Personal information

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Date of birth	19 September 1992

Summary

I am a computational biologist motivated by the applications of machine learning and artificial intelligence to the field of biology. During my academic career I developed computational methods to reveal biological insights by the integration of multi-modal data (the most popular one being MOFA). I also worked in collaboration with experimental biologists to generate and analyse large single-cell multi-modal atlases of embryonic development. Currently, I work as a Senior Research Scientist at the Institute of Computation at Altos Labs, where I focus on modelling gene perturbation screens to infer the regulatory networks that underlie cellular rejuvenation programming.

Education

PhD in Statistical Genomics, European Bioinformatics Institute and Cambridge University (2016-2020).
MSc in Bioinformatics, Copenhagen University (2014-2016).
BSc in Human Biology, Pompeu Fabra University (2010-2014).

Academic research

Postdoctoral Scientist at the Babraham Institute
Duration: January 2021 - January 2022
Supervisor: Wolf Reik
Research topic: Multi-modal profiling of mouse embryonic development at single-cell resolution

PhD thesis at the European Bioinformatics Institute (EMBL-EBI, Cambridge)
Duration: October 2016 - December 2020
Supervisors: John Marioni and Oliver Stegle
Title: Statistical methods for the integrative analysis of single-cell multi-omics data (Link to PhD thesis)

MSc thesis at the Statistical genomics and systems genetics group at EMBL-EBI (Cambridge)
Duration: February 2016 - August 2016
Supervisor: Oliver Stegle
Title: Bayesian Factor Analysis models for data integration (Link to MSc thesis)

BSc thesis at the Computational Molecular Biology Group at the Freie Universitat Berlin
Duration: April 2014 - July 2014
Supervisor: Kashif Sadiq
Title: Kinetic characterization of the mature HIV-1 protease by constructing Markov models from Molecular Dynamics Simulations (Link to BSc thesis)

Industry jobs

Research Scientist. Altos Labs, Institute of Science; February 2022 - September 2022

Senior Research Scientist. Altos Labs, BioML and Institute of Computation; September 2022 - Present

Selected publications

- Clark S*, **Argelaguet R*** et al. Joint profiling of chromatin accessibility, DNA methylation and transcription in single cells. <u>Nat Comms</u>. 2018;9(1):781
- **Argelaguet R***, Velten B*, et al. Multi-Omics Factor Analysis: an unsupervised framework for the integration of multi-omics data. <u>Mol Sys Bio</u>. 2018. 14, e8124
- **Argelaguet R***, Clark S*, et al. Multi-omics profiling of mouse gastrulation at single-cell resolution. <u>Nature</u>. 2019
- **Argelaguet R***, Arnol D*, et al. MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. <u>Genome Biology</u>. 2020
- Haak BW*, **Argelaguet R***, et al. Intestinal transkingdom analysis on the impact of antibiotic perturbation and critical illness. <u>mSystems</u>. 2020
- Kapourani CA*, **Argelaguet R***, et al. scMET: Bayesian modelling of DNA methylation heterogeneity at single cell resolution. <u>Genome Biology</u>. 2020
- Lohoff T, Ghazanfar S, Missarova A, Koulena N, Pierson N, Griffiths JA, Tyser RCV, **Argelaguet R**, Guibentif C, Srinivas S, Hadjantonakis AK, Gottgens B, Reik W, Nichols J, Cai L, Marioni JC. Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <u>Nature Biotechnology</u>. 2021
- Velten B, Braunger JM, **Argelaguet R**, Arnol D, Stegle O. Identifying temporal and spatial patterns of variation from multi-modal data using MEFISTO. <u>Nature methods</u>. 2022
- **Argelaguet R***, Clark S*, Lohoff T, Li G, Krueger F, Velten L, Reik W. Decoding gene regulation in the mouse embryo. <u>bioRxiv</u>. 2022
- **Argelaguet R***, Clark S*, Lohoff T*, Krueger F, Drage D, Gotggens B, Marioni JC, Nichols J, Reik W. Single-cell multi-omics profiling links dynamic DNA methylation to cell fate decisions during early mammalian organogenesis. <u>Genome Biology</u>. 2022
- Rosen L, Stapel C, **Argelaguet R**, Barker CG, Yang A, Reik W, Marioni JC. Inter-gastruloid heterogeneity revealed by single cell transcriptomics time course: implications for organoid based perturbation studies. <u>bioRxiv</u>. 2022

- Full list of publications: [Google scholar, ORCID.](#)

Reviews

- **Argelaguet R**, Cuomo A, Stegle O, Marioni J.C. Computational principles and challenges in single-cell data integration. <u>Nature Biotechnology</u>. 2021
- Pau Badia-i-Mompel, Lorna Wessels, Sophia Müller-Dott, Rémi Trimbour, Ricardo O Ramirez Flores, **Ricard Argelaguet**, Julio Saez-Rodriguez. Gene regulatory network inference in the era of single-cell multi-omics. <u>Nature Reviews Genetics</u>. 2023

Teaching experience

- **Instructor at the EMBO course "Integrative Analysis of Multi-Omics Data** [Course link](#). EMBL Heidelberg (Germany). February 2024.
- **Instructor at the VIB course "Using MOFA for integration of omics data"** ([Course link](#)). Leuven (Belgium). Running yearly 2019-2024
- **Adjunct professor at Universitat Pompeu Fabra; Fundamentals of computational biology, BSc Human Biology** ([Course link](#)). Barcelona (Spain). September 2021 - December 2021
- **Instructor at the MSc course "Information Extraction from Omics Technologies" at Universitat Pompeu Fabra** ([Course link](#)). Barcelona (Spain). May 2020

- **Instructor at the course "Introduction to multi-omics data Integration"** ([Course link](#)). EMBL-EBI, Cambridge (UK). Running yearly 2018-2024.
- **Instructor ELIXIR-SE Omics Integration and Systems Biology course** ([Course link](#)). (Sweden, Online), September 2021

- **Instructor at the course "Systems Biology: From Large Datasets to Biological Insight"** (Course link). EMBL-EBI, Cambridge (UK). May 2019
- **Supervisor at the BSc course "Mathematical Biology"** (Course link). Cambridge University (UK). October 2017 - July 2020
- **Instructor at the Multi-Omics Factor Analysis workshop** (Course link). Heidelberg (Germany). September 2019
- **Teaching assistant at the MSc course "Biological Sequence Analysis"** (Course link). Copenhagen University (Denmark). September 2015 - December 2015

Software developed

- **MOFA**: Multi-Omics Factor Analysis. Webpage
- **MEFISTO**. Functional Integration of Spatial and Temporal Omics data. Webpage
- **scMET**: Bayesian modelling of single-cell DNA methylation, Github repository
- **SingleCellMultiModal**: A collection of processed single-cell multi-modal datasets in Bioconductor. Webpage.

Invited speaker and oral presentations

- 4th Bioinformatics and Genomics Symposium (Barcelona, 2016)
- From Single- to Multiomics: Applications and Challenges, conference (Heidelberg, 2017)
- Annual Meeting of Mathematical and Statistical Aspects of Molecular Biology (St. Andrews, 2018)
- German Conference in Bioinformatics (Heidelberg, 2019).
- Single-cell Genomics conferenc e(Boston, 2019).
- EMBL-EBI Industry Programme Workshop on single-cell multi-omics (Cambridge, 2019).
- German Conference in Bioinformatics (Heidelberg, 2019).
- Life Science Masterclass, Addenbrooks Biomedical Campus (Cambridge, 2019).
- Machine Learning Discussion Group, Cavendish Laboratories (Cambridge, 2019).
- Universite Cote d'Azur Seminar (Nice, 2019).
- PRBB Computational Genomics Seminar (Barcelona, 2019).
- Workshop on Methods in Integrative Genomics, organised by the Royal Statistical Society and the Centre for Methodology at the London School of Hygiene and Tropical Medicine (London, 2020)
- GOS Institute of Child Health Research Symposium (London, 2020).
- Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Types (Banff, 2020).
- Challenges in Omics data integration (EU-LIFE online workshop, 2020).
- UK Festival of Genomics (virtual, 2020)
- Bristol Meyers Squibb computational seminar (Online, 2021).
- 10x Genomics webinar on single-cell multi-modal analysis (Online, 2022).
- Harvard Medical school, Computational biology seminar (Online, 2023).
- Astrazeneca, computational biology seminar(Cambridge, 2024).
- Cambridge AI club for Biomedicine, seminar (Cambridge, 2024).
- Center for Health Data Science, computational seminar (Copenhagen, 2025).

Languages

Catalan (native), Spanish (native), English (fluent), Portuguese (intermediate).

Computational skills

- Programming languages (proficient): Python and R

- Machine learning / data science: working experience with a variety of machine learning and data science frameworks, including probabilistic modelling, Bayesian inference, (generalised) linear models, discrete and continuous latent variable models, neural networks (Pytorch), Markov models.

- Omics data processing pipelines with nf-core: bulk RNA-seq, scRNA-seq, DNAm via bisulfite sequencing, ATAC-seq, ChIP-seq.

- Workflow management with Nextflow and Snakemake.

- [Personal github account]

PhD thesis jury

PhD candidate: Lise Mangiante

Title: Disentangling heterogeneity of Malignant Pleural Mesothelioma through deep integrative omics analyses

Institution: IARC-WHO (Lyon, France)

December 2021

MSc thesis jury

I evaluated the MSc thesis of several students from the MSc Bioinformatics

Institution: Universitat Pompeu Fabra (Barcelona, Spain)

June 2021

Student supervision

PhD candidate: Bart Theeuwes (2021-2022)

Title: Deciphering gene regulatory network control of embryonic haematopoiesis

Institution: Stem Cell Institute, University of Cambridge

PhD candidate: Brendan Terry (2021 - 2022)

Title: Multi-modal CRISPR screenings at single-cell resolution

Institution: Babraham Institute

MSc candidate: Yonatan Deloro (2018)

Title: Building Factor Analysis Models for Genomics

Institution: Ecole des Ponts ParisTech (Paris, France)

BSc candidate: Jingyu Li (2021 - 2022)

Title: Integrative analysis of single-cell multi-omics data

Institution: Babraham Institute

Scolarships

Graduate studies   "La Caixa" International Graduate Studies Scholarship (2014-2016)

Undergraduate studies   "Collaboration grant" to allow students to combine studies and research for 6 months (2013). Awarded by the Spanish Government

Journals reviewed for

Bioinformatics (3), Nature Methods (3), Nature Biotechnology (2), Nature communications (2), BMC Bioinformatics (1), Genome Research (1), eLife (1), Statistical Applications in Genetics and Molecular Biology (2), Nucleic Acids Research (1), PLOS Comp Bio (5)

Grants reviewed

ERC Starting Grants 2023