

JACQUES SERIZAY

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University of Cambridge, UK

Educational background

- **2016:2020 – PhD in Genomics – University of Cambridge, United Kingdom**
Julie Ahringer lab – Gurdon Institute / Department of Genetics
Thesis: Spatiotemporal control of gene expression in *C. elegans*
- **2016 – MSc in Genetics – Ecole Normale Supérieure de Paris-Saclay**
Partnership with Pasteur Institute
Graduated with highest honors.
First (UK) / *summa cum laude* (USA)
- **2013 – BSc in Biology and Health – Ecole Normale Supérieure de Paris-Saclay**

Research experience

- 2016 - current **Julie Ahringer Lab**
University of Cambridge UK

Multi-omics (ChIP-seq, RNA-seq, ATAC-seq, MNase-seq), single-cell approaches, sequencing data analysis, data integration, data visualization
- 2016 (5 months) **Raphael Margueron Lab**
Institut Curie, France
MSc thesis: *Functional role of BAP1 in the control of gene transcription*

ChIP-seq, SILAC & Mass spectrometry, sequencing data analysis, data visualization
- 2014 - 2015 (10 months) **Kathrin Plath Lab**
Department of Biological Chemistry, University of California Los Angeles, USA
Xist 5'-located repeats and their role in Xist cloud formation (personal project);
Importance of Xist repeats and their interacting proteins for the initiation of X Chromosome Inactivation (shared project).

RNA Antisense Purification (RAP-seq), Nascent-RNA sequencing, DNA/RNA-FISH, sequencing data analysis, data visualization
- 2014 - (2 months) **Maite Huarte Lab**
Center for Applied Medical Research – University of Navarra, Spain
Long intergenic non-coding RNA frequently amplified or deleted in cancerous cells play a role in cancer phenotypes.

RT-qPCR, Bioinformatics
- 2013 - (2 months) **Edith Heard Lab**
Institut Curie, France
BSc thesis: *Study of random monoallelic expression of autosomal genes.*

Entrepreneurial experience

- 2018 – 2019
5 months **EnterpriseTECH PhD+ program**
Cambridge Judge Business School – University of Cambridge, UK

Distributed ledger for genomic data: opportunities & road to market (Project leader)

Qualifications

Computing basics	Bash (advanced) R (expert) Python (intermediate) Web design: HTML, CSS (intermediate) Latex (intermediate)
Bio-informatics	R/Bioconductor Genome-wide sequencing (RNA/ATAC/ChIP/others) in-depth analysis Mapping/analysis pipeline automation Advanced data visualization
Data analysis	SQL databases (sqlite3, MySQL) Interactive dashboards (Shiny, Dash)
English	Fluent (TOEIC 2014: 955/990, TOEFL 2016: 110/120)
French	Native language
Spanish	Intermediate

Awards & funding

2018	Winner of the Cambridge Genomics Hackathon > sudo: sequence . Conceptualized and designed a platform to integrate patient's genomic data in an interactive platform to facilitate decision making by non-expert clinicians.
2016	Medical Research Council Doctoral Training Grant School of Biological Sciences PhD funding (3 ½ years) Sackler Fund (£6,000) Diploma of the Ecole Normale Supérieure de Paris-Saclay
2015	Diploma of the Pasteur Institute ('Genome Analyses' course)
2012-2016	Ecole Normale Supérieure de Cachan: 4-year studentship funding

Scientific references

Julie Ahringer	ja219@cam.ac.uk
Kathrin Plath	kplath@mednet.ucla.edu
Maite Huarte	maitehuarte@unav.es
Edith Heard	edith.heard@curie.fr

Other interests

Movie box-office data investigator – https://github.com/js2264/moviestats
Micro-entrepreneur in jewelry (3+ years) – Funded Fovea Paris (https://foveaparis.com/)

Scientific communication

Publications	In preparation:	periodicDNA: an R package to investigate oligonucleotide periodicity , <u>Jacques Serizay</u> , Julie Ahringer
	In preparation:	The analysis of copy number alterations from a lncRNA perspective reveals a mediator of NSCLC immune evasion , Alejandro Athie, Jovanna González, Teresa Lozano, Ivan Raimondi, Oskar Marin-Bejar, <u>Jacques Serizay</u> , Dannys Martínez, Juan Sandoval, Luis Montuenga, Chandrasekhar Kanduri, Juan José Lasarte, Maite Huarte
	In review:	A phase-separated multi-molecular assembly formed by Xist, PTBP1, MATR3, CELF1 and TDP-43 is essential for Xist localization and gene silencing during X-inactivation , Amy Pandya-Jones, Yolanda Markaki, <u>Jacques Serizay</u> , Tsothe Chitashvili, Walter Mancia, Andrey Damianov, Costantinos Chronis, Bernadett Papp, Chun-Kan Chen, Robin McKee, Anthony Chau, Heinrich Leonardt, Sika Zheng, Mitchell Guttman, Douglas L. Black, and Kathrin Plath, <i>bioRxiv</i> (DOI: 10.1101/2020.03.09.979369)
	2020:	Ubiquitous, germ line, and somatic genes have distinct regulatory architecture in <i>C. elegans</i> , <u>Jacques Serizay</u> , Yan Dong, Jürgen Jänes, Chiara Cerrato, Julie Ahringer, <i>bioRxiv</i> (DOI: 10.1101/2020.02.20.958579)
	2018	Genome organization at different scales: nature, formation and function , <u>Jacques Serizay</u> and Julie Ahringer, <i>Current Opinion in Cell Biology</i> (DOI: 10.1016/j.ceb.2018.03.009)
Scientific communication		Chromatin accessibility dynamics across <i>C. elegans</i> development and ageing , Jurgen Janes [§] , Yan Dong [§] , Michael Schoof [★] , <u>Jacques Serizay</u> [★] , Alex Appert, Chiara Cerrato, Carson Woodbury, Ron Chen, Carolina Gemma, Ni Huang, Djem Kissiov, Przemyslaw Stempor, Annette Steward, Eva Zeiser, Sascha Sauer, Julie Ahringer, <i>Elife</i> (DOI: 10.7554/eLife.37344)
	2020:	Systems Biology: Global Regulation of Gene Expression [CSHL] (Poster) (Selected)
	2019:	International <i>C. elegans</i> Conference [UCLA] (Talk) (Selected)
	2018:	Research in Genetics Conference [Cambridge] (Poster)
	2017:	sciLife / LMB Bioscience Symposium [Cambridge University, UK] (Poster)
		International <i>C. elegans</i> Conference [UCLA] (Poster) (Selected)
		Conference on Everything [Cambridge University, UK] (Poster) (Selected)
Bioinformatic resources		Shell Research Prize [Cambridge University, UK] (Poster) (Selected)
	periodicDNA	https://github.com/js2264/periodicDNA/ – R package to study k-mers periodicity at small and large scale in genomes
	VplotR	https://github.com/js2264/VplotR/ – R package to easily generate V-plots of paired-end sequencing data
	RegAtlas	https://ahringerlab.com/RegAtlas/ – Developmental and tissue-specific regulatory atlas in <i>C. elegans</i> – Shiny app
Teaching	<i>Caenorhabditis elegans</i> genome browser	https://ahringerlab.com/Browser/ – Genome browser for exploratory data analysis of developmental and tissue-specific chromatin organization in <i>C. elegans</i>
		Introduction to Multi-omics Data Integration and Visualisation (European Bioinformatics Institute, UK) 1A Biology of the Cells (University of Cambridge, UK) BTEC Higher National Diploma, Biotechnology (Gif s/ Yvette, France) Supervision of master students (4–6 months lab internships) Student supervision (Sixth form students, first year undergraduates)