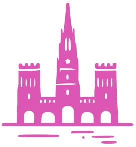
JOBIM 2024

25>28 JUIN
Toulouse

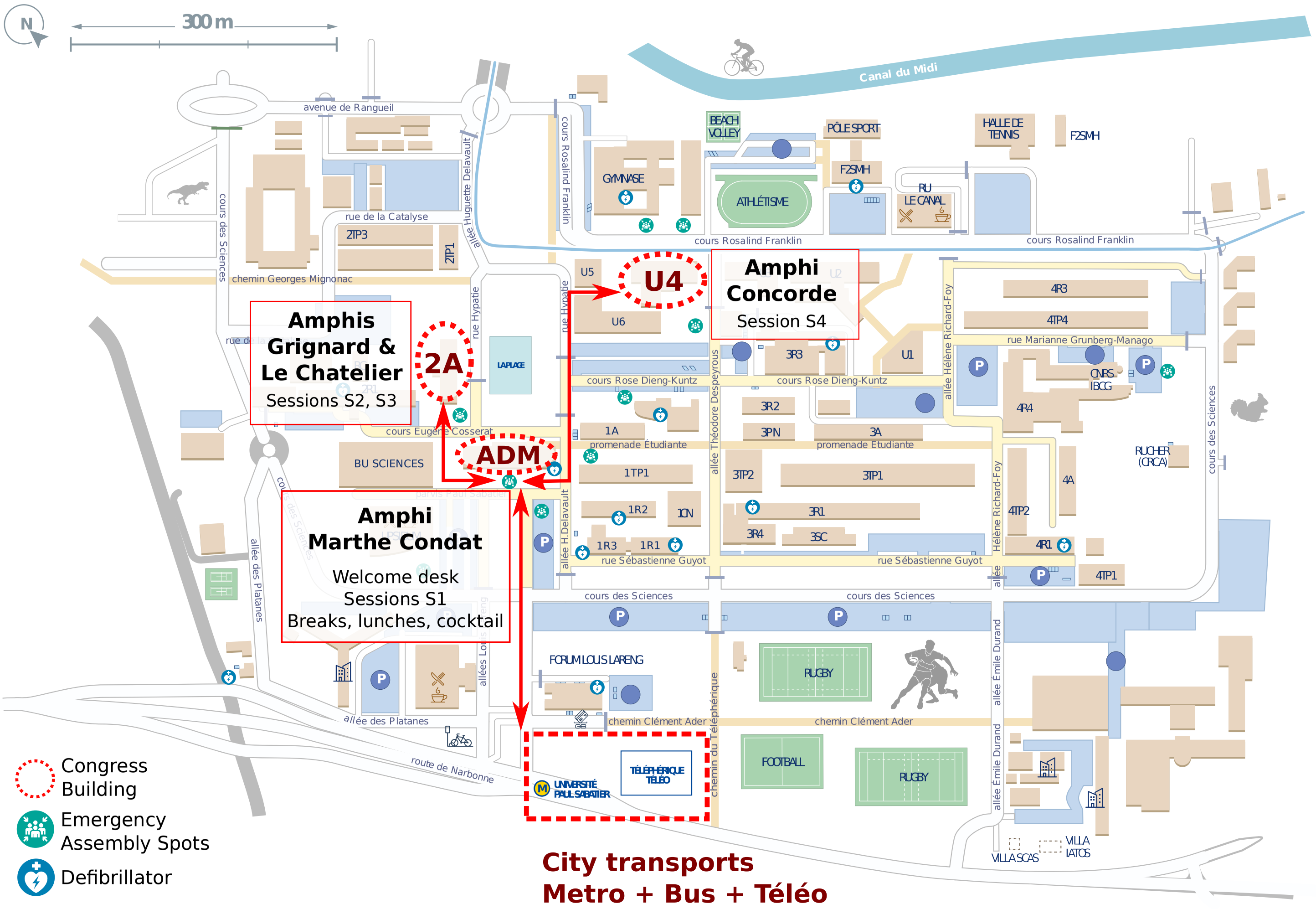
Journées Ouvertes en Biologie, Informatique et Mathématiques

POCKET PROGRAM

https://jobim2024.sciencesconf.org





Amphis Grignard & Le Chatelier

Sessions S2, S3

Amphi Marthe Condat

Welcome desk

Sessions S1

Breaks, lunches, cocktail

Amphi Concorde

Session S4

City transports Metro + Bus + Téléo

- ⭕ Congress Building
- Emergency Assembly Spots
- Defibrillator

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
- Benoit Aliaga, benoit.aliaga@inserm.fr

GOOD CONDUCT

In the event of a disrespectful behaviour or harassment, please contact :
- Sarah Djebali : sarah.djebali@inserm.fr
- Guillaume Devailly : 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

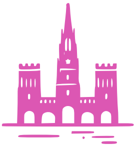
EDUSPOT

With login/password given on request at the reception
Un identifiant / mot de passe pourra être remis à l'accueil

#jobim2024 x.com/jobim2024

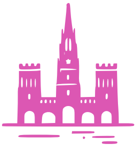
Please refrain from using your 4/5G mobile hotspots to reduce CO2 emissions and to share the rooms' bandwidths with your colleagues.

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

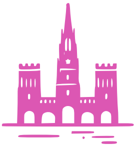
12:30 - 13:45	Registration, Building ADM, main Hall
13:45 - 14:00	Welcome & opening remarks, ADM, amphi Marthe Condat
14:00 - 15:00	Keynote: Nelle Varoquaux *ADM, amphi Marthe Condat, chair: Nathalie Vialaneix* Machine Learning Adventures in Biology: Overcoming Hurdles and Harvesting Biological Insights
15:00 - 16:00	Posters' flash presentations, ADM, amphi Marthe Condat
16:00 - 16:30	Break & Coffee, ADM main hall
16:30 - 17:30	**S1:** Statistics, Machine Learning and AI - ADM, *Marthe Condat* • Semi-supervised learning improves regulatory sequence prediction with unlabeled sequences - *R. Mourad* • scEVE: a scRNA-seq ensemble clustering algorithm that leverages the extrinsic variability to prevent over-clustering - *Y. Asloudj* • localScore: an R package to highlight optimal and suboptimal segment in a sequence with associated p-val computation - *S. Mercier* **S2:** Workflows, reproducibility & Open Science - *2A, Grignard* • PhaseImpute: a NF-Core pipeline for genetic imputation - *L. Le Nézet* • Benchmarking feature selection and feature extraction methods to improve the performances of machine-learning algorithms for patient classification using metabolomics biomedical data - *J. Labory* • Constructing a robust framework to benchmark deconvolution algorithms - *E. Amblard* **S3:** Evolution: Concepts - *2A, Le Chatelier* • Beyond Recombination: Exploring the Impact of Meiotic Frequency on Genome-wide Genetic Diversity - *L. Ollivier* • When lianas and trees talk DNA: new insights into genetic exchanges in plants - *E. Aubin* • Unzipped genome assemblies of polyploid root-knot nematodes reveal unusual and clade-specific telomeric repeats - *E.G.J. Danchin*
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* • RNAdvisor: 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* • Pangenome graph construction from genome alignments with Minigraph-Cactus, *J. Monlong* **S3:** Statistics and machine learning for clinical applications - *2A, Le Chaltelier* • 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 Flicek *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

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, Bioinfo-fr.net

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
ADM, amphi Marthe Condat, chair: Anais Baudot
Tracing genomic adaptations in emerging fungal pathogens.

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

10:30 - 11-30

S1: Evolution: analyses - ADM, *Marthe conda*

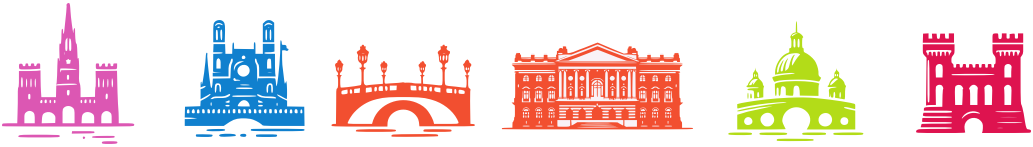
- Modeling the mosaic structure of bacterial genomes to infer their evolutionary history, *F. Massip*
- Can we Predict Evolution ? *R. Bricout*
- Origins and Functional Significance of Eukaryotic Protein Folds, *M Carpentier*

S2: Platform & services: annotation &omics - *2A, Grignard*

- Advancing genome annotation with long-read RNA sequencing: Insights from the IGDRion Facility, *T. Derrien*
- MicroScope: 20 years of expertise in microbial genomics, *A. Calteau*
- A benchmark study of bioinformatics methods for single cell RNA-seq Nanopore long reads data, *A. Hamraoui*

S3: Functionnal & integrative genomics - *2A, Le Chatelier*

- MethyLasso: a segmentation approach to analyze DNA methylation patterns and identify differentially methylation regions from whole- genome datasets, *A.F. Bardet*
- DiffSegR: an RNA-seq data driven method for differential expression analysis using changepoint detection, *A. Liehrmann*
- InteractORF, prediction of human sORF functions from an interactome study, *M. Slivak*



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-SYMPOSIA

S1: Articicial Intelligence in Lifes Sciences - implications for our professions - ADM, *Marthe Condat*

S2: New horisons in computationnal approaches for deconvolving heterogeneous biological samples from bulk transcriptomic profiles - 2A, *Grignard*

S3: Chromatine 3D structure and Hi-C data analysis - *2A, Le Chatelier*

S4: Towards accessible and reproducible computational systems biology analysis - *U4, Concorde*

16:00 - 16:30 Lunch break, ADM main hall

16:30 - 18:30 MINI-SYMPOSIA

S1: Machine learning and statistics in genomics & metagenomics - *ADM, Marthe Condat*

S2: Unravelling Cellular Landscapes : Advances in spacial transcriptomics - *2A, Grignard*

S3: Digital Twins for Human Health : the role of bio-informatics and computational biology - 2A, *Le Chatelier*

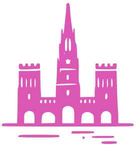
S4: WASM Technology : a revolution for bioinformatics learning - *U4, Concorde*

20:00 - 00:00 Gala dinner (details on last pages)

DAY 4 - Friday June 28th

9:30 - 10:30 **S1:** Systems biology and metabolomics - ADM, Marthe Condat

- Comparative constraint-based modelling of fruit development across species highlights nitrogen metabolism in the growth-defence trade-off - *C. Beaumont*
- Improving Snoussi constraints in the Thomas framework for Gene Networks - *G. Grataloup*
- Large-scale computational modelling of the M1 and M2 synovial macrophages in rheumatoid arthritis - *A. Niarakis*






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

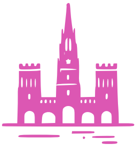
Exploration of microbial ecosystems: from compositional patterns to metabolic models

12:00 - 12:30

Conference closing words

12:30 - 14:00

Lunch / boxed lunch



Information related to social events

TUESDAY, JUNE 26th, 18:30

Welcome cocktail

Bulding ADM, main hall.

WEDNESDAY, JUNE 27th, 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

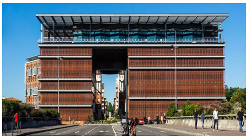
18h30 : Downtown activities

- 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 28th, 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



sfbi

société française de bioinformatique

IFB

INSTITUT FRANÇAIS DE BIOINFORMATIQUE

cnrs

GDR Groupement de recherche

BIMMM Bio-Informatique Moléculaire : Modélisation et Méthodologie

INRAE

GDR GÉNOMIQUE ENVIRONNEMENTALE

BGI

Pierre Fabre

iMEAN

cimi

Centre International de Mathématiques et d'Informatique

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Genotoul Bioinfo

CBI Toulouse

Centre de Biologie Intégrative

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La Région Occitanie Pyrénées - Méditerranée