

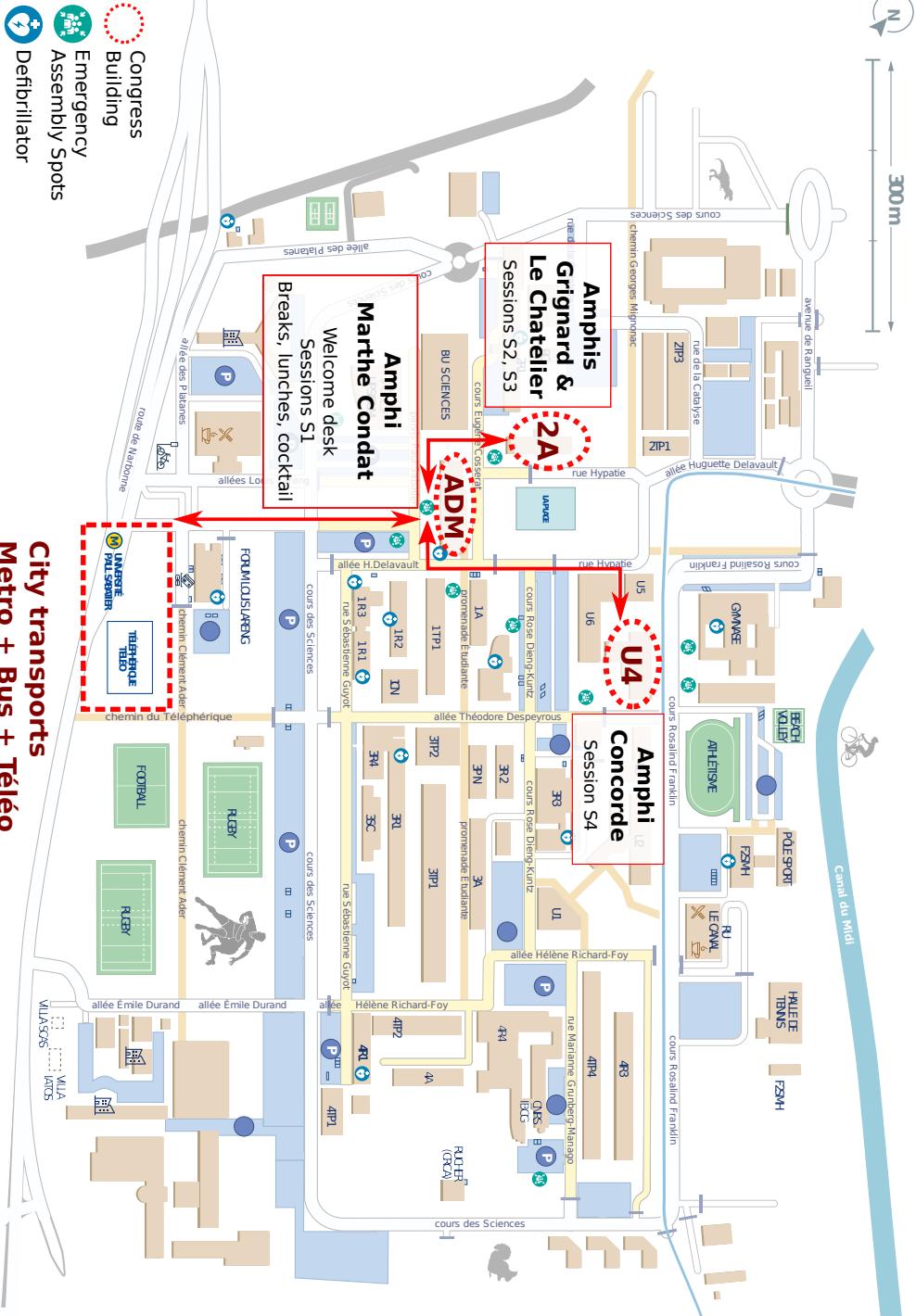


## Journées Ouvertes en Biologie, Informatique et Mathématiques

POCKET PROGRAM

<https://jobim2024.sciencesconf.org>







## MAGNETIC LOOP

The Grignard and Le Chatelier lecture halls are equipped with a magnetic loop for the hearing impaired.

## HANDICAP INFORMATION

For handicap-related enquiries, please contact :

- Sarah Maman, [sarah.maman@inrae.fr](mailto:sarah.maman@inrae.fr)
- Benoit Aliaga, [benoit.aliaga@inserm.fr](mailto:benoit.aliaga@inserm.fr)

## GOOD CONDUCT

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

- Sarah Djebali : [sarah.djebali@inserm.fr](mailto:sarah.djebali@inserm.fr)
- Guillaume Devailly : [guillaume.devailly@inrae.fr](mailto:guillaume.devailly@inrae.fr)

## ORANGE ARMBANDS

For other enquiries : organisers are wearing orange armbands.

## EDUROAM

*To use in priority with your usual login/password*

*A utiliser en priorité avec votre identifiant / mot de passe*

## EDUSPOT

*With login/password given on request at the reception*

*Un identifiant / mot de passe pourra être remis à l'accueil*



#jobim2024 x.com/jobim2024

Please refrain from using your 4/5G mobile hotspots to reduce CO2 emissions and to share the rooms' bandwidths with your colleagues.

Il vous est demandé d'éviter le partage de connexion de votre téléphone 4/5G afin de réduire notre impact en CO2 et pour mieux partager la bande passante avec vos collègues.



# DAY 1 - Tuesday June 25th

12:30 - 13:45	Registration, Building ADM, main Hall
13:45 - 14:00	Welcome & opening remarks, ADM, amphi Marthe Condat
14:00 - 15:00	<p>Keynote: Nelle Varoquaux <i>ADM, amphi Marthe Condat, chair: Nathalie Vialaneix</i> Machine Learning Adventures in Biology: Overcoming Hurdles and Harvesting Biological Insights</p>
15:00 - 16:00	Posters' flash presentations, ADM, amphi Marthe Condat
16:00 - 16:30	Break & Coffee, ADM main hall
16:30 - 17:30	<p><b>S1:</b> Statistics, Machine Learning and AI - ADM, <i>Marthe Condat</i></p> <ul style="list-style-type: none"><li>• Semi-supervised learning improves regulatory sequence prediction with unlabeled sequences - <i>R. Mourad</i></li><li>• sceVE: a scRNA-seq ensemble clustering algorithm that leverages the extrinsic variability to prevent over-clustering - <i>Y. Aslouadj</i></li><li>• localScore: an R package to highlight optimal and suboptimal segment in a sequence with associated p-val computation - <i>S. Mercier</i></li></ul> <p><b>S2:</b> Workflows, reproducibility &amp; Open Science - 2A, <i>Grignard</i></p> <ul style="list-style-type: none"><li>• PhaselImpute: a NF-Core pipeline for genetic imputation - <i>L. Le Nézet</i></li><li>• Benchmarking feature selection and feature extraction methods to improve the performances of machine-learning algorithms for patient classification using metabolomics biomedical data - <i>J. Labory</i></li><li>• Constructing a robust framework to benchmark deconvolution algorithms - <i>E. Amblard</i></li></ul> <p><b>S3:</b> Evolution: Concepts - 2A, <i>Le Chatelier</i></p> <ul style="list-style-type: none"><li>• Beyond Recombination: Exploring the Impact of Meiotic Frequency on Genome-wide Genetic Diversity - <i>L. Ollivier</i></li><li>• When lianas and trees talk DNA: new insights into genetic exchanges in plants - <i>E. Aubin</i></li><li>• Unzipped genome assemblies of polyploid root-knot nematodes reveal unusual and clade-specific telomeric repeats - <i>E.G.J. Danchin</i></li></ul>
17h45 - 18:45	Poster session 1, ADM main hall
18:45 - 20:00	Welcome Cocktail, ADM main hall



## DAY 2 - Wednesday June 26th

9:00 - 10:00

Keynote: Elodie Laine

*ADM, amphi Marthe Condat, chair: Raphaël Mourad*

From sequences to fitness and motions, protein language models to the rescue?

10:00 - 10:30 Break & Coffee, ADM main hall

10:30 - 11:30

**S1:** Structural bionfo. and proteomics - *ADM, Marthe Condat*

- Automatic exploration of the natural variability of RNA non-canonical geometric patterns with a parameterized sampling technique, *T. Boury*
- MDverse: Shedding Light on the Dark Matter of Molecular Dynamics simulations. *P. Poulain*
- RNAvisor: a comprehensive benchmarking tool for the measure and prediction of RNA structural model quality, *C. Bernard*

**S2:** Metagenomics & pangenomics - *2A, Grignard*

- CroCoDeEL: accurate detection of cross-sample contamination in metagenomic data, *G. Gautreau*
- Integration of metataxonomic datasets into microbial association networks highlights shared bacterial community dynamics in fermented vegetables, *R. Junker*
- Pangome graph construction from genome alignments with Minigraph-Cactus, *J. Monlong*

**S3:** Statistics and machine learning for clinical applications - *2A, Le Châtelier*

- hdmax2, an R package to perform high dimension mediation analysis, *F. Pittion*
- Advancing Drug-Target Interactions Prediction: Leveraging a Large-Scale Dataset with a Rapid and Robust Chemogenomic Algorithm, *G. Guichaoua*
- AttOmics: Attention-based architecture for diagnosis and prognosis from Omics data, *A. Beaude*

11:30 - 12:30 Poster session 2, ADM main hall / Demos Marthe Condat

12:30 - 14:00 Lunch, ADM main hall

14:00 - 15:00

Keynote: Paul Flliceck

*ADM, amphi. Marthe Condat, chair: Benoit Ballester*

Using data science to build a bridge from model systems to human disease



15:00 - 16:00	Assemblée Générale SFBI, Bioinfo-fr.net
16:00 - 16:30	Break & Coffee, ADM main hall
16:30 - 17:30	Network presentations - ADM, amphi Marthe Condat IFB, GDR BIMMM, JeBif, PCI, MERIT
17:30 - 19:30	CULTURAL ACTIVITIES (details on last pages) On-site : Retro-gaming : ADM, 1st floor near Marthe Condat Origami : ADM, Marthe Condat Downtown, via metro stations : Karaoke, Toulouse Secrète, Urban Challenge, Balade du patrimoine

## DAY 3 - Thursday June 27th

9:00 - 10:00	Keynote: Toni Gabaldon <i>ADM, amphi Marthe Condat, chair: Anais Baudot</i> Tracing genomic adaptations in emerging fungal pathogens.
10:00 - 10:30	Break & Coffee, ADM main hall
10:30 - 11:30	<b>S1:</b> Evolution: analyses - ADM, Marthe conda <ul style="list-style-type: none"> <li>Modeling the mosaic structure of bacterial genomes to infer their evolutionary history, <i>F. Massip</i></li> <li>Can we Predict Evolution ? <i>R. Bricout</i></li> <li>Origins and Functional Significance of Eukaryotic Protein Folds, <i>M Carpentier</i></li> </ul> <b>S2:</b> Platform & services: annotation &omics - 2A, Grignard <ul style="list-style-type: none"> <li>Advancing genome annotation with long-read RNA sequencing: Insights from the IGDRion Facility, <i>T. Derrien</i></li> <li>MicroScope: 20 years of expertise in microbial genomics, <i>A. Calteau</i></li> <li>A benchmark study of bioinformatics methods for single cell RNA-seq Nanopore long reads data, <i>A. Hamraoui</i></li> </ul> <b>S3:</b> Functionnal & integrative genomics - 2A, Le Chatelier <ul style="list-style-type: none"> <li>MethyLasso: a segmentation approach to analyze DNA methylation patterns and identify differentially methylation regions from whole- genome datasets, <i>A.F. Bardet</i></li> <li>DiffSegR: an RNA-seq data driven method for differential expression analysis using changepoint detection, <i>A. Liehrmann</i></li> <li>InteractORF, prediction of human sORF functions from an interactome study, <i>M. Slivak</i></li> </ul>



11:30 - 12:30	Posters session 3, ADM, main hall / Demos Marthe Condat
12:30 - 14:00	Lunch break, ADM main hall
14:00 - 16:00	MINI-SYPOSIA  <b>S1:</b> Artificial Intelligence in Life Sciences - implications for our professions - ADM, <i>Marthe Condat</i> <b>S2:</b> New horizons in computational approaches for deconvolving heterogeneous biological samples from bulk transcriptomic profiles - 2A, <i>Grignard</i> <b>S3:</b> Chromatin 3D structure and Hi-C data analysis - 2A, <i>Le Chatelier</i> <b>S4:</b> Towards accessible and reproducible computational systems biology analysis - U4, <i>Concorde</i>
16:00 - 16:30	Lunch break, ADM main hall
16:30 - 18:30	MINI-SYPOSIA  <b>S1:</b> Machine learning and statistics in genomics & metagenomics - ADM, <i>Marthe Condat</i> <b>S2:</b> Unravelling Cellular Landscapes : Advances in spatial transcriptomics - 2A, <i>Grignard</i> <b>S3:</b> Digital Twins for Human Health : the role of bio-informatics and computational biology - 2A, <i>Le Chatelier</i> <b>S4:</b> WASM Technology : a revolution for bioinformatics learning - U4, <i>Concorde</i>
20:00 - 00:00	Gala dinner (details on last pages)

## DAY 4 - Friday June 28th

9:30 - 10:30	<b>S1:</b> Systems biology and metabolomics - ADM, Marthe Condat <ul style="list-style-type: none"> <li>Comparative constraint-based modelling of fruit development across species highlights nitrogen metabolism in the growth-defence trade-off - <i>C. Beaumont</i></li> <li>Improving Snoussi constraints in the Thomas framework for Gene Networks - <i>G. Grataloup</i></li> <li>Large-scale computational modelling of the M1 and M2 synovial macrophages in rheumatoid arthritis - <i>A. Niarakis</i></li> </ul>
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9:30 - 10:30

**S2:** Platform & services: best practices - 2A, *Grignard*

- Misconceptions about Galaxy debunked by the (French) Galaxy Community. - *R. Libouban*
- nf-core a community dedicated to best-practices Nextflow workflows - *M. Garcia*
- codabench, a web-plateform to organize scientific competitions - *M. Richard*

**S3:** Knowledge representation, omics & cancer - 2A, *Le Chatelier*

- Graph representation learning and semantic distribution application to omic expression data - *I. Andr*
- Intégration reproductible d'informations de haut niveau dans des graphes de connaissances sémantiques avec OntoWeaver et BioCypher, applications en oncologie et en écologie - *J. Dreo*
- Characterizing intergenic transcription at RNA polymerase II binding sites in normal and cancer tissues - *B. Ballester*

10:30 - 11:00 Break & Coffee, ADM hall

11:00 - 12:00 Keynote: Clémence Frioux

*ADM, amphi. Marthe Condat, chair: Ludovic Cottret*

Exploration of microbial ecosystems: from compositional patterns to metabolic models

12:00 - 12:30 Conference closing words

12:30 - 14:00 Lunch / boxed lunch



## Information related to social events



TUESDAY, JUNE 25th, 18:30

### Welcome cocktail

Bulding ADM, main hall.

WEDNESDAY, JUNE 26th, 17h45 or 18:30

### Social events:



**17h35 : Group departures to downtown activities.  
Rendez-vous at ADM building, main hall.**

**17h45 : On-site activities, building ADM**

(*food & drinks strictly forbidden*)

- **Retro-gaming:** 1st floor, front of amphi. Marthe Condat
- **Origami:** Amphitheatre Marthe Condat

**18h30 : Downtown activities**

#### **- Balade du patrimoine / Toulouse secrète :**

Office de tourisme de Toulouse / Donjon du Capitole

2 square Charles-de-Gaulle(metro: line A, Capitole station)

#### **- Urban Challenge**

Place Saint Etienne (metro: line A, Esquirol station)

#### **- Karaoke**

58 rue Riquet (metro: line B, Jean Jaures station)



THURSDAY, JUNE 27th, from 19:00

### Gala dinner:

#### **Espaces Vanel**

1 Allée. Jacques Chaban-Delmas, 31500

**Metro:** line A, Marengo-SNCF station

**Bus :** fast line L9, Marengo-SNCF stop



