

Personal information

Surname(s) / First name(s) **Argelaguet, Ricard**
Address(es) 10 Coldhams Lane, CB1 3EP, Cambridge, UK
Telephone(s) +34677039424 (Spain) 07732811468 (UK)
Email(s) ricard.argelaguet@gmail.com
Nationality(-ies) Catalan, Spanish
Date of birth 19 September 1992
Gender Male

Interests

I develop computational methods to decipher the gene regulatory processes that underlie cellular diversity during embryonic mammalian development. For this, I analyse data from high-throughput molecular profiling technologies at single-cell resolution, including scRNA-seq, scATAC-seq, Cut&Tag and scNMT-seq. My current goal is to leverage these set of statistical methods and experimental assays to understand and improve cellular rejuvenation programming.

Current work

Research Scientist. Altos Labs, February 2022 -

Education

PhD in Computational Biology.

European Bioinformatics Institute and Cambridge University, October 2016 - December 2020

MSc in Computational Biology.

Copenhagen University, 2014 – 2016

BSc in Human Biology.

Pompeu Fabra University, 2010 – 2014

Academic experience

Postdoctoral Scientist at the Babraham Institute

Duration: December 2020- January 2022

Supervisor: Wolf Reik

Title: Multi-omics 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

URL: <https://www.repository.cam.ac.uk/handle/1810/315822>

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

BSc thesis at the Computational Molecular Biology Group at the Freie Universität 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

Summer internship at the Genetic Systems Lab at the Centre for Genomic Regulation (Barcelona)

Duration: July 2015 - September 2015

Supervisor: Fran Supek and Ben Lehner

Title: Machine learning to predict protein epistasis patterns from Deep Mutational Sequencing Data.

Publications

Google scholar: <https://scholar.google.com/citations?user=8xGSu9EAAAAAJ>

Clark S*, **Argelaguet R*** et al. Joint profiling of chromatin accessibility, DNA methylation and transcription in single cells. *Nat Comms*. 2018;9(1):781

Argelaguet R*, Velten B*, et al. Multi-Omics Factor Analysis: an unsupervised framework for the integration of multi-omics data. *Mol Sys Bio*. 2018. 14, e8124

Argelaguet R*, Clark S*, et al. Multi-omics profiling of mouse gastrulation at single-cell resolution. *Nature*. 2019

Argelaguet R*, Arnol D*, et al. MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. *Genome Biology*. 2020

Haak BW*, **Argelaguet R***, et al. Intestinal transkingdom analysis on the impact of antibiotic perturbation and critical illness. *mSystems*. 2020

Kapourani CA*, **Argelaguet R***, et al. scMET: Bayesian modelling of DNA methylation heterogeneity at single cell resolution. *Genome Biology*. 2020

Lohoff T, Ghazanfar S, Missarova A, Kouloua N, Pierson N, Griffiths JA, Bardot ES, Eng CHL, Tyser RCV, **Argelaguet R**, Guibentif C, Srinivas S, Briscoe J, Simons BD, Hadjantonakis AK, Gottgens B, Reik W, Nichols J, Cai L, Marioni JC. Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. *Nature Biotechnology*. 2021

Argelaguet R*, Cuomo A, Stegle O, Marioni J.C. Computational principles and challenges in single-cell data integration. *Nature Biotechnology*. 2021

LeCao, Kim-Anh and Abadi, Al J. and Davis-Marcisak, Emily F. and Hsu, Lauren and Arora, Arshi and Coullomb, Alexis and Deshpande, Atul and Feng, Yuzhou and Jeganathan, Pratheepa and Loth, Melanie and Meng, Chen and Mu, Wancen and Pancaldi, Vera and Sankaran, Kris and Righelli, Dario and Singh, Amrit and Sodicoff, Joshua S. and Stein-O'Brien, Genevieve L. and Subramanian, Ayshwarya and Welch, Joshua D. and You, Yue and **Argelaguet, Ricard** and Carey, Vincent J. and Dries, Ruben and Greene, Casey S. and Holmes, Susan and Love, Michael I. and Ritchie, Matthew E. and Yuan, Guo-Cheng and Culhane, Aedin C. and Fertig, Elana. Community-wide hackathons to identify central themes in single-cell multi-omics. *Genome Biology*. 2021

Velten B, Braunger JM, **Argelaguet R**, Arnol D, Stegle O. Identifying temporal and spatial patterns of variation from multi-modal data using MEFISTO. *Nature methods*. 2022

Taubenschmid-Stowers J., Rostovskaya M., Fatima S., Ljung S., **Argelaguet R.**, Krueger F., Nichols J., Reik W. 8C-like cells capture the human zygotic genome activation program in vitro. *Cell Stem Cell*. 2022

Eckenrode KB, Righelli D, Ramos M, **Argelaguet R**, Vanderaa C, Geistlinger L, Culhane C, Gatto L, Carey V, Morgan M, Risso D, Waldron L. Curated Single Cell Multi-modal Landmark Datasets for R/Bioconductor. *bioRxiv*. 2022

Argelaguet R*, Clark S*, Lohoff T, Li G, Krueger F, Velten L, Reik W. A multi-omics roadmap of mouse early organogenesis. In preparation

Argelaguet R*, et al. Multi-omics profiling of human preimplantation embryos. In preparation

Argelaguet R*, Clark S*, Lohoff T*, Krueger F, Drage D, Gottgens B, Marioni JC, Nichols J, Reik W. Single-cell multi-omics profiling links dynamic DNA methylation to cell fate decisions during early mammalian organogenesis. *Under review*

Teaching experience

Adjunct professor at Universitat Pompeu Fabra. Barcelona (Spain). Duration: September 2020 - December 2021

Supervisor at the BSc course "Mathematical Biology" at Cambridge University. Cambridge, (UK). Duration: October 2017 - July 2020

Demonstrator at the course "Using MOFA for integration of omics data". Vlaams Instituut voor Biotechnologie. Leuven (Belgium). Duration: 6 hours, February 2019

Demonstrator at the course "Systems Biology: From Large Datasets to Biological Insight". EMBL-EBI, Cambridge (UK). Duration: 3 hours, May 2019

Demonstrator at the course "Introduction to multi-omics data Integration". EMBL-EBI, Cambridge (UK). Duration: 2 hours, February 2018

Teaching assistant at the MSc course "Biological Sequence Analysis" at Copenhagen University. Copenhagen (Denmark). Duration: September 2015 - December 2015

Demonstrator at the Multi-Omics Factor Analysis workshop. Heidelberg (Germany). Duration: 4 hours, September 2019

Demonstrator ELIXIR-SE Omics Integration and Systems Biology course. Sweden (Virtual). Duration: 4 hours, September 2021

Demonstrator at the MSc course "Information Extraction from Omics Technologies (IEO)" at Universitat Pompeu Fabra. Barcelona (Spain). Duration: 6 hours, May 2020

Software developed

MOFA: Multi-Omics Factor Analysis, <https://biofam.github.io/MOFA2/>

scMET: Bayesian modelling of single-cell DNA methylation, <https://github.com/andreaskapou/scMET>

MEFISTO. Functional Integration of Spatial and Temporal Omics data <https://biofam.github.io/MOFA2/MEFISTO.html>

SingleCellMultiModal: A collection of processed single-cell multi-modal datasets in Bioconductor, <https://bioconductor.org/packages/release/data/experiment/html/SingleCellMultiModal.html>

Virtual ChIP-seq: in silico prediction of Transcription Factor binding sites from single-cell multi-omics data. *In preparation...*

Invited speaker

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)

EIPP Bioinformatics Predocs Course, keynote speaker (Cambridge, 2022).

Contributed oral presentations

Integrative methods for multi-omics data integration. Talk at the **German Conference in Bioinformatics** (Heidelberg, 2019).

Single-cell multi-omics profiling reveals a hierarchical epigenetic landscape during mammalian germ layer specification. Talk at the conference **Single-cell Genomics**. Boston, 2018.

MOFA: an unsupervised framework for the integration of multi-omics data. Talk at the **Annual Meeting of Mathematical and Statistical Aspects of Molecular Biology**. St. Andrews, 2018.

Joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Talk at the conference **From Single- to Multiomics: Applications and Challenges**. Heidelberg, 2017

Disentangling the different sources of variation in multi-omics single-cell sequencing data. Talk at the **4th Bioinformatics and Genomics Symposium**. Barcelona, 2016

Contributed poster presentations

MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. Presented at the conference **Single-cell Genomics**. Stockholm, 2019.

Single cell multi-omics profiling reveals a hierarchical epigenetic landscape during mammalian germ layer specification. Presented at the conference **Biology of Genomes**. Cold Spring Harbor, 2019.

MOFA: an unsupervised framework for the integration of multi-omics data. Presented at the **3rd European Conference on Translational Bioinformatics**. Barcelona, 2018.

scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Presented at the conference **Single-cell Genomics**. Tel Aviv, 2017.

Disentangling the different sources of variation in multi-omics single-cell sequencing data. Presented at the workshop **Statistical Challenges in Single-Cell Biology**. Ascona, 2017.

Group Factor Analysis to disentangle sources of variability between different molecular layers. Presented at the **EMBL PhD symposium**. Heidelberg, 2016.

Languages

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

Computational skills

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, Markov models, Gaussian Processes.

Programming languages (proficient): Python and R

GitHub

<https://github.com/rargelaguet>

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

MSc candidate: Yonatan Deloro

Title: Building Factor Analysis Models for Genomics

Institution: Ecole des Ponts ParisTech (Paris, France)

Duration: February 2018 - July 2018

BSc candidate: Jingyu Li

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

Institution: ZheJiang University

Duration: April 2021 - June 2022

Scholarships

Graduate studies

"La Caixa" International Graduate Studies Scholarship (2014-2016) to course the MSc in Bioinformatics at Copenhagen University. "La Caixa" grants are designed to reward academic excellence and to cover the full cost of matriculation, travel expenses and monthly allowances for the entire MSc period. Awarded by "Obra Social La Caixa".

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 (1), 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)