Detailed Program

JOBIM 2026
30 JUIN>3 JUIL
Strasbourg

Tuesday June 30th 2026

11:30 – 13:00 Hall	**Registration**
13:15 – 13:30 Amphi Cavailles	**Opening remarks**
13:30 – 14:30 Amphi Cavailles	**Keynote - Hugues Roest Crollius** - Chair: Isabel Alves The evolution of 568 vertebrate genomes during 400 million years
14:30 – 14:40 Amphi Cavailles	**Sponsored Talk - Jules Deforges** (Transgene) From neoantigen prediction to clinical response: bioinformatics-driven development of individualized cancer vaccines
Amphi Cavailles	**Session: Genomic Variation and Sequence Analysis Methods -** Chair: Audrey Bihouée
14:45 – 15:05	NanoVar: a comprehensive workflow for structural variant detection to uncover the genome's hidden patterns - Touati Benoukraf
15:05 – 15:25	DrMAB: Framework to track mutations of concern in respiratory viruses - Jérôme Bourret
15:25 – 15:45	Pangenome graph node-phenotype association shows GWAS-like quality results but using only few individuals - Camille Carrette
Amphi 3	**Session: Biological Networks and Systems Modeling** - Chair: Yannis Nevers
14:45 – 15:05	Fast and robust graph construction from KEGG metabolic and genomic data - Florent Cabret
15:05 – 15:25	Backtrack-free network propagation with in-degree normalization - Jędrzej Kubica
15:25 – 15:45	KGATE: A tool for graph representation learning applied to Biomedical Knowledge Graphs - Benjamin Loire
Amphi 4	**Session: Protein Dynamics and Conformational Landscapes -** Chair: Claudine Mayer
14:45 – 15:05	Exploration of multiconformers to extract Information about structural deformation undergone by a protein target: Illustration on the Bcl-xL target - Leslie Regad
15:05 – 15:25	Closing the sampling-scoring gap: a MassiveFold study in CASP16 - Nessim Raouraoua
15:25 – 15:45	Benchmark bias and conformational dynamics in allosteric site prediction - Victor Pryakhin
15:45 – 16:15 Hall	**Coffee Break**
Amphi Cavailles	**Session: Evolving Genomes** - Chair: Isabel Alves
16:15 – 16:35	Epidemics of temperate phages and what's left of them in bacterial genomes - Julien Guglielmini
16:35 – 16:55	De novo genes in diatoms - Alix Boutheroue-Desmarais
16:55 – 17:15	Decoupling phenotypic from genetic pleiotropy during evolution on a complex genotype-phenotype-fitness map - Théotime Grohens
Amphi 3	**Session: RNA Biology and Transcriptomics** - Chair: Anne Friedrich
16:15 – 16:35	Long and small RNA annotation reveals extensive gene expression changes during chicken and pig development - Cervin Guyomar
16:35 – 16:55	Cluefish: a workflow for comprehensive biological interpretation of transcriptomic data series - Ellis Franklin
16:55 – 17:15	phyloDS: An RNA-seq data-driven method for differential splicing analysis across species - Arnaud Liehrmann

Amphi 4	**Session: From Molecular Motions to Generative Drug Design** - Chair: Claudine Mayer
16:15 – 16:35	BeeRNA: tertiary structure-based RNA inverse folding using Artificial Bee Colony - Mehyar Mlaweh
16:35 – 16:55	Visualization-driven pipeline for drug design through generative AI - Lucas Rouaud
16:55 – 17:15	Intrinsic Conformational Dynamics of Apo HIV-2 Protease Reveal Two Dynamical Phases and Multiple Closed Flap States - Marine Baillif

Amphi 3	**Demos 1**
17:15 – 17:45	SaVanache : Interactive Visualization of Pangenomic Diversity -Mourdas Mohamed
17:45 – 18:15	Gaston 2, a C++ library and an R package for large-scale genotype data - Hervé Perdry

Amphi 4	**Demos 2**
17:15 – 17:45	madbot, a metadata and data brokering online tool to ensure the adoption of standards and FAIR principles in an open science context - Imane Messak

17:15 – 18:15 Hall	**Posters A**

1 Sponsor Transgene - VacDesignR®: a computational tool to optimize viral-based individualized neoantigen therapeutic vaccine production - Anne-Isabelle Moro
2 Summary of the MERIT/SFBI Survey on the Working Conditions of Bioinformaticians - Merit Bureau
3 MIMEco: Multi-objective metabolic modeling to predict and explain pairwise ecosystem interactions - Anna Lambert
4 Multi-omics network integration across disease progression in myotubular myopathy - Supriya Priyadarshani Swain
5 A mathematical framework to accurately reconstruct cell lineage from single cell transcriptomics on barcoded cells: application for therapeutics optimization - Annabelle Ballesta
6 InSillyClo: How to make large-scale golden gate cloning and MoClo workflows user-friendly and reproducible - Bryan Brancotte
7 Unravelling hyperglycemia in diabetic cardiomyopathy: a multivalued computational approach - Sahar Aghakhani
8 DynAA: Characterizing the dynamics of antibody-antigen interfaces using Molecular Dynamics simulations - Louise Lam
9 Generating Chain Mappings in Large Protein Structures - Pierre Berriet
10 Understanding the Structural Landscape of Self-Incompatibility in Arabidopsis halleri through AI-Driven Protein Interaction Modeling. - Thomas Binet
11 Mfd's connectors at the heart of its extensive reshaping - Thomas Marino
12 AlphaFold-Multimer Predictions : Which Scores Best Identify True Protein–Protein Interactions in the TGF-β Activation Network? - Elisa Chenel
13 A benchmark dataset for analyzing the functional fate of duplicate gene pairs in the model plant Arabidopsis thaliana - Erine Benoist
14 Comparative genomics of phenotypic convergence and diversity in fishes - Alice Regnier
15 Elucidation and modeling of the insertion mechanism driving high pathogenicity avian influenza emergence - Aldair Martin Martinez Pineda
16 Reproducible SNP-based phylogenomics reveals the population structure of multidrug-resistant Salmonella enterica serovar Kentucky ST198 in Burkina Faso - Marguerite Edith Malatala Nikiema
17 An integrated long-read bioinformatics pipeline for resolving the genetic diversity of Plasmodium falciparum csp in Burkina Faso - Emilie Badoum
18 Transposable element dynamics in a conserved genomic segment of Pea revealed by comparative and pangenomic analysis - Mathieu Cartier
19 T2T genome assembly of a basal nematode reveals a plant horizontal gene transfer and a complete epigenetic regulation toolkit - karine Robbe-Sermesant
20 Unlocking Microbial Dark Matter genomes using microscopy and Single-Cell Sequencing - Lucile Martin
21 Unravelling the fine-scale genotype diversity and evolution of grapevine fanleaf virus - Sélim Ben Chéhida
22 Charting the Evolution of Protein Splice Variations Across the Tree of Life - Hugues Richard
23 Defining Populations in the Presence of Admixture: Insights from Saccharomyces cerevisiae Genomics - Louis Ollivier
24 PanExplorer2 : Explore multi-scale genetic markers derived from pangenome graphes for interactive comparative genomics and diversity analyses - Alexis Dereeper
25 Investigating the evolution of phototrophy in Pseudomonadota - Timothée Salzat-Hervouette
26 Profylo: A Python Package for Phylogenetic Profile Comparison and Analysis - Martin Schoenstein
27 Designing genome annotation tools to investigate the evolution of bioenergetic enzymes - Alexis Nguyen
28 MSEABOARD: An open source and web-based interactive platform for linked visualization and analysis of bioinformatics data - Luca Nesterenko
29 eHGTDB: A web platform for the exploration and visualization of horizontal gene transfer events in eukaryotes - Corinne Rancurel

30 Automated construction of Boolean models using knowledge graphs - Nina Alger
31 Geom@nnot: Environmental Metadata Enrichment from Biosample Coordinates - Mélodie Fleury
32 Data mining of public genomic repositories: harnessing off-target reads to expand microbial pathogen genomic resources - Damien Richard
33 LLM Training Dataset for Plant Biology & Food Processing Literature - Tom Colombu
34 Extending the Semantic Metabolomics Data Lake: Integrating Plant and Food Transformation Ontologies for Enhanced Knowledge Graphs - Isaac Karaman
35 Community Detection in a Plant-based Fermentation Knowledge Graph - Zoé Le Roux
36 A Multiomic Atlas of Human Microprotein-Coding Intronic Polyadenylation Isoforms - Matthaus Sirvent
37 MicroScope, an Integrated Platform for the Annotation and Exploration of Microbial Gene Functions through Genomic, Pangenomic and Metabolic Comparative Analysis - Noëlle Haddad
38 Digital Twins of Organoids: a Knowledge Graph of human organoids omics dataset - Kenza Zeghari
39 SNPer, a web app for annotated variant mining - Frédérique Bitton
40 RO-crate as a metadata source for the FAIDARE global federation – Etienne Bardet
41 Spirochase, easy-to-navigate portal to explore proteomes in Spirochaetes phylum - Elodie Chapeaublanc
42 pan2met: predicting metabolic networks at the scale of microbial pangenomes - Samuel Ortion
43 HaploExplore, a software specifically designed for the detection of minor allele (MiA-) haploblocks - Samuel Hiet
44 A Course-Undergraduate Research Experience (CURE) to explore the effect of structural variants on gene expression in C. elegans balancers - Tatiana Maroilley
45 International Society for Computational Biology Student Council Regional Student Group France (RSG France) : Association of Young Bioinformaticians of France (JeBiF) - Elisabeth Hellec
46 Inferring Cell Fate Trajectories in Time-Resolved Metabolic RNA Labeling data - Anna Audit
47 D-Genies2 : dot plot large genomes in an interactive, more efficient and simpler way - Christophe Klopp
48 Minimal feature set selection for spatial transcriptomics data clustering and preventing over-clustering - Tess Chilliet
49 Bridging Scales: A Multi-Level Graph Neural Network for Protein Function Prediction - Antoine Toffano
50 Revisiting Effector Prediction Datasets using Protein Language Model Embedding Spaces - Fanny Xie
51 Prédiction d’expression différentielle à partir des variants génomiques - Elliot Butz
52 Development of a metabolic score predictive of survival in patients with Multiple Myeloma - Philippe Laurent
53 An integrated R package for interpretable deep learning on multi-omics data in system immunology - Philippe Stocker
54 Robust genotyping of grapevine fanleaf virus variants using amplicon-based Illumina sequencing - Pierre Mustin
55 CurateMake: a reproducible multi-source workflow for ITS reference database curation in metabarcoding - Auguste Gardette
56 Automatic characterization of regulatory elements in the human genome using multimodal integration of '-omics' data - Julien Raynal
57 Evaluation of 7 jDR methods for multi-omics survival prediction: a benchmark study on 18 cancer datasets - Vincent Le Goff
58 scRAW: Representation learning for rare cell population identification - Victoria Bourgeais
59 Genome-wide DNA methylation profiles identify molecular predictors of measurable residual disease in the MIDAS Trial - Céline Chevalier
60 Methodological approach for RNA edition analysis: a brain tissue case study - Julie Le Borgne
61 PasteurAIze: A Multi-Agent Platform for Secure Natural Language Biomedical Data Analysis - Rémi Planel
62 Text2Meta: Automated Extraction and Structuring of RNA-seq Metadata from Scientific Publications using Large Language Models - Dylan Pin
63 Improving viral protein clustering using both diversified protein profiles and structural information - Quentin Nugier
64 AI-stro: a neuro-symbolic approach to astrocyte regulation in artificial neural networks - Anne Jeannin-Girardon
65 Stability selection algorithm for biomarkers selection in high dimensional data - Thomas Carvaillo
66 Assessing the structure of DNA embedding spaces using graph-based comparisons - Juliette Francis
67 Knowledge graph–driven discovery of drought tolerance genes in sorghum - Quentin Secher
68 Preliminary work on the development of a Knowledge-Distillation based framework able to handle missing modalities in the context of multi-omics integration - Mary Savino
69 Comparative Evaluation of Genomic Foundation Models for Regulatory Sequence Classification in Plant Genomes - Pierre Larmande
70 Computational deciphering and mathematical modeling of the regulatory networks controlling plasmacytoïd dendritic cell biology - Arafate Idrissou
71 Statistical learning for predicting gene expression from transcription factor expression - Manal Bezia
72 Family-level classification of viral contigs using deep learning - Emma Soufir
73 Evaluation of Helixer for structural genome annotation in non-model organisms - Audrey Onfroy
74 Assessing Dorado pseudourydilation RNA modification prediction on Arabidopsis thaliana ribosomal RNA - Emma Rodriguez
75 Latent Differential Graphical model for Multi-Tissue and Multi-Omics integration to model molecular interaction networks under multiple Radiation Exposure groups - Asma Nouira

76 Preliminary evaluation of the Transfer Learning capabilities of MOTL for multi-omics cancer survival analysis - Arnaud Gloaguen
77 KmerExploR: Fast and easy biological quality control of RNA-Seq data based on k-mers - Camelia Sennaoui
78 A bioinformatics pipeline for de novo detection of tandem repeats in common bean genomes - Maisen Hassani
79 DeCovarT: Network-Driven Deconvolution of Transcriptomics data to dissect organoid Cellular Heterogeneity - Bastien Chassagnol
80 Computational prediction of transcription factor binding to DNA using deep learning - Agathe Bancquart
81 NARCOD: Non-Arbitrarily Reproducible Clustering of transcriptOmics Data - Christophe Le Priol
82 Functional AI-nnotation: Unlocking the "Orphan" Proteome - Damien Mornico
83 Are deep learning methods accurate to predict protein functions in marine organisms? - Rodrigo Salinas
84 Augmentating Pangenome Variation Graph With Low-coverage Sequencing for Haplotype Inference - Julien Chevreau
85 Scalable machine learning for large-scale genomic source attribution of L. monocytogenes - Isis Lorenzo
86 InterProScan 6: a modern large-scale protein function annotation pipeline - Matthias Blum
87 Evaluating protein representations from domain architectures - Sheyenne Nguyen
88 PASTEC: An Automatic Transposable Element Classification Tool - Mohamad Yassine
89 Large-scale single-cell characterization of tumor cell subpopulations in breast cancer - Quentin Rott
90 Automatic Mapping of UnLabelled Extracellular Transcripts (AMULET) for sparse spatial transcriptomics data - Gabriel Duval
91 Few-shot learning strategy for Predicting Meropenem Resistance genes in Escherichia coli - Meriem Youssef
92 Characterization of grapevine fanleaf virus diversity and recombination events using complementary sequencing approaches - Jeanne Juquel
93 Optimizing Grapevine Fanleaf Virus Diagnostics: A Statistical Model for Representative Sampling in Infected Vineyards - Eva Chevalier
94 The Virome@tlas project: from systematic harmonization of nucleotide sequence archives metadata to large-scale One Health applications - Elea Pauliat

18:15 - 19:30 Hall	**Welcome Cocktail**

Wednesday July 1st 2026

9:00 – 10:00 Amphi Cavailles	**Keynote - Laura Cantini** - Chair: Anaïs Bardet Multi-modal learning for single-cell multi-omics integration
10:00 – 10:30 Hall	**Coffee Break**
Amphi Cavailles	**Session: Spatial and Single-Cell Genomics** - Chair: Laura Cantini
10:30 – 10:50	Spatial transcriptomic analysis reveals region-specific glial activation during epileptogenesis - Adrien Dufour
10:50 – 11:10	Spatiotemporal regulation of cell cycle states within the complex tumor microenvironment - Gianni Zanardelli
11:10 – 11:30	A consensus-driven framework for building and sharing single-cell atlases applied to pancreatic ductal adenocarcinoma - Lucie Lamothe
Amphi 3	**Session: Knowledge Graphs and Biomedical Data Integration** - Chair: J. van Helden
10:30 – 10:50	Knowledge graph mining linking endometriosis and pollutants – Meije Mathé
10:50 – 11:10	Holograph: a generic RDF schema to handle data from agroecological holobionts - Marie Lahaye
11:10 – 11:30	Combining phenotypic similarity and network propagation to improve performance and clinical consistency of rare disease diagnosis - Maroua Chadil
Amphi 4	**Session: Machine and Representation Learning** - Chair: Yannis Nevers
10:30 – 10:50	Adversarial Domain Adaptation Enables Knowledge Transfer Across Heterogeneous RNA-Seq Datasets - Kevin Dradjat
10:50 – 11:10	Phage evolutionary relationships emerge from protein language model-based proteome representation - Swapnesh Panigrahi
11:10 – 11:30	PLM-View : Protein Language Models for fast, accurate, interpretable functional classification - Vinh-Son Pho

Amphi 3 11:30 – 12:00	**Demos 3** VCFProcessor: a complete toolbox for improved VCF file analysis - Thomas Ludwig
Amphi 4 11:30 – 12:00	**Demos 4** MOAL - Multi-omic analysis at lab - a R package to improve the accessibility and accessibility and reproducibility of omics analysis - Florent Dumont
11:30 – 12:00 Hall	**Posters A** – Identical to previous day (Please remove your poster on Wednesday afternoon)
12:00 – 13:30	**Lunch** - Resto U Paul Appell
13:30 – 14:30 Amphi Cavailles	**Keynote IFB - Christophe Dessimoz** - Chair: Morgane Thomas-Chollier Open biological databases as strategic infrastructure: from research to competitiveness and sovereignty
14:30 – 15:30 Amphi Cavailles	**Assemblée Générale Société Française de Bio-Informatique** (AG SFBI)
15:30 – 16:00 Hall	**Coffee Break**
16:00 – 17:00 Amphi Cavailles	**Bioinformatics Networks** (SFBI, IFB, GDR BIMMM, MERIT...)
17:00 – 20:00	**Social activities** (see below)

Thursday July 2nd 2026

9:00 – 10:00 Amphi Cavailles	**Keynote - Daniel Jost** - Chair: Charles Lecellier Deciphering the structure-function relationship of chromatin: from experiments to modeling and back
10:00 – 10:30 Hall	**Coffee Break** (Group Photo on the terrace at 10:00)
Amphi Cavailles	**Session: Epigenomics and Genome Regulation** - Chair: Anaïs Bardet
10:30 – 10:50	Sister-chromatid analysis to study strand-specific DNA methylation maintenance during DNA replication - Manon Coulée
10:50 – 11:10	Circulating DNA reveals nucleosome occupancy patterns that are associated with nucleosome-DNA affinity and are affected in cancer - Marianne Richaud
11:10 – 11:30	Genomic analysis of the factors influencing the localization of recombination events and the segregation of genetic determinants of quality in an interspecific context in the genus Vitis - Léonie Chrétien
Amphi 3	**Session: Microbial Genomics and Metagenomics** - Chair: Mahendra Mariadassou
10:30 – 10:50	Updating and using a Hidden Markov Models-based algorithm to detect Anti-Microbial Resistance sequences in French soils metagenomes - Zéphyrin Enaux
10:50 – 11:10	De novo assembly pipeline for the characterization of the Mandrillus sphinx microbiome using massive sequencing data - Raphaël Ribes
11:10 – 11:30	Advancing Neisseria Gonorrhoeae Surveillance through Long-Read Sequencing, Pangenome Graphs, and Mass Spectrometry - Hugues Richard
Amphi 4	**Session: Data Analysis Methods and Scientific Workflows** - Chair: Yannis Never
10:30 – 10:50	A Statistical Workflow Combining Full-Scan and Targeted Analyses for Identifying Candidate Volatile Compounds from SIFT-MS Data - Axel Mercier
10:50 – 11:10	ShareFAIR-KG, a centralised knowledge base of scientific workflows - Marie Schmit
Amphi 4 11:10 – 11:30	AlignMarkers: a pipeline for accurate context sequence-based placing of molecular markers across genomes and assemblies - Camille Auneau

Amphi 3
11:30 – 12:00

Demos 5
Pixitainer: frictionless apptainer image generation from a pixi workspace - Raphaël Ribes

Amphi 4
11:30 – 12:00

Demos 6
Depictio: an open-source platform for building interactive dashboards from bioinformatics workflow outputs - Thomas Weber

11:30 – 12:00
Hall

Posters B

1 Sponsor Transgene - VacDesignR®: a computational tool to optimize viral-based individualized neoantigen therapeutic vaccine production - Anne-Isabelle Moro
2 Summary of the MERIT/SFBI Survey on the Working Conditions of Bioinformaticians - Merit Bureau
3 Scientific Workflow Reuse in Practice: An Empirical Study of Nextflow Pipelines - Lénora Buggenhoudt
4 Enhancing Genomic Prediction Accuracy for Complex Traits in Cassava (Manihot esculenta) Through Pangenome-Informed Variant Calling - Isaac Abegunde
5 Open Science: A Catalogue of European Tools Supporting Research Data Management - Saliha Zenboudji-Beddek
6 Building a cassava pangenome to explore the genetic diversity of local cassava varieties from Côte d'Ivoire - Cyrielle Ndougonna
7 Modernizing ATGC Bioinformatics Services: Migration to a Shared Meso-Centre and API-Driven Delivery - Christophe Menichelli
8 Comparing reference-based SNP analysis and k-mer approaches to assess genomic diversity of yam accessions from Burkina Faso within West African germplasm - Sory Siedou
9 Inter-individual variability in transcriptomes: what methods can already be used and why should it be analysed? - Simon Thiry
10 Leveraging atlas-level single cell resources as reference panels for bulk RNA-seq deconvolution - Massimiliano Cocca
11 Optimizing de novo assembly of RCA-enriched circular ssDNA viral genomes using long-read sequencing - Pakyendou Estel Name
12 Bridging the gap in computational biology: genomic surveillance and bioinformatic innovation for plant health and food security in Africa - Justin S. PITA
13 Refining a Knowledge Graph Embedding library for reproducibility: the example of KGATE - Célia Brahimi
14 Bioinformatic development for Nanopore epigenomics: building reproducible workflows for methylation analysis and beyond - Mélina Farshchi
15 Tackling the scRNA-seq integration challenge with a reproducible benchmarking framework - Sara Boughaba
16 mETHYLotest: a unified toolkit for multi-platform DNA methylation analysis - Nicolas Doldi
17 Genome annotations in ATLASea: using BEAURIS for their generation, FAIR handling and exploration within genomic web portals - Romane Libouban
18 CARTOMIX: A generic web tool for the exploration of genome organization - Wolimata Diaw
19 Frhap: A flexible Snakemake Workflow for haplotype frequency estimation in tGBS data - Abdelkarim Wahnou
20 A snakemake pipeline to genotype large sets of short reads on a pangenome using pangenie - Martin Racoupeau
21 DeconvolisSTa - Deconvolution of Spatial Transcriptomics dAta - Slim Karkar
22 PHAREOM: streamlining multi-omics for translational research - Olivier Feudjio
23 madbot national working group : join us to participate to the development and adoption of madbot for FAIR data and metadata management - Thomas Denecker
24 Developping a reusable and robust microbiota analysis pipeline using non-robust methods - Corentin Lucas
25 GPU pipeline and interactive interface for large-scale single-cell data analysis and visualization - Astrid Delépine
26 Development in R of a processing pipeline integrated into an interface for flow cytometry data analysis - Camellia Lambert
27 Structuring and Interoperability of Thematic Data Management Plans for Research Entities - Sylvain Milanesi
28 ONTmethPLANT: a reproducible pipeline for integrated analysis of DNA methylation and genomic variants from Oxford Nanopore data in plants - Mame Seynabou Fall
29 SnakeVir: A Snakemake Workflow for Viral Metagenomics - Florian Charriat
30 OpenMetaBar & BarCodeR: two complementary tools for metabarcoding analyses - Matéo Léger-Pigout
31 RDMkit efficiently manages metabarcoding and metagenomic data - Clara Emery
32 Improving accessibility of machine learning models in bioinformatics - Pauline Le Corre
33 ATLASea : Challenges in building a comprehensive dataset in marine genomics - Isaline Guerin
34 OSPIL, save your data, save the world - Loik Galtier
35 ATLASea BYTE-Sea: Navigating IT Systems and Web Portals for Sample Tracking and Marine Data Exploitation - Loraine Brillet-Guéguen
36 IFB-Biosphère Cloud, Multi-Cloud Infrastructure for Life Sciences - Christophe Blanchet

37 Pipeline for the detection and quantification of ribosomal RNA nucleotidic variants from long read Oxford nanopore sequencing datasets - Allyson Moureaux
38 BYTE-Sea: Advances in the development of the digital infrastructure for ATLASea, the French marine genome sequencing programme - Annie Lebreton
39 How metagenomic analysis strategy shapes functional inference? Metabolic landscapes from Le French Gut Cohort - Toubal Sarah
40 Cloud4SAMS: a trusted research environment to handle human gut microbiome data - Nicolas Pons
41 Balancing Open Science and Data Privacy: The Challenge of Human Microbiome Research - Guillaume Gautreau
42 A long-read metagenomic pipeline for deciphering yam virome: overcoming host-integrated sequences challenges - Maimouna Kone
43 MetaPanG: a pangenome graph-based method for strain-level profiling of prokaryotic microbiomes - Téo Lemane
44 Could the methylome be a new lever for steering microbial communities? - Benjamin Prehaud
45 A reproducible genomic and predictive modelling framework for characterising clinical antimicrobial resistance: A long-read sequencing study in Burkina Faso - Nènè Sthella Ky
46 Deciphering virus-host-environment relationships guided by large scale metagenomics data integration: the Dziani Dzaha hypersaline lake virome case study - Maël Rimeur
47 From Waste to Enzymes: A Metagenomic Approach to Uncover Plastic-Degrading Microbes in Brazil - Julia Cantuti Gendre
48 How Data Pre-processing Shapes Conclusions in Metagenomics: A Reproducible Benchmark to Guide Microbiome Analysis - Emile Mardoc
49 PanGBank: a Database of Pangenome Graphs for Comparative Microbial Genomics - Jean Mainguy
50 Large-scale meta-omics: identifying functional signatures of marine parasitism through sequence similarity networks - Valentin Fourdraine
51 {affiliationExplorer} a Shiny webapp to resolve taxonomy conflicts - Cédric Midoux
52 Identification of microorganisms in dairy systems using shotgun metagenomic data - Oriane Lamy
53 FROGS 5: A redesigned, modular pipeline for the comprehensive analysis of metabarcoding data - Agoutin Gabryelle
54 Microbial transfers in dairy compartments under two farming systems - Anne-Laure Abraham
55 Investigating genome reduction and evolutionary strategies in freshwater actinomycetes - Maxime ARQUE
56 Systematic and robust integration of bulk and single-cell RNA-seq to resolve the ion channel repertoire in Apis mellifera - Louis Closson
57 Comparative analysis of regeneration transcriptomic landscape across animals - Yves Clément
58 Stress Adaptation Pathways and Druggable Vulnerabilities in MTUS1-Low Triple Negative Breast Cancer - Gwenn Guichaoua
59 Integrative gene network analysis of genome-wide association data in myalgic encephalomyelitis / chronic fatigue syndrome - Katia Antonenko
60 Multi-reference STARR-seq analysis reveals candidate enhancers associated with the 2La inversion in Anopheles - Adrien Pain
61 Spatial and transcriptomic profiling reveal cell-specific mechanisms of epilepsy in Focal Cortical Dysplasia Type II - Franz Dervis
62 Effect of ultra-processed food consumption on the human sperm epigenome – Elza Bersanoukaeva
63 Remarkable repeated sequences in one of the most compact vertebrate genome - Faustine Collignon
64 Can somatic mutations be spatially localized using 10x Visium spatial transcriptomics? - Sacha Schutz
65 Deciphering the photoperiod-driven life cycle of the non-model algae Tisochrysis lutea through Single-Cell Transcriptomics - Antoine Daussin
66 Interplay between R-Loops and m6A RNA modification in transcriptional regulation using Drosophila S2R+ cell line - Paul Terzian
67 The BioInformatics and Genomics (BIG) Platform at Institut Sophia Agrobiotech: Expertise and Resources for Multi-Omics Data Analysis in Plant Health Research - Corinne Rancurel
68 Unveiling the dynamic transcriptome of the microsporidia parasite Anncaliia algerae during Human cell invasion - Ivan Wawrzyniak
69 In Silico Prediction of Transcription Factor Binding Sites in Proximal Promoter Regions Using TSS-Relative Positional Enrichment - Margot Correa
70 Automated structural annotation of marine eukaryotic genomes in the ATLASea project - Khaoula Ziane
71 Spatiotemporal mapping of cellular dynamics during epileptogenesis - Raphaël Edery
72 Inference of ligand–receptor interactions guiding neuronal wiring in the developing mouse somatosensory cortex - Tangra Draia-Nicolau

73 Recovering informative multiplex contacts from chimeric Hi-C and Micro-C reads using a split-and-parse workflow - Samir Bertache
74 Computationnal approaches for studying readthrough transcripts biogenesis and functions in neuroblastoma cells - Lou-Sahra Khourab
75 ParasiTE: detection of chimeric gene-transposon transcripts in plants - Jérémy Berthelier

76 ArmVar: a novel approach to identify cancer cells from single-cell RNA-sequencing datasets - Mehdi Marchand
77 Neuronal epigenetic plasticity in polyaddictions - Yahia Hadj-Arab
78 Investigating stop codon readthrough using ribosome profiling and protein structure prediction - Enora Corler
79 An Integrative Deep Learning and Structural Workflow for Accurate Annotation of Insect Odorant Receptors - David Gilardot
80 SNPs functional annotation tools using eQTL and meQTL data - Lucie Troubat
81 Profiling the escape from X chromosome inactivation in endometriosis - Nur Syahirah Binte Ruhazat
82 Polygenic architecture of morbid obesity in individuals of European ancestry : a UK Biobank study - Lucille Herbay
83 Study of mouse brain development transcriptome at transcript and exon level with ONT sequencing - William Desaintjean
84 ICEs and IMEs Delineation : Leveraging Pangenome and Machine Learning Approaches - Mamadou Aliou Diallo
85 The Genotoul-Bioinfo platform - Christophe Klopp
86 Building a Regional Bioinformatics Community in West Africa: Interdisciplinary Collaboration for Genomics and Health Research – RABIAS network - Julie Orjuela
87 GenomiqueENS, the IBENS Genomics core facility - Laurent Jourdren
88 cgMLST typing in the ABRomics web platform - Julie Lao
89 Deciphering translational regulation during infection with the Sindbis virus - Lauryn Trouillot
90 Retrieval-Augmented Generation over Genomic Reports in the ABRomics Platform: Towards AI-Assisted Antimicrobial Resistance Research - Raphaël Tackx
91 Automating image-based severity assessment of watermelon mosaic virus symptoms in melon using deep learning - Matthieu Deloget
92 Workflow development for automatically using Large Language Models to extract entities from a predefined corpus of scientific papers: creation of a knowledge graph for the fungal species Podospora anserina - Anakim Gualdoni
93 FiFi: Functional Inference from Fungal ITS, A bioinformatics tool to infer fungal metagenomes from ITS data - Maëlle Pomiès
94 BioloGrist: Using Grist for Biological Data Management - From Field Samples to Submission of Associated Sequencing Data - Alexis Dereeper

12:00 – 14:00	**Lunch** - Resto U Paul Appell
14:00 – 15:00 Amphi Cavailles	**Keynote - Sarah Cohen-Boulakia** - Chair: Hélène Chiapello Reproducibility by Design in Bioinformatics: Research challenges and opportunities
15:00 – 16:00 Amphi Cavailles	**Mini-Symposium** - Spatial Biology: principles, tools and applications for translational research in oncology
15:00 – 16:00 Amphi 3	**Mini-Symposium** - International bioinformatics connection spotlighting sequencing technologies applied to One Health
15:00 – 16:00 Amphi 4	**Mini-Symposium** - Is the structural annotation of genes in eukaryotic genomes still a challenge?
15:00 – 16:00 Amphi 5	**Mini-Symposium** - Orchestrating data flows throughout their lifecycle
16:00 – 16:30 Hall	**Coffee Break**
16:30 – 18:00 Amphi Cavailles	**Mini-Symposium** - Spatial Biology: principles, tools and applications for translational research in oncology
16:30 – 18:00 Amphi 3	**Mini-Symposium** - International bioinformatics connection spotlighting sequencing technologies applied to One Health
16:30 – 18:00 Amphi 4	**Mini-Symposium** - Is the structural annotation of genes in eukaryotic genomes still a challenge?
16:30 – 18:00 Amphi 5	**Mini-Symposium** - Orchestrating data flows throughout their lifecycle
19:00 – 00:00	**Gala Dinner - Restaurant Le Tigre** (Bring your badge!) (see below)

Friday July 3rd 2026

Amphi Cavailles	**Session: Cancer Genomics and Tumor Evolution** - Chair: Charles Lecellier
9:00 – 9:20	A Probabilistic Framework for Clonal Reconstruction in chronic lymphocytic leukemia (CLL) - Vidhi Vidhi
9:20 – 9:40	Unifying genetic differentiation statistics: mathematical constraints and application to tumour evolution - Yuliya Lim
9:40 – 10:00	K-mer-based exploration of large RNA sequencing collections reveals diagnostic transcriptomic variants in acute myeloid leukemia - Chloé Bessiere
Amphi 3	**Session: Microbial Interactions and Metabolic Systems** - Chair: Mahendra Mariadassou
9:00 – 9:20	In situ viral regulation of bacterial successions during organic matter turnover - Domitille Jarrige
9:20 – 9:40	Multi-objective metabolic modeling of cross-feeding interactions in a microalgae-bacteria consortium under nutritional stress - Marinna Gaudin
9:40 – 10:00	METAFLUX: A method for predicting metabolic fluxes by integrating proteomic data into a genome-scale constraint-based metabolic model - Maëla Sémery
Amphi 4	**Session: Bioinformatics Workflows and Data Platforms** - Chair: Erwan Corre
9:00 – 9:20	SIDURI: an integrated data and analysis portal supporting data-driven innovation in food fermentation - Emilie Fernandez
9:20 – 9:40	Supporting Workflow Reproducibility by Linking Bioinformatics Tools across Papers and Executable Code - Clémence Sebe
9:40 – 10:00	Revisiting SIF abstraction rules with SPARQL for querying BioPAX - Cécile Beust
10:00 – 10:30 Hall	**Coffee Break**
Amphi 3	**Demos 7**
10:30 – 11:00	IFB-Biosphère: Open access to adaptable computing resources within reproducible environments - Matis Zouari
11:00 – 11:30	MetroFlow: automatic, interactive metro-map visualisation for enhancingtransparency and comprehensibility of Nextflow workflows - George Marchment
Amphi 4	**Demos 8**
10:30 – 11:00	Virome@tlas-explorer: Putting the virosphere on the map - Luca Nesterenko
11:00 – 11:30	ViromeChat-AI: a conversational interface to explore viral metagenomic data in the Virome@tlas project - Romuald Marin
10:30 – 11:30 Hall	**Posters B** – Identical to previous day
11:30 – 12:30 Amphi Cavailles	**Keynote - Judith Zaugg** - Chair: Anaïs Bardet Understanding disease mechanisms through the lens of gene regulation at single-cell and spatial resolution
12:30 – 13:00 Amphi Cavailles	Closing Remarks
11:30 – 13:30 Hall	Lunch Bag

Going from the conference (le Patio) to lunch (Resto U Paul Appell)

After lunch coffee served at the conference venue

Social activities

Wednesday July 1st – 5pm-8pm

(Check your badge to see your registration)

More info on the activities

Activity	Times	Location / Departure point
River Cruise	18:30 – 19:45	[Place du Marché aux Poissons, Strasbourg]
Lieu d'Europe Exhibition	18:00 – 19:00	[Lieu d'Europe, Strasbourg]
Guided tour of European District	18:00 – 19:15	[parvis du Conseil de l'Europe, Strasbourg]
Guided City Tour	18:00 – 19:30	[Office de Tourisme de Strasbourg]
Wine Tasting	17:00 – 18:00	Conference location (le Patio) Cafétéria
Fresque du numérique **Digital Collage**	17:00 – 20:00	Conference location (le Patio) *Rooms* : 3R-E01 ; 3R-E02
Board Games	17:00 – 18:30	Conference location (le Patio) *Room* : 3R-E03

Activity	Times	Location / Departure point
Gala Dinner	19:00 – 24:00	[Restaurant Le Tigre 5 Rue du Faubourg-National, Strasbourg]

Practical information

Wireless network

During the conference, you can use the following Wi-Fi network **Osiris**:

- Login: conf-jobim2026
- Password: JOBIM2026

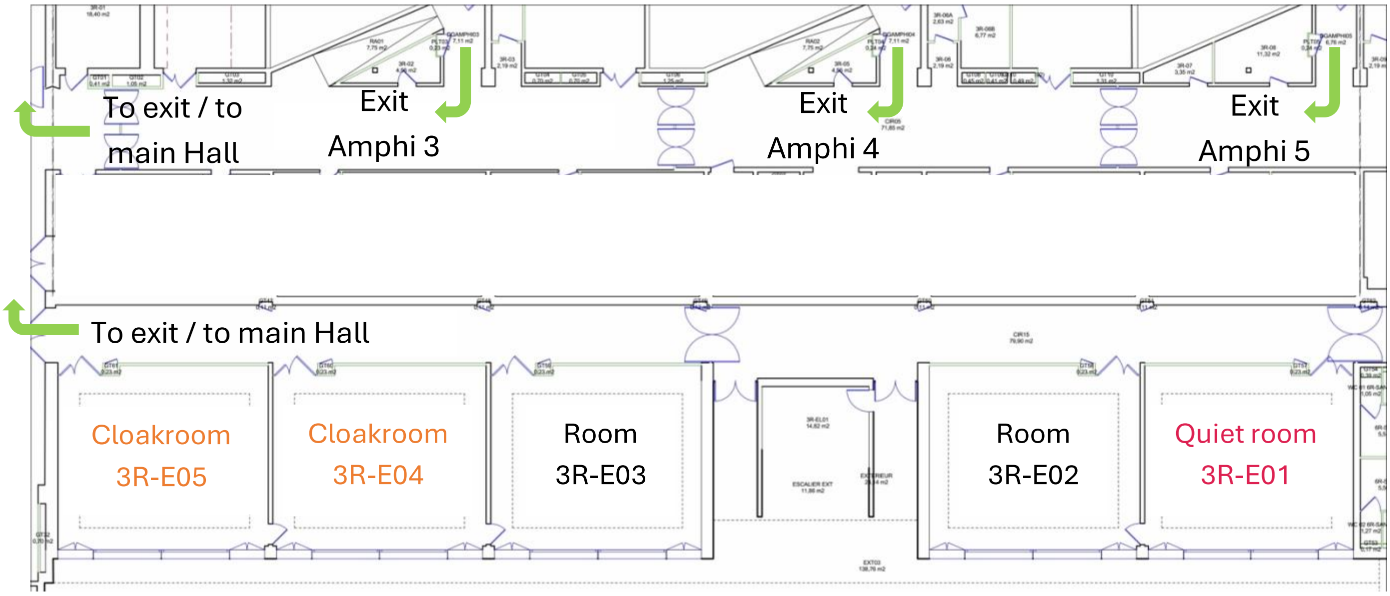
Badge

Your badge will be given to you at the welcome desk. Please wear it at all times during the conference, social activities, and the gala dinner.

You can unfold it to find important information, including: Wi-Fi details, the conference map, and your personal choices (mini-symposium, gala dinner, social activities).

Maps

Groundfloor



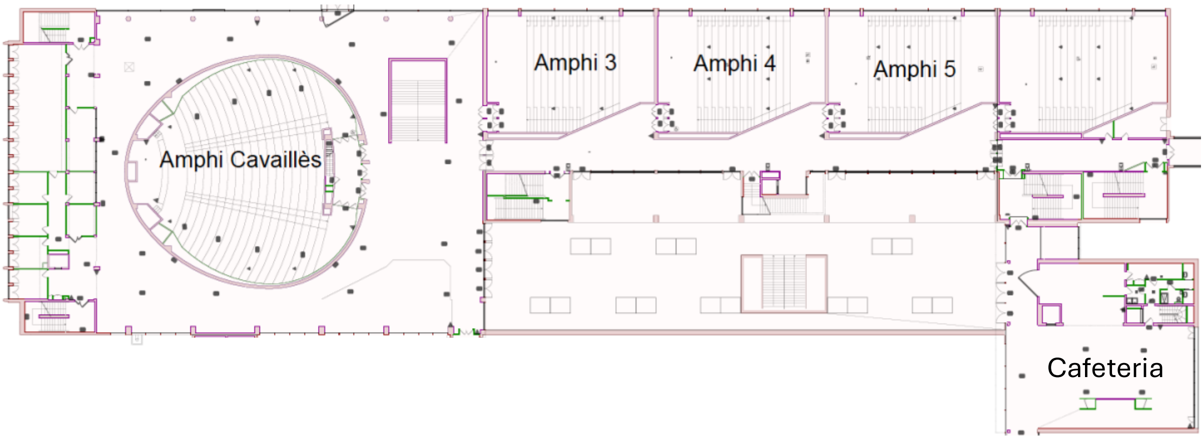
Restrooms are in the groundfloor.

Cloakrooms will be available at the following locations:

- 3R-E05
- 3R-E04
- 3R-E03 (open on Friday only)

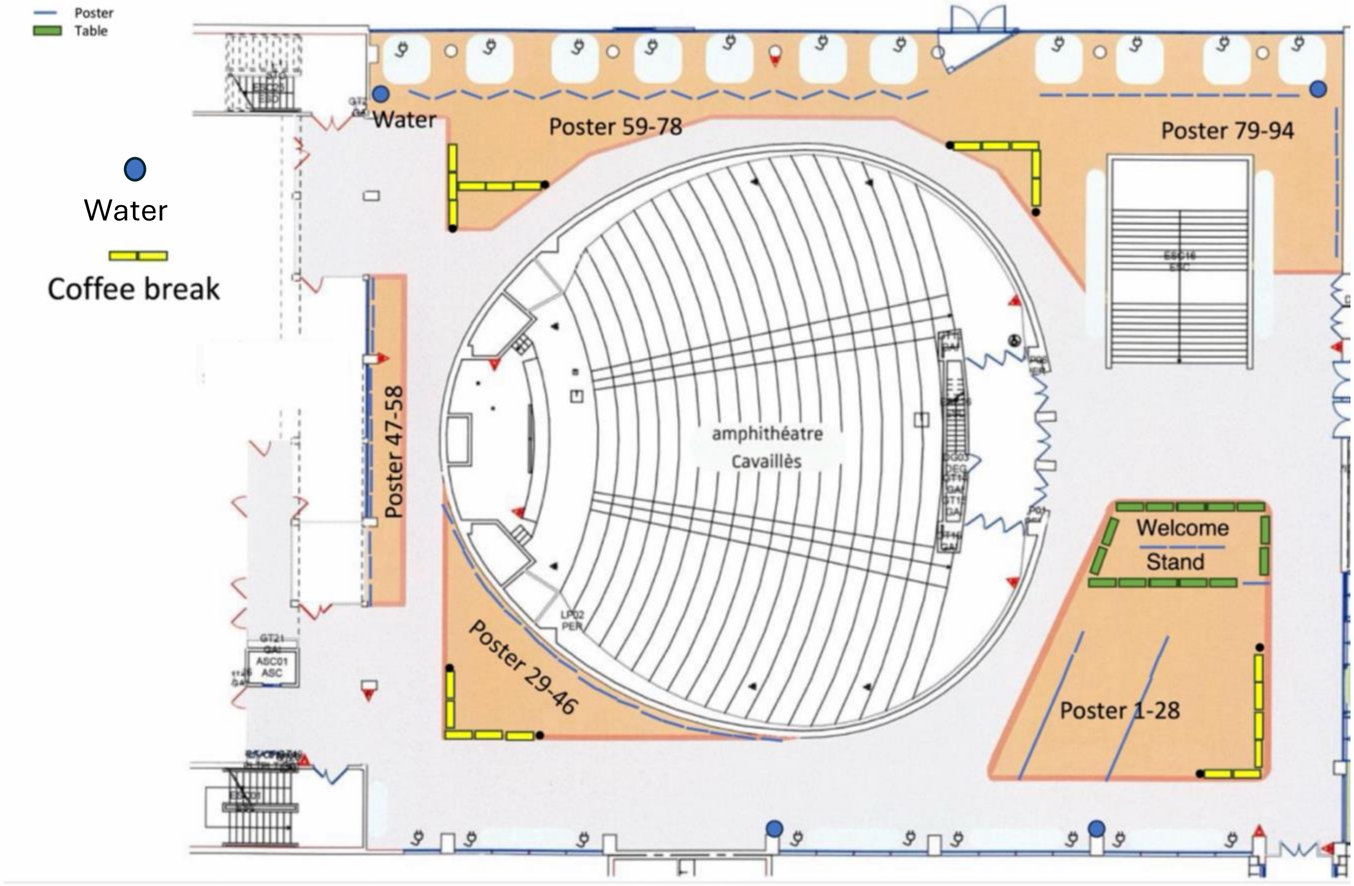
A **quiet room** will be available throughout the entire conference.

1st floor



JOBFAIR will take place in the Cafeteria.

- Zoom on the main hall



Coffee will be served at 4 stations in the main hall and in the cafeteria.

The **welcome cocktail** on Tuesday evening will take place in the main hall.

Certificates of participation

Certificates of participation can be asked by email at jobim2026@premc.org.

Cloakroom (Bagagerie)

The cloakroom is located on the ground floor of Le Patio building. Feel free to spread out across the available rooms.

Opening hours:

- Tuesday, June 30: 11:30 – 13:30 and 17:30 – 19:45
- Friday, July 3: 8:30 – 14:00

Remember to take a photo of your cloakroom ticket—this will allow you to retrieve your luggage even if you lose the physical ticket.

Free public transport in Strasbourg

As a conference participant, you have received a code to activate the CTS Strasbourg Event Pass, giving you free access to trams and buses for 96 hours from activation.
Important: Only activate it when you're ready to start using it.
The TER between the airport and the train station is also included in the pass.

Eco-cup

To make your eco-cup uniquely yours - and avoid drinking from your neighbor's - markers will be available in the Patio hall.

Recycling

Join our effort to reduce waste at JOBIM 2026: please use your eco-cup and sort your waste!

Code of conduct

We are committed to ensuring a safe and respectful environment for everyone. As part of your registration, you agreed to comply with the code of conduct throughout the event.

If you experience gender-based or sexual violence or harassment during the conference, please contact us at the welcome desk or email vhss-jobim2026@inrae.fr.

Social media

Want to stay updated? Follow us on:

- Linked-in
- Bluesky

Find help

Find us at the welcome desk or ask people wearing a green bandana.

sfbi
société française de bioinformatique

cnrs

GDR Groupement de recherche
BIMMM Bio-Informatique Moléculaire : Modélisation et Méthodologie

IFB
INSTITUT FRANÇAIS DE BIOINFORMATIQUE

BGI

FRANCE 2030

IA Grand Est
ENACT

FRANCE GENOMIQUE

CANCÉROPÔLE Est
Régions Bourgogne-Franche-Comté / Grand Est

sfé²
GREENOMICS
GENOMICS RESEARCH FOR ECO-EVOLUTION AND ENVIRONMENT

iCUBE

IMC Bio

Biologie moléculaire
& cellulaire intégrative | IMCBio+
Les Instituts thématiques interdisciplinaires
de l'Université de Strasbourg & cnrs & Inserm

INRAE ALIMH

INRAE BAP

INRAE GA

INRAE PHASE

INRAE SPE

INRAE SA

Inria

Loria

LINCA

RNA networks Net RNA

Strasbourg.eu
eurometropole

transgene

Université de Strasbourg

IBMP
Institut de biologie moléculaire des plantes

igbmc
institut de génétique et de biologie moléculaire et cellulaire

INCI

gmgm
Génétique Moléculaire ■ Génomique ■ Microbiologie

SVQV
Santé de la Vigne & Qualité du Vin