Jacques Serizay

POST-DOCTORATE FELLOW IN GENOMICS

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Research fellow with 8 years of experience in the analysis, visualization and **integration of multi-omics data**, for both bulk and single cell analyses. I am interested in developing scientific projects that bridge the experimental and computational sides of epigenomics to uncover meaningful biological information.

My formal training in molecular biology and genomics, combined with years of experience in genome-wide data generation and analysis, puts me in a strategic position to understand and communicate with experimentalists. I strongly support collaborations to gain new insights into biological problems, I actively promote reproducibility, FAIR principles, knowledge dissemination and I train best practices for data management.

Education

PhD in Genomics   *Cambridge, UK*
Julie Ahringer lab, Gurdon Institute | Department of Genetics, University of Cambridge   *2016-2020*

EntrepriseTECH programme   *Cambridge, UK*
Judge Business School, University of Cambridge   *20018-2019*

Ecole Normale Superieure de Paris-Saclay Diploma   *Paris, France*
Biology Department, ENS Paris-Saclay   *2016*

M.Sc. in Genetics   *Paris, France*
ENS Paris-Saclay & Magistère Européen de Génétique   *2014-2016*

B.Sc. in Biology & Health   *Paris, France*
ENS Paris-Saclay & Université Orsay Paris Sud   *2013*

Research Experience

Institut Pasteur & Ecole Normale Supérieure   *Paris, France*
Post-doctorate fellow, Romain Koszul lab & Nathalie Spassky lab   *Sep 2020 - Current*
- Investigated the role of DNA sequence composition for the chromatinization of foreign chromosomes.
- Implemented biocomputational approaches to investigate single-cell transcriptomics during cell cycle variants.
- Developed a unified syntax and methodolgy to manipulate epigenomics data.

University of Cambridge   *Cambridge, UK*
PhD student, Julie Ahringer lab   *Sep 2016 - Aug 2020*
PhD thesis: Spatiotemporal control of gene expression in C. elegans
- Profiled chromatin landscape and transcriptome in *C. elegans* tissues isolated by flow cytometry and nuclei sorting.
- Designed & developed a biocomputational approach to resolve tissue-specific chromatin interactions *in silico*.
- Implemented single-cell RNA-seq and ATAC-seq experimental approaches and analysed data during *C. elegans* embryonic development.

Institut Curie   *Paris, France*
Master student, Raphaël Margueron lab   *Jan 2016 - May 2016*
Project: hBAP1 acts as a transcriptional activator independently of its H2A-K119Ub deubiquitinase activity
- Performed and analysed ChIP-seq, SILAC & Mass spectrometry, RNA-seq

University of California Los Angeles   *Los Angeles, California*
Placement year, Kathrin Plath lab   *Sep 2014 - Jul 2015*
Project: Role of Xist RNA repeats in X Chromosome Inactivation
- Performed and analysed long non-coding RNA Antisense Purification (RAP-seq), Nascent-RNA sequencing
- Performed and analysed ChIP-seq, RNA-seq and CLIP-seq, DNA/RNA-FISH

University of Navarra   *Pamplona, Spain*
Summer internship in Maite Huarte lab   *Jun 2014 - Aug 2014*
Project: Role of frequent long intergenic non-coding RNA amplifications or deletions in cancer phenotypes

Institut Curie   *Paris, France*
Summer internship in Edith Heard lab   *Jun 2013 - Aug 2013*
Project: Study of random monoallelic expression of autosomal genes

Skills

Basic computing	• Linux, Bash (advanced) • R (expert), Python (intermediate) • High-Performance Computing (slurm, AWS, Spark)
Bioinformatics	• **Integrative analysis of bulk and single-cell multiomics** • **10+ years using R/Bioconductor, 10+ public packages** • Automation of mapping and analysis pipelines • Data visualization
Data analysis	• Data mining using R (**9+ years**) or Python (**5 years**) • Data visualization using interactive dashboards (Shiny, Dash) • SQL databases (sqlite3, MySQL)
Workflow & data management	• CI/CD automation (git, Github Actions, Makefile, Snakemake, Nextflow) • Containerization and deployement (Docker, Singularity, Kubernetes, AWS) • Transparency & reproducibility (Quarto, Github Pages)
Web	• Static web: HTML5, CSS, Bootstrap, Hugo, Quarto
Languages	• English: fluent (TOEFL 2016: 110/120) • French: native • Spanish: intermediate

Selected bioinformatic resources

tidyCoverage	Extract and aggregate genomic track signals **[Bioconductor]**	*js2264/tidyCoverage*
HiCExperiment	Data structure for Hi-C in R **[Bioconductor]**	*js2264/HiCExperiment*
HiContacts	In-depth Hi-C investigation in R **[Bioconductor]**	*js2264/HiContacts*
HiCool	Process raw Hi-C data in R **[Bioconductor]**	*js2264/HiCool*
plyinteractions	Genomic grammar for genomic interactions **[Bioconductor]**	*js2264/plyinteractions*
OHCA	Orchestrating Hi-C analysis with Bioconductor **[Book]**	*js2264/OHCA*
BiocBook	Write, containerize and publish versioned Quarto books **[Bioconductor]**	*js2264/BiocBook*
periodicDNA	K-mers periodicity at small and large scale **[Bioconductor]**	*js2264/periodicDNA*
VplotR	Fragments density plots methodology **[Bioconductor]**	*js2264/VplotR*
RegAtlas	Tissue-specific regulatory atlas in C. elegans **[Shiny app]**	*js2264/RegAtlas*

Awards & funding

2023	**Travelling grant**, Gordon Conference *Chromosome Dynamics*	*Tuscany, IT*
2022	€2,400 (**1st place**), Hackathon **Digital 4 Genomics**: Predicting physical interactions between nuclear parasites and host chromosomes	*Evry, FR*
2022	€94,833, Post-doctorate fellowship from the Association pour la Recherche sur le Cancer	*Paris, FR*
2018	£500 (**1st place**), Cambridge Genomics Hackathon **>sudo: sequence**: Building an interactive platform to improve drug treatment decisions	*Cambridge, UK*
2016	£50,976, Medical Research Council Doctoral Training Grant	*Cambridge, UK*
2016	£6,000, Sackler Fund	*Cambridge, UK*
2012	€63,168, Studentship from École Normale Superieure Paris-Saclay	*Paris, FR*

Teaching

2022-2023	Workshop: Developing R/Bioconductor package for Genomics	*Physalia Courses*
2021-2023	Workshop: Single-cell RNA-seq analysis with R/Bioconductor	*Physalia Courses*
2021-2023	Workshop: NGS analysis for gene regulation and epigenomics	*Physalia Courses*
2020	Workshop: Introduction to Multi-omics Data Integration and Visualisation	*European Bioinfo. Institute, UK*
2018-2019	Teaching Assistant: Setting up and supervising practicals [NST 1A BoC]	*University of Cambridge, UK*
2017-2019	Supervision of master students (6 months lab internships)	*University of Cambridge, UK*

Publications

Equal contributions are marked with †, Ψ | All corresponding authors are marked ✉

In revision

- **Serizay J.** ✉, Koszul R.: "Summarising and visualising genomic track coverage with tidyCoverage". *Initial review at Bioinformatics* [bioRxiv: 10.1101/2024.01.27.577537]

- Chapard C. Ψ, Meneu L. Ψ, **Serizay J. Ψ** ✉, Westbrook A., Routhier E., Ruault M., Bignaud A., Thierry A., Gourgues G., Lartigue C., Piazza A., Taddei A., Beckouët F., Mozziconacci J. ✉ and Koszul R. ✉: "Exogenous chromosomes reveal how sequence composition drives chromatin assembly, activity, folding and compartmentalization". *Invited for revision after review at Science* [bioRxiv: 10.1101/2022.12.21.520625]

Published

- **Serizay J.** ✉, Matthey-Doret C., Bignaud A., Baudry L., Koszul R.: "Orchestrating chromosome conformation capture analysis with Bioconductor". *Nature Communications (2024)*. 10.1038/s41467-024-44761-x

- Hutchison W. J. Ψ, Keyes T. J. Ψ, Crowell L. H., **Serizay J.**, Soneson C., Yuan V., Davis E. S., Sato N., Moses L., Tarlinton B., Nahid A. A., Kosmac M., Clayssen Q., Yuan V., Mu W., Park J., Mamede I., Ryu M. H., Axisa P. P., Paiz P., Poon C. L., Tang M., , Gottardo R., Morgan M., Lee S., Lawrence M., Hicks S. C., Nolan G. P., Davis K. L., Papenfuss A. T. ✉, Love M. ✉, Mangiola S. ✉: "The tidyomics ecosystem: Enhancing omic data analyses". *Nature Methods (2024)*. 10.1101/2023.09.10.557072

- **Serizay J.** ✉, Ahringer J.: "Generating fragment density plots in R/Bioconductor with VplotR". *Journal of Open-Source Software (2021)*. 10.21105/joss.03009

- **Serizay J.** ✉, Ahringer J. ✉: "periodicDNA: an R/Bioconductor package to investigate k-mer periodicity in DNA". *F1000Research (2021)*. 10.12688/f1000research.51143.1

- **Serizay J.**, Dong Y., Jänes J., Chesney M., Cerrato C., Ahringer J. ✉: "Distinctive regulatory architectures of germline-active and somatic genes in C. elegans". *Genome Research (2020)*. 10.1101/gr.265934.120

- Pandya-Jones A., Markaki Y., **Serizay J.**, Chitiashvili T., Mancia Leon W. R., Damianov A., Chronis C., Papp B., Chen C.-K., McKee R., Wang X.-J., Chau A., Sabri S., Leonhardt H., Zheng S., Guttman M., Black D. L. ✉, Plath K. ✉: "A protein assembly mediates Xist localization and gene silencing". *Nature (2020)*. 10.1038/s41586-020-2703-0

- Athie A., Marchese F. P., González J., Lozano T., Raimondi I., Kumar Juvvuna P., Abad A., Marin-Bejar O., **Serizay J.**, Martínez D., Ajona D., Jose Pajares M., Sandoval J., Montuenga L. M. , Kanduri C., Lasarte J. J., Huarte M. ✉: "Analysis of copy number alterations reveals the lncRNA ALAL-1 as a regulator of lung cancer immune evasion". *Journal of Cell Biology (2020)*. 10.1083/jcb.201908078

- Jänes J. †, Dong Y. †, Schoof M. Ψ, **Serizay J. Ψ**, Appert A., Cerrato C., Woodbury C., Chen R., Gemma C., Huang N., Kissiov D., Stempor P., Steward A., Zeiser E., Sauer S., Ahringer J. ✉: "Chromatin accessibility dynamics across C. elegans development and ageing". *eLife (2018)*. 10.7554/eLife.37344

- **Serizay J.**, Ahringer J. ✉: "Genome organization at different scales: nature, formation and function". *Current Opinion in Cell Biology (2018)*. 10.1016/j.ceb.2018.03.009

Selected scientific communication

9th Gordon Conference *Chromosome Structure and Function*, Rhode Island (USA) — 2024 | Talk: Emergence of vertebrate heterochromatin features in foreign DNA integrated into a eukaryotic nucleus (selected)

JOBIM, Toulouse (France) — 2024 | Talk: Integrating Hi-C data in multi-omics studies (invited)

20th annual Bioconductor Conference, Michigan (USA) — 2024 | Workshop: Applying tidy principles to investigate chromatin composition and architecture (organizer)

Replication, Repair, Recombination, Leucate (France) — 2024 | Talk: Rescuing replication during the multiciliation cell cycle variant (selected)

European Bioconductor Conference, Ghent (Belgium) — 2023 | Developer session: writing versioned online documentation with Bioconductor (organizer)

19th annual Bioconductor Conference, Boston (Massachusetts) — 2023 | Package demonstration: Orchestrating Hi-C analysis with Bioconductor (selected)

9th Gordon Conference *Chromosome Dynamics*, Tuscany (Italy) — 2023 | Talk: Cyclin-dependent chromatin remodeling in cell cycle variant (selected)

5th EMBO European Cilia Conference, Cologne (Germany) — 2022 | Talk: Identification of a new cell cycle variant during multiciliated cell differentiation (selected)

2nd annual Qlife conference (Online) — 2021 | Talk: Co-opting the mitotic machinery to differentiate (invited)

Systems Biology: Global Regulation of Gene Expression, CSHL (New York) — 2020 | Poster: Distinct regulatory architectures of germline and soma genes in *C. elegans* (selected)

International *C. elegans* Conference, UCLA (California) — 2019 | Talk: Distinct regulatory architectures of germline and somatic genes (selected)

International *C. elegans* Conference, UCLA (California) — 2017 | Poster: Profiling tissue-specific chromatin parameters during *C. elegans* development (selected)

Shell Research Conference (Cambridge, UK) — 2017 | Poster: Functional roles of chromatin dynamic organization in tissue-specific gene regulation (selected)