.jl

<https://github.com/chronchi/proteinpersistent.jl>

- Package that provides an interface for some functions of BioPython. It also calculates the persistent homology of a protein using the python package ripser.

## MapperMDS.jl

<https://github.com/chronchi/mappermds.jl>

- Mapper is an algorithm from topological data analysis that helps visualize high dimensional data. This is an implementation in Julia that accepts a distance matrix as input.

## PersistenceImage.jl

<https://github.com/chronchi/persistenceimage.jl>

- Persistence image is a vectorization method for persistence diagrams. This is an implementation of the algorithm in Julia.

## 3dPD

<https://github.com/chronchi/3dPD>

- Visualization tool for optimal cycles (w.r.t. number of edges) and persistence diagrams of three-dimensional datasets. Developed as part of my master thesis.

## HSP.jl

<https://github.com/chronchi/hsp.jl>

- Julia implementation of a package to calculate the optimal Hansen Solubility Parameters.

## Events

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Feb. 2024	<b>Perspectives on cancer prevention</b> , Talk: EMBER creates a unified space for independent breast cancer transcriptomic datasets enabling precision oncology	<i>Lausanne, Switzerland</i>
Jun. 2023	<b>International workshop on cancer prevention</b> , Transcriptomic based molecular landscape provides a framework for precision medicine in breast cancer	<i>Ghent, Belgium</i>
Jul. 2023	<b>Science and policy summer schoool</b> , Organized by EPFL and ETH PhD students	<i>Beatenberg, Switzerland</i>
Feb. 2023	<b>World Cancer Day</b> , Could algorithms and computers help us with cancer prevention?	<i>Lausanne, Switzerland</i>
Nov. 2022	<b>Talks at AstraZeneca</b> , Understanding hormone signaling and its risks on estrogen receptor-positive breast cancer	<i>Cambridge, UK</i>
Oct. 2022	<b>II Congreso Internacional de Topología y Afines</b> , TDA in action: using two-tier mapper to understand breast cancer	<i>Lima, Peru</i>
Aug. 2022	<b>43rd Annual Conference of the International Society for Clinical Biostatistics</b>	<i>Newcastle, UK</i>
Jun. 2022	<b>Open Science Summer School</b> , @EPFL, organized by EPFL and ETH PhD students	<i>Lausanne, Switzerland</i>
Jun. 2022	<b>International workshop on cancer prevention</b> , Understanding hormone signaling and its risk on estrogen receptor-positive breast cancer	<i>Pollone, Italy</i>
Sep. 2021	<b>Basel Computational Biology Conference - BC2</b> , Estrogen signature and gene coexpression network for breast cancer stratification and survival analysis	<i>Basel, Switzerland</i>
Oct. 2019	<b>XII Regional Topology Meeting</b> , A topological approach to protein stability	<i>Águas de Lindóia, Brazil</i>
May 2019	<b>Geometric Data Analysis</b> , Persistent homology and the protein folding problem	<i>Chicago, USA</i>
Apr. 2019	<b>Data Driven Dynamics: Algebraic Topology, Combinatorics and Analysis</b> , Persistent homology and the protein folding problem	<i>Montreal, Canada</i>
Aug. 2018	<b>8th Workshop of Thesis and Dissertations of ICMC</b> , Optimal cycles and applications in machine learning	<i>São Carlos, Brazil</i>
Aug. 2018	<b>XXI Brazilian Topology Meeting</b> , Optimal cycles and applications in machine learning	<i>Niteroi, Brazil</i>
Aug. 2018	<b>TRIPODS Summer Bootcamp: Topology and machine learning</b> , Optimal cycles and applications in machine learning	<i>Providence, USA</i>
Oct. 2015	<b>Automatic sequences, Number Theory, Aperiodic Order</b>	<i>Delft, The Netherlands</i>
Oct. 2015	<b>Panorama of Mathematics</b>	<i>Bonn, Germany</i>

## Honors & Awards

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2010	<b>Bronze medal</b> , National Astronomy Olympiad	<i>Curitiba, Brazil</i>
2011	<b>Bronze medal</b> , National Astronomy Olympiad	<i>Curitiba, Brazil</i>
2018	<b>Best Poster Presentation</b> , 8th Workshop of Thesis and Dissertations at ICMC - USP	<i>São Carlos, Brazil</i>