



POCKET PROGRAM

<https://jobim2025.labri.fr/>



HANDICAP INFORMATION

For handicap-related enquiries, please contact:

- Patricia Thébault: thebault@labri.fr

GOOD CONDUCT

In the event of a disrespectful behaviour or harassment, please contact:

any organiser with a bandana or: jobim2025-resp@diff.u-bordeaux.fr

RED BANDANAS

For other enquiries: organisers are wearing red bandanas.

EDUROAM

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to reduce CO2 emissions and to share the rooms' bandwidths with your colleagues.**

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réduire notre impact en CO2 et pour mieux partager la bande passante avec vos
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DAY 1 – Tuesday, July 8th

Main Hall 12:30 - 13:30	Registration, ENSEIRB
Main Amphi 13:30 - 14:00	Welcome & opening remarks
Main Amphi 14:00 - 15:00	Keynote: Anamaria Necsulea - <i>Chair: Guy Perrière</i> Deciphering the genomic basis of convergent phenotypic evolution
Main Amphi 15:00 - 15:20	Session: Statistics, Machine Learning, and AI for Biology and Health - <i>Chair: Victoria Bourgeois</i> Explainable AI for Marine Ecological Quality Prediction: Integrating Microbiome Data, Metadata, and Diversity - Houria Braikia
15:20 - 15:40	Evaluating deep learning models for plant protein function prediction - Minh Ngoc Vu
15:40 - 16:00	Variable selection in transcriptomics data using knockoffs in a classification framework - Julie Cartier
Amphi D 15:00 - 15:20	Session: Algorithms and data structures for sequences - <i>Chair: Raphaël Mourad</i> Structural Space of Microproteins with Protein Language Models - Simon Herman
15:20 - 15:40	MetagenBERT: a Transformer Architecture using Foundational Read Embedding Models to enhance Disease Classification - Gaspar Roy
15:40 - 16:00	SpecPeptidOMS Directly and Rapidly Aligns Mass Spectra on Whole Proteomes and Identifies Peptides That Are Not Necessarily Tryptic: Implications for Peptidomics - Géraldine Jean
Amphi E 15:00 - 15:20	Session: Evolution, phylogeny and comparative genomics - <i>Chair: Sophie Abby</i> Evolutionary dynamics of centromeric DNA in guenon might end an old anthropocentric dogma - Julien Pichon
15:20 - 15:40	Natural selection acting on gene expression and regulation in mole-rats - Maëlle Daunesse
15:40 - 16:00	A Comprehensive Study of Inverted Repeats in Prokaryotic Genomes: Enrichment, Depletion, and Taxonomic Variations - Victor Banon Garcia
Main Hall 16:00 - 16:30	Break & Coffee
Main Amphi 16:30 - 16:50	Session: Statistics, Machine Learning, and AI for Biology and Health - <i>Chair: Romain Bourqui</i> Joint Embedding-Classifer Learning for Interpretable Collaborative Filtering - Clémence Réda
16:50 - 17:10	Models for protein domain embedding - Louison Silly
17:10 - 17:30	Benchmarking Data Leakage on Link Prediction in Biomedical Knowledge Graph Embeddings - Galadriel Brière
Amphi D 16:30 - 16:50	Session: Metagenomics, Metatranscriptomics, and Microbial Ecosystems Statistics - <i>Chair: Rayan Chikhi</i> Metatranscriptomic classification in the study of microbial translocation - Antonin Colajanni
16:50 - 17:10	Fast answers to simple bioinformatics needs and capacity building in an island context, a focus on microbial omics data analysis - David Couvin
17:10 - 17:30	OneNet—One network to rule them all: Consensus network inference from microbiome data - Magali Berland
Amphi E 16:30 - 16:50	Session: Functional and Integrative Genomics - <i>Chair: François Sabot</i> AntiBody Sequence Database - Nicolas Maillet
16:50 - 17:10	The Pfam protein families database: embracing AI/ML - Typhaine Paysan-Lafosse
17:10 - 17:30	MethMotif 2024 Suite Reveals the Epigenetic Blueprint of Context-Specific Transcription Factor Binding Sites - Touati Benoukraf



- 3 REPET v4.0: A robust and accessible tool for TE annotation - Etienne Bardet
- 4 Digital Concord: Cultivating links between Discord and the secrets of the genome - Franck Samson
- 5 Refining eDNA taxonomic assignments with a phylogenetic approach - Enora Geslain
- 6 Evolaps 3: Next-Level Phylogeographic Visualization - Thomas Vitre
- 9 Mechanistic Modeling of Cell Viability Assays with in silico Lineage Tracing - Aurore Amrit
- 11 A meta-model for representing bioinformatics workflow to improve reproducibility - Mouna El Garb
- 13 Single-cell profiling reveals distinct immune profile in anti-Yo paraneoplastic neurological syndrome - Anna Tran
- 14 COSMIQ-4C: quantifying 3D genome interactions of retroviral proviruses at the single-clone level - Nicolas Fontrodona
- 15 HoloOligoDB: Exploring Mammalian Milk Oligosaccharides - Hajar Bouamout
- 16 InDeepNet a web platform for predicting and validating protein-protein interaction binding sites - Fabien Mareuil
- 17 Metage2Metabo-PostAViz: exploring and visualising the wealth of metabolic modelling predictions to compare microbial communities - Leonard Brindel
- 19 Exploring the challenges of Dinoflagellate transcriptome assembly with long-read data - Lauryn Trouillot
- 20 Computational investigation of chemosensory receptors in salmonid species - Emma Mathieu
- 21 Generation of gene annotations including UTRs for Bulk and Single-Cell RNASeq analyses - Salomé Brunon
- 22 GenomiqueENS, the IBENS Genomics core facility - Laurent Jourden,
- 23 Building an atlas of transcription factor DNA-binding properties in Arabidopsis thaliana - Alice Jegou
- 25 Beyond species: towards the modeling and prediction of marine plankton ecological associations biogeography - Marinna Gaudin
- 26 Seed2LP: seed inference in metabolic networks for reverse ecology applications - Chabname Ghassemi Nedjad
- 27 The Genotoul-Bioinfo platform - Matthias Zytnicki
- 28 MOAL: Improving the Reproducibility of OMICS Bioanalysis - Florent Dumont
- 31 MLOps best practices for bioinformatics - Pauline Le Corre
- 33 CroCoDeEL: accurate control-free detection of cross-sample contamination in metagenomics data - Lindsay Goulet
- 35 A multi-modal and temporal antibiotic resistance knowledge graph - Brieuc Quemeneur
- 36 ABRomics-analysis: Developing Metagenomic Workflows for National Antibiotic Resistance Surveillance Platform - Hugo Lefeuve
- 37 Annotating Bioconductor packages using the EDAM ontology - Claire Rioualen
- 38 StatOmique: sharing experience on statistical analysis of omics data - Julie Aubert
- 39 Evolutionary Dynamics of G-Quadruplexes in Human and Other Great Ape Telomere-to-Telomere Genomes - Saswat Mohanty
- 40 KGATE, an Autoencoder Training Environment for exploring and benchmarking Knowledge Graph Embedding models - Benjamin Loire
- 47 Exploring the Richness of the French Galaxy Ecosystem - Bérénice Batut
- 48 Galaxy Training: A powerful framework for teaching! - Bérénice Batut
- 51 Genome Annotation tooling in Galaxy: contributions of the EuroScienceGateway project - Romane Libouban
- 54 Investigating the habitat range of yeast species - Thomas Biscop
- 55 Unraveling gut microbiome latent structures: enterosignatures and microbial guilds - Mathilde Sola
- 57 fastCNV: Fast and Accurate CNV prediction from scRNA-Seq and Spatial Transcriptomics Data - Gadea Cabrejas
- 61 Characterizing the landscape of genomic rearrangements associated to double-strand breaks associated to transcribed loci (TC-DSB) - Amel Benarbia
- 63 Generation Mechanisms and Species-Specific Properties of Beta Oscillations in the Basal Ganglia - Elena Nicollin
- 66 Plant-PLMview: a web-tool and in silico method for identifying cis-regulatory elements in gene-proximal regions of plants - Franck Samson and Cécile Guichard
- 68 Normalization Strategies in Lipidomic Profiling: Implications for Ewe's Milk Lipolysis Biomarker Discovery - Alyssa Imbert
- 69 Microbial transfers in dairy systems under changing climate and farming practices - Sébastien Theil
- 71 A web platform for taxonomic exploration of metabarcoding databanks - Olivier Rué
- 72 Lifting the veil on Challenging Medically Relevant Filaggrin Gene - Victor Grentzinger
- 74 A Robust Computational Framework to Characterize the Genetic Diversity Across 3,570 Strains in *S. cerevisiae* - Louis Ollivier
- 77 Pan1c: A Snakemake Workflow for Chromosome-Level Pangenome Construction and analysis - Martin Racoupeau
- 78 Viral RNA meets RIG-I: insights from RNA-Seq - Rachel Legendre
- 79 Long-read sequencing of the 16S-ITS-23S operon enables maternal microbiota transmission study at the strain-level resolution - Maëlle Pomiès
- 80 Microplastic effects on Mosquito Gene Expression and Microbiota - Ahamed Tchatakoura
- 177 Comprehensive Identification of Pleiotropic Associations for Chronic Lymphocytic Leukemia - Anthony Haidamous
- 178 The Good, the Bad and the Ugly: methodological and conceptual pitfalls in single-cell data science - Yanis Asloudj
- 191 OLGA: Local Accession Management Tool for Biological Resources Centres (BRC) - Jacques Lagne
- 202 Using OntoWeaver to Integrate Heterogeneous Information in the OncodashKB Semantic Knowledge Graph for Finding Personalized Actionable Drugs in Ovarian Cancer - Matthieu Najm



Amphi D	Session Demo - Chair: Nicolas Tourasse
17:30 - 18:00	ABRomics-analysis: a web service for the analysis of Antibiotic Resistance in bacterial genomes - Julie Lao
18:00 - 18:30	WHOOPER: Web application for Hands-On identification of protein co-Occurrence among Phyla, focused on user ERgonomics - Sylvain Marthey
Amphi E	Session Demo - Chair: Elodie Darbo
17:30 - 18:00	Bridging the Gap Between R and Python in Bulk Transcriptomic Data Analysis with InMoose - Maximilien Colange
18:00 - 18:30	Interactive toolbox for cell-type deconvolution of spatial transcriptomics data - Lucie Gaspard-Boulinc
Main Hall 18:30 - 20:00	Welcome Cocktail

DAY 2 - Wednesday July, 9th

Main Amphi 9:00 - 10:00	Keynote: Simona Cocco - Chair: Morgane Thomas-Chollier SARS-CoV-2 viral evolution and antibody resilience
Main Hall 10:00 - 10:30	Break & Coffee
Main Amphi	Session: Structural Bioinformatics and Proteomics - Chair: Daniel Gautheret
10:30 - 10:50	Comparative Analysis of Deep Learning-Based Algorithms for Peptide Structure Prediction - Clément Sauvestre
10:50 - 11:10	Searching for variable structural motifs in RNA graphs using simple descriptors - Camille De Amorim
11:10 - 11:30	RNA3DClust: unsupervised segmentation of RNA 3D structures using density-based clustering - Quoc Khang Le
Amphi D	Session: Systems Biology - Chair: Sarah Djebali
10:30 - 10:50	Regulatory response of maize to water deficit mediated by distal cis-regulatory elements - Thomas-Sylvestre Michau
10:50 - 11:10	Predictive modelling of Acute Promyelocytic Leukaemia resistance to Retinoic Acid therapy - Denis Thieffry
11:10 - 11:30	Building a modular and multi-cellular virtual twin of the synovial joint in Rheumatoid Arthritis - Anna Niarakis
Amphi E	Session: Statistics, Machine Learning, and AI for Biology and Health - Chair: Nathalie Vialaneix
10:30 - 10:50	Ten years of the Pasteur's Bioinformatics and Biostatistics Hub: achievements and perspectives - Hervé Ménager
10:50 - 11:10	Developing machine-learning-based amyloidogenicity predictors with Cross-Beta DB - Valentin Gonay
11:10 - 11:30	Leveraging multi-omics integration to uncover childhood trauma-related mechanisms in bipolar disorder. - Margot Derouin



- 53 Building a Standardized Database for Honey Bee Microbiome: Addressing Metadata and Data Comparability gaps - Bérénice Batut
- 56 A database to predict safety risks of raw milk cheeses from farming practices in climate change context - Sébastien Theil
- 82 Accounting for defective genomes in influenza consensus genome reconstruction - Kévin Da Silva
- 83 Exploration of non-coding and structural variations in early-onset Alzheimer disease patients: contribution of PacBio HiFi long-read sequencing - Fatima-Zahra Abani
- 84 BYTE-Sea: the digital infrastructure of ATLASea, the French marine genome sequencing programme - Annie Lebreton
- 85 Identification of transcriptional regulatory networks underlying variable human immune responses - Anthony Bertrand
- 86 Multi-omics data integration in constraint-based modeling of metabolic networks to study the metabolism of adipose-derived stem cells - Maximilian Stingl
- 87 EuphausiDB: A Transcriptomic reference Database for Krill Species - Triskell Cumunel
- 89 Generation of metabolomic-informed models of metabolism in complex microbial communities - Coralie Muller
- 90 Assessing rhythmicity in the marine diatom *P. tricornutum* circadian transcriptome - Irelka Colina Moreno
- 94 Detection of Somatic Copy Number Alterations from Single-Cell Multiomics Data with the R package muscadet - Marie Denoulet
- 95 Exploring Rare Genetic Variants in French Centenarians: A Path to Understanding Longevity - Assia Benmehdia
- 97 InterPro: Accelerating Protein Annotation with AI - Matthias Blum
- 98 Uncovering the sweetpotato virome in Burkina Faso using Nanopore-based metagenomics and bioinformatics approaches - Pakyendou E. Name
- 99 SeaGO: A Scalable and High-Performance Platform for Functional Annotation and Genomic Data Visualization - Said Ait Salah
- 103 Gammaproteobacteria Operons for polysaccharide utilization: from Algae to a Larger Scope (GOALS project) - Matthieu Boulinguez
- 105 GRIS: Gene Repertoires Indexes of Similarity - Julien Guglielmini
- 106 A strategy for balanced haplotype-resolved de novo assembly of the autotetraploid genome of *Medicago sativa* - Christophe Klopp
- 109 Integrases as Key Players in Shaping Pangenome Hotspots in Enterobacteriaceae - Romane Junker
- 112 MEMHDX v2: Advanced Preprocessing and Enhanced Analysis of HDX-MS Datasets - Stevonn Volant
- 113 Comprehensive Herpesviruses Antiviral drug Resistance Mutation Database (CHARMD) - Daniel Diaz Gonzalez
- 114 Overall genetic characterization of a 3D iPSC-derived cell therapy for Parkinson Disease through a multi-omic approach - Elodie Babina
- 115 SIDURI: from an integrative information system to a user-friendly portal for data analysis and visualisation dedicated to fermentation - Agnès Barnabé
- 116 Optimizing in silico drug discovery: simulation of connected differential expression signatures and applications to benchmarking - Catalina Gonzalez Gomez
- 117 GrAuFlow: A snakemake workflow for pangenome graph augmentation using assembled short-read data - Antoine Malet
- 118 Data stewardship strategy of the Ferments du Futur grand challenge - Erwan Le Floch
- 119 Gradiv: a tool to compute diversity statistics from a pangenome graph - Margaux Imbert
- 120 Bridging gene-level and sequence-level pangenome graph to explore microbial diversity - Hanin Ali
- 122 Large Language Models-driven Reconstruction of Sequence Read Archive Metadata for Cancer Research - Fiona Hak
- 123 POMODO database: a Pan OMics cOLlection of tOMato undeR biOtic stress - Alexina Damy,
- 124 Towards new therapeutic strategies for protein x-deficient Triple-Negative Breast Cancers - Gwenn Guichaoua
- 126 Genomic Approaches for Nematode Systematics: UCEs and Machine Learning - Lucy Jimenez
- 128 Evolutionary process of breast cancer metastasis - Zakia Tariq
- 129 LoRa-com: INRAE's Shared LoRaWAN Platform for Agro-environmental Research - Jacques Lagnel
- 132 International Society for Computational Biology Student Council Regional Student Group France (RSG France): Association of Young Bioinformaticians of France (JeBiF) - Magis Papail
- 133 cMFA for multi-omics data integration in microbial community models - Sthyye Tatho
- 134 Towards reproducible single-cell transcriptomics analysis - Audrey Onfroy
- 135 Assessing the contribution of ancient genomic data to the inference of historical demographic parameters - Arnaud Quelin
- 136 iKISS: A Reference-Free Pipeline for Inferring Domestication Traces in Plants - Julie Orjuela
- 141 The Environmental Cost of Bioinformatics: A Perspective from GenOuest, a Bioinformatics Platform - Rémy Siminel
- 142 Large-scale proteomics and Deep learning for the generation of protein-protein interaction (PPI) maps at atomic resolution - Caroline Sancho
- 144 Data modeling in agroecology, a first schema to characterize plant holobiont and environmental data - Marie Lahaye
- 146 IFB/ELIXIR-FR contributions to the ELIXIR Training Platform Programme - Olivier Sand
- 147 Protein fold diversity and evolution in Archaea: from adaptation to extreme environments to the origin of biodiversity - Ambre Baumann
- 148 Bread wheat pangenome graph provides access to gene diversity, structural variations and key agronomic loci architecture - Pauline Lasserre-Zuber
- 149 Computational modeling of JAK inhibitors in patients with Rheumatoid Arthritis - Elisa Mages
- 150 Transient RNA structures and recombination in H7NX high pathogenicity Avian Influenza virus - Aldair Martin Martinez Pineda
- 152 DigiDermA: Modeling Interactions between Mast Cells and Sensory Neurons in Atopic Dermatitis
- 154 ABRAAM: Agent-Based Rheumatoid Arthritis Model for personalised therapy
- 158 SynOmics: A Synthetic Data Pipeline for Transcriptomics and Clinical Data Accelerating Benchmarking Study - The-Chuong Trinh



Amphi D	Session Demo - Chair: Fleur Mougín
11:30 - 12:00	Network-centric identification and analysis of a model of post-traumatic stress disorder with NORDic - Fabien Romano
12:00 - 12:30	Demonstrating OntoWeaver to Integrate Heterogeneous Information in the OncodashKB Semantic Knowledge Graph for Finding Personalized Actionable Drugs in Ovarian Cancer - Matthieu Najm
Amphi E	Session Demo - Chair: Simon Labarthe
11:30 - 12:00	CroCoDeEL: accurate control-free detection of cross-sample contamination in metagenomics data - Lindsay Goulet
12:00 - 12:30	LAGOON-MCL: A Nextflow pipeline for comprehensive protein sequence annotation and comparison - Jérémy Rousseau
Main Hall	Lunch
12:30 - 14:00	
Main Amphi	Keynote speaker: Eric Rivals - Chair: Raluca Uricaru.
14:00 - 15:00	On n'a pas de terres rares, mais on a des idées. Partitionnement en classe d'équivalence pour le test d'algorithmes du texte.
Main Amphi	Assemblée Générale SFB
15:00 - 16:00	
Main Hall	Break & Coffee
16:00 - 16:30	
Main Amphi	Network presentations - IFB, GDR BIMM, JEBIF, MERIT, PCI, Bioinfo-Dag
16:30 - 17:30	
17:30 - 20:00	CULTURAL ACTIVITIES (details on last pages)

DAY 3 - Thursday July, 10th

Main Amphi	Keynote speaker: Emma Schymanski - Chair Sylvain Prigent
9:00 - 10:00	Open Science Data Processing and Integration Workflows in Metabolomics and Exposomics
Main Hall	Break & Coffee
10:00 - 10:30	
Main Amphi	Session Systems Biology - Chair: Damien Eveillard
10:30 - 10:50	Metagenome-scale metabolic modelling for the characterization of cross-feeding interactions in freshwater cyanobacteria-associated microbial communities - Juliette Audemard
10:50 - 11:10	Met4J: a library, a toolbox and a workflow suite for graph-based analysis of metabolic networks - Clément Frainay
11:10 - 11:30	Methods for a species-specific genome-scale metabolic model designed for eukaryotes and applied to the <i>Ascophyllum nodosum</i> macroalga - Pauline Hamon-Giraud
Amphi D	Session: Algorithms and data structures for sequences - Chair: Matthias Zytnicki
10:30 - 10:50	Vizitig: context-rich exploration of sequencing datasets - Bastien Degardin
10:50 - 11:10	Reindeer2: practical abundance index at scale - Yohan Hernandez Courbevoie
11:10 - 11:30	OREO: Optimizing Read Order for practical compression - Mathilde Girard
Amphi E	Session Workflows, Reproducibility, and Open Science - Chair: Erwan Corre
10:30 - 10:50	Madbot, a metadata and data brokering online tool to ensure the adoption of standards and FAIR principals in an open science context - Imane Messak
10:50 - 11:10	Assessing bioinformatics software annotations: bio.tools case-study - Ulysse Le Clanche
11:10 - 11:30	A decade of strengthening bioinformatics in West Africa: HPC infrastructure, training, and scientific collaboration - Ezechiel B. Tibiri



Main Hall
11:30 - 12:30 **POSTERS – Session 3**

- 2 URGI – A scientific facility dedicated to plant bioinformatics - Mariène Wan
- 50 Breaking Myths: The Reality of Galaxy's Capabilities and Impact - Bérénice Batut
- 65 GBOT upgrade: a loci comparison tool dedicated to the exploration of duplications and syntenies - Franck Samson
- 67 A priori estimation of reproducibility odds informs the sizing of omic data cohorts - Maximilien Colange
- 155 The HARMONI project: Evaluating advanced microbiota characterization methods for host and environmental samples using DNA metabarcoding and metagenomic sequencing - Lindsay Goulet
- 159 A High-Throughput Approach and Pipeline for Single-Bacterium Transcriptomics - Ngoc Chau Pham
- 162 Assessing phenomic prediction in the plant species *Stevia rebaudiana* B - Patricia Homobono Brito de Moura
- 164 French Bioinformatics Institute's Initiatives for Biodiversity Genomic Data Management - Clara Emery
- 165 Investigating taxonomy-based clustering of HiFi reads for de novo assembly of complex metagenomes - Nicolas Maurice
- 168 gwas-pipe: a Nextflow pipeline for GWAS analyses incorporating quality control - Jacques Lagnel
- 169 Identifying subtypes in neurological disease patients - Julie Segueni
- 180 Virome@tlas, a digital platform for the virosphere surveillance - Elea Pauliat and Paul Tissot
- 181 Interpretable Multi-Class Classification of the Microbiome Using Predomics - Fabien Kambu Mbuangi
- 182 Deciphering codon choice: how deep learning models select between synonymous codons - Helene Bret
- 183 A refined strategy linking transcriptomics and metabolic models for deciphering chemical induced changes - Maxime Lecomte
- 185 Evolutionary divergence of regulatory chromatin contacts following gene duplication - Victor Lefebvre
- 187 Integrative Bulk and Single-Cell Multiomic Framework for Tracing (Sub)clonal Evolution in Multiple Myeloma - Nils Giordano
- 189 Virus–host–ecosystem studies at large-scale: Please check your sequence metadata! - Paul Tissot and Elea Pauliat,
- 192 Spatial transcriptomic analysis of neuroinflammation and brain dysfunction induced by bacterial meningitis in juvenile mice - Alicia Gouge
- 193 Data-Driven Discovery of Novel Antigen Targets: A Scalable Bioinformatics Pipeline - Lea Meunier
- 194 SnoBoard: surfing on ncRNA modifications and snoRNA guides - Philippe Bordron
- 195 Size optimization of RNA sequences in the RNA World context.
- 196 Gpredomics: rapid, interpretable and accurate prediction models for compositional data - Matteo Bettati
- 199 GaaS: Galaxy as a Service - Rémi Planel
- 200 Protein Function Prediction: Graph Neural Networks as Multi-modal Aggregators of Sequences, Networks, and Ontologies - Antoine Toffano
- 201 Characterization of swine influenza viruses infections in pig herds: A machine learning approach identifying key environmental, physiological, immunological and virological determinants - Elisabeth Hellec
- 203 Integrating proteomics data into a genome-scale metabolic model to predict metabolic fluxes in maize leaf - Maëla Sémerly
- 206 Co-building a Sustainable Bioinformatics Training Program: The International Certificate in Bioinformatics and Genomics in West Africa - Ezechiel B. Tibiri
- 207 Identification and characterization of inversions' content in *Pseudogymnoascus destructans* - Hugo Bellavoir
- 208 Models and Methods for de novo Identification of Transposable Elements in short-read RNAseq data - Sasha Darmon
- 210 A pipeline for Trans-kingdom small RNAs analysis - Alexis Bourdais
- 214 Methods for identifying associations between plant genomes and symbioses despite the presence of paralogues - Pierre Géroton
- 215 Recursivity improves spatial transcriptomics data clustering quality - Christophe Le Priol
- 220 Using PhysiCell modelling to simulate the PDAC tumor microenvironment response to therapies based on patients' spatial omics data - Owen Griere
- 223 SCANS: Assessing lncRNA conservation across species - Aurore Besson
- 224 Predictive metabolomic to decipher plant eco-evolutionary tendencies - Cathleen Mirande-Ney
- 225 Single-cell classification of breast cancer and identification of cell surface protein targets - Quentin Rott
- 227 Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1L444P/WT mouse model: Implications for Parkinson disease pathogenesis - Mallia Geiger
- 229 Probabilistic motif search and differentials in pangenome graphs - Benjamin Linard
- 233 vvv2_align_SE, vvv2_align_PE / vvv2_display: Galaxy workflows and software to compute, summarize and visualize variant calling and annotations of a viral assembly - Fabrice Touzain
- 235 DLScaff: Deep Learning for Hi-C Assembly Correction and Scaffolding - Alexis Mergez
- 236 MSpangpop: Simulating complex structural variants under advanced demographic scenarios using the coalescent - Lucien Piat
- 237 Predicting Non-Response to Cystic Fibrosis Modulators from Microbiota Using Standard and Custom Machine Learning - Céline Hosteins
- 239 Multi cohort investigation of the AML tumour microenvironment in relation to mutational profiles - Emilie Montaut
- 240 Comparative Evaluation of Short-Read, Long-Read, and Hybrid Assemblies for MAG Recovery in Human Fecal Metagenomes - Baptiste Hennecart
- 241 Evolutionary genomics of the *Aedes aegypti* Mosquitoes in the West Indies: Impact of Transposable Elements in their Adaptation - Meron Tsetargachew
- 242 CellTFusion: A novel approach to unravel cell states via cell type deconvolution and TF activity estimated from bulk RNAseq data identifies cell niches potentially predictive of cancer progression- Marcelo Hurtado
- 247 Mapping the Human Small Intestinal Microbiome: A Statistical Learning Approach - Zakaria Tougui
- 253 A computational workflow to map and evaluate the impact of human genetic variation on the interactome - Thomas Stosskopf
- 255 GraDex, a set of indexes for sequence graphs in GFA format - Mourdas Mohamed
- 256 A workflow for the analysis of QuantSeq FWD data - Pascal G P Martin



Amphi D	Session Demo - Chair: Sylvain Prigent HUMESS: A tool to integrate quantitative transcriptomic and metabolic network modelling to unveil context specific gene signatures - Louis Paré 11:30 - 12:00 12:00 - 12:30 SynFlow: a Syri based interactive viewer - Marilyne Summo
Amphi E	Session Demo - Chair: Pascal Martin 11:30 - 12:00 Gratools a tool for easy manipulation of GFA - Camille Carette 12:00 - 12:30 REPET v4.0: A Comprehensive Tool for Transposable Element Analysis - Etienne Bardet
Main Hall	Lunch 12:30 - 14:00
Main Amphi	Keynote speaker: Björn Grüning - Chair: Jacques Van Helden 14:00 - 15:00
Main Amphi	Mini-symposium: Comment concilier nos activités en bioinformatique avec les limites planétaires ? 15:00 - 18:00
Amphi D	Mini-symposium: AI in Healthcare: From Fundamentals to the Clinic 15:00 - 18:00
Amphi E	Mini-symposium: The Genomics of Biodiversity 15:00 - 18:00
Amphi B	Mini-symposium: Methods for Interfacing with Graphs of Genomic Sequences: novel pangenome paradigms 15:00 - 18:00
19:00 - 00:00 Gala dinner (details on last pages)	

DAY 4 - Friday July, 11th

Main Amphi	Session Algorithms and data structures for sequences - Chair: Sèverine Bérard 9:30 - 9:50 SVJedi-Tag: a novel method for genotyping large inversions with linked-read data - Mélody Temperville 9:50 - 10:10 GrAnnoT, a tool for efficient and reliable annotation transfer through pangenome graph - Nina Marthe 10:10 - 10:30 Facilitating genome annotation using ANNEXA and long-read RNA sequencing - Nicolai Hoffmann
Amphi D	Session Statistics, Machine Learning, and AI for Biology and Health - Chair: Sophie Schbath 9:30 - 9:50 Exhaustive Identification of Pleiotropic Loci for Serum Leptin Levels in the NHGRI-EBI Genome-Wide Association Catalog - Anthony Haidamous 9:50 - 10:10 jsPCA enables fast, interpretable and parameter-free domain identification in 3D spatial transcriptomics data - Ines Assali 10:10 - 10:30 RITHMS: An advanced stochastic framework for the simulation of transgenerational hologenomic data - Solène Pety
Amphi E	Session Functional and Integrative Genomics - Chair: Sylvain Foissac 9:30 - 9:50 rnaends: an R package targeted to study the exact RNA ends at the nucleotide resolution - Tomas Caetano 9:50 - 10:10 Strain-dependency of metabolic pathways within 1,494 genomes of lactic bacteria evidenced with Prolipipe, an in silico screening pipeline - Noé Robert 10:10 - 10:30 Benchmarking circRNA Detection Tools from Long-Read Sequencing Using Data-Driven and Flexible Simulation Framework - Anastasia Rusakovich
Main Hall	Break & Coffee 10:30 - 11:00
Main Amphi	Keynote: Jean Monlong - Chair: Claire Lemaitre 11:00 - 12:00 Integrating structural variants in genomic studies of rare and complex diseases with long-read sequencing and pangenomes
Main Amphi	Conference closing words 12:00 - 12:30
Main Hall	Lunch Box 12:30 - 14:00



Information about social events

Tuesday, July 8th



Welcome cocktail

ENSEIRB building, main hall.
18:30-20:00

Wednesday, July 9th



Social events:

Meeting for bus departure at 17:40, ENSEIRB building

Wine tasting by ISVV

Institut des Sciences de la Vigne et du Vin, 210 Chemin de Leysotte,
Villenave d'Ornon

Initiation Salsa - Jardin Public

Jardin Public Cours de Verdun, Bordeaux
Tramway B: STOP Quinconces (+ 7 mn walk)

Escalade, Arkose

170 Cr du Médoc Galerie Tatry, 33300 Bordeaux
Tramway B: STOP Cours du Médoc (+ 16 mn walk)
Remember to bring sportwear

On-site activity at 17:45, ENSEIRB

Online Game – GeoGuessr:

On-site: Amphitheatre D - Bring your laptop

<https://inrae-fr.zoom.us/j/91754534311?pwd=fAnMskBpcVA6P9KnHQo2ki2kDPuB6c.1>

Downtown on-site meeting at 18:00

Karaoke

BAM Karaoke Box Chartrons, 38 rue Cornac, Bordeaux
Tramway B: STOP CAPC Musée d'Art Contemporain (+ 6 mn walk)

Escape Game John Doe

7 rue d'Alembert Bordeaux
Tramway B: STOP Victoire (+ 3 mn walk)

Downtown on-site meeting at 18:30

Bordeaux City Tour (~1.5 hours)

Rendez-Vous monument des Girondins, 2792 Pl. des Quinconces, Bordeaux
Tramway B: STOP Quinconces (+ 2 mn walk)

Thursday, July 10th, from 19:00



Gala dinner

Bordeaux Palais de la Bourse - BPB

17 Pl. de la Bourse, Bordeaux
Tramway B: STOP Grand Théâtre (+ 6 mn walk)



