Jacques Serizay

Post-doctorate Fellow in Genomics

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Research fellow with 10+ 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. I support **strong collaborations** to gain new insights into biological problems and I actively promote **reproducibility**, **FAIR principles** and **knowledge dissemination**.

Education

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

EntrepriseTECH Degree — *Cambridge, UK*
Judge Business School, University of Cambridge — *2018-2019*

Ecole Normale Superieure de Paris-Saclay Degree — *Paris, France*
ENS Paris-Saclay, Biology Department — *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*

Recent research experience

Institut Pasteur & Ecole Normale Supérieure — *Paris, France*
Post-doctorate fellow, Romain Koszul lab & Nathalie Spassky lab — *Sep 2020 - Current*

- Developed collaborations that advanced understanding of chromatinization in foreign chromosomes, bridging experimental and computational perspectives.
- Spearheaded cross-laboratory research integrating single-cell transcriptomics and epigenomics to investigate chromatin dynamics.
- Led development of biocomputational tools, establishing new methodologies for data integration and visualization in large-scale epigenomic studies.

University of Cambridge — *Cambridge, UK*
PhD student, Julie Ahringer lab | Thesis: Spatiotemporal control of gene expression in C. elegans — *Sep 2016 - Aug 2020*

- Led pioneering studies on chromatin architecture in *C. elegans* using a combination of flow cytometry, high-throughput genomics and bioinformatics.
- Developed in silico pipelines for analyzing tissue-specific chromatin interactions, improving genome-wide data processing capabilities.

Scientific and professional appointments

Elected member of the Technical Advisory Board — *International*
Bioconductor consortium — *2024 - Current*

- Contribute to strategic decisions and technical leadership for advancing bioinformatics research.
- Spearhead initiatives promoting open-source tool development within the consortium.

Certified Carpentries Instructor — *International*
The Carpentries organization — *2024 - Current*

- Lead workshops to teach foundational programming and data science skills to researchers.
- Advocate for accessible education in computational skills, improving research capacity.

Package reviewer — *International*
Bioconductor consortium — *2024 - Current*

- Engage in reviewing new tools, fostering innovation across the Bioconductor ecosystem.
- Ensure quality and adherence to coding standards for bioinformatics packages.

Founding member of the Tidyomics working group *International*

Bioconductor consortium *2023 - Current*

- Develop and promote tidy principles for multi-omics data analysis.
- Facilitate collaborations to enhance reproducibility and data integration practices.

Skills

Core Programming **R** *[expert]*, **Python** *[advanced]*, **HPC** *[Slurm, TileDB]*, **Cloud** *[AWS, GCP, Azure]*, **versioning** *[git, GitHub]*

Data analysis **Machine learning** *standard, deep-learning*, **SQL** *[sqlite3, MySql]*, **interactive dashboards** *[Shiny, Dash]*

- Adapt and optimize machine-learning approaches to solve biological problems.
- Implement cloud-native framework to store, manipulate and analyze high-dimensional datasets.
- Develop bespoke data analysis pipelines to streamline biological discovery and hypothesis testing.
- Full-stack development of interactive dashboards to visualize complex multi-omics datasets for real-time data exploration.

Data management **CI/CD** *[Nextflow, Makefile, Snakemake, Github Actions]*, **Containerization** *[Docker, Singularity, Kubernetes]*

- Implement CI/CD procedures to automate workflows, ensure reproducibility and scalability.
- Lead initiatives to enhance data versioning and workflow automation, improving collaboration across interdisciplinary teams.

Bioinformatics **Package development** *[R, Bioconductor]*, **Multi-omics integration**

- Specialize in the integration and analysis of multi-omics datasets, with a focus on chromatin interactions, gene regulation, and epigenomics.
- Employ bioinformatics tools to address complex biological questions, contributing to new discoveries in regulatory genomics.

Selected bioinformatic resources

Full list of public projects on Github: github.com/js2264

momics	Cloud-native tool to manage and manipulate large-scale genomic data **[Pypi]**	*pypi/momics*
tidyCoverage	Extract and aggregate genomic track signals **[Bioconductor]**	*js2264/tidyCoverage*
plyinteractions	Genomic grammar for genomic interactions **[Bioconductor]**	*js2264/plyinteractions*
OHCA	Orchestrating Hi-C analysis with Bioconductor **[Technical book]**	*js2264/OHCA*
HiCExperiment	Data structure for Hi-C in R **[Bioconductor]**	*js2264/HiCExperiment*
HiContacts	In-depth Hi-C investigation in R **[Bioconductor]**	*js2264/HiContacts*
BiocBook	Write, containerize and publish versioned Quarto books **[Bioconductor]**	*js2264/BiocBook*
periodicDNA	K-mers periodicity at small and large scale **[Bioconductor]**	*js2264/periodicDNA*
RegAtlas	Tissue-specific regulatory atlas in C. elegans **[Shiny app]**	*js2264/RegAtlas*

Awards & funding

National and international recognition of my scientific achievements

2024	**Best presentation**, Gordon Research Conference *Chromosome Structure and Function*	*Rhode Island, USA*
2023	**Travelling grant**, Gordon Research Conference *Chromosome Dynamics*	*Tuscany, IT*
2022	**1st place (€2,400)**, Hackathon **Digital 4 Genomics**: Predicting physical interactions between nuclear parasites and host chromosomes	*Evry, FR*
2022	**Research fellowship (€94,833)**, Association pour la Recherche sur le Cancer	*Paris, FR*
2018	**1st place (€500)**, Cambridge Genomics Hackathon **>sudo: sequence**: Building an interactive platform to improve drug treatment decisions	*Cambridge, UK*
2016	**Student fellowship (£56,976)**, Medical Research Council Doctoral Training Grant	*Cambridge, UK*
2012	**Student fellowship (€63,168)**, Studentship from École Normale Superieure Paris-Saclay	*Paris, FR*

Teaching

Carpentries-certified Instructor strongly engaged in teaching

2022-2025	Workshop: Developing R/Bioconductor package for Genomics	*Physalia Courses*
2021-2025	Workshop: Single-cell RNA-seq analysis with R/Bioconductor	*Physalia Courses*
2021-2025	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-today	Supervision of PhD students (3) and Master students (4)	*France, UK*

Publications

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

Peer-reviewed

• Meneu L. Ψ, Chapard C. 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. ✉: "Sequence-dependent activity and compartmentalization of foreign DNA in a eukaryotic nucleus". ***Science*** *(In press).* 10.1101/2022.12.21.520625

• **Serizay J.** ✉, Khoury Damaa M., Boudjema A.-R., Balagué R., Faucourt M., Delgehyr N., Zaragosi L.-E., Barbry P., Spassky N., Koszul R., Meunier A. ✉: "Cyclin switch tailors a cell cycle variant to orchestrate multiciliogenesis". ***Cell Reports*** *(In press).* 10.1101/2024.05.22.595357

• Khoury Damaa M., **Serizay J.**, Balagué R., Boudjema A.-R., Facourt M., Delgehyr N., Cameron J., Lu H., Roy S., Legendre M., Omran H., Arnold S., Gil-Gómez G., Zaragosi L.-E., Magnone V., Barbry P., Koszul R., Spassky N., Meunier A. ✉: "Cyclin O is a driver of multiciliated cells differentiation cell-cycle variant". ***Cell Reports*** *(In press).* 10.1101/2024.05.22.595363

• **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

• **Serizay J.** ✉, Koszul R.: "Summarising and visualising genomic track coverage with tidyCoverage". ***Bioinformatics*** *(2024).* 10.1093/bioinformatics/btae487

• 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

In revision

• Singh P. Ψ, **Serizay J. Ψ**, Couble J. Ψ, Cabahug M. D., Rosa C., Chen P., Scherf A., Koszul R., Baumgarten S., Bryant J. M. ✉: "Micro-C reveals MORC/ApiAP2-mediated links between distant, functionally related genes in the human malaria parasite". ***Nature Microbiology*** [bioRxiv: 10.1101/2024.08.28.610079]

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

JOBIM, Toulouse (France) — 2024
Talk: Integrating Hi-C data in multi-omics studies (invited)
Center for Theoretical Biological Physics meeting: *Physics meets Biology*, Paris (France) — 2024
Talk: DNA sequence dictates transcriptional activity of exogenous DNA integrated in yeast
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)