JOBIM 2022

05>08 JUIL

Université de Rennes 1 | RENNES

Journées Ouvertes en Biologie, Informatique et Mathématiques

POCKET PROGRAM

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DAY 1 - TUESDAY JULY 5TH

12:00 - 14:00	Registration & welcome coffee
14:00 - 14:30	Welcome & opening remarks *Amphi A+B*
14:30 - 15:30	Keynote: **Cédric Notredame** ***Nextflow and NF-Core : growing your analysis with the right data sprinkler*** *Amphi A+B*
15:30 - 16:20	*Workflows, reproducibility & open science - Amphi A* • *UseGalaxy.fr: a Galaxy server for the French bioinformatics community,* **Anthony Bretaudeau** • *EMERGEN-BioInfo : The digital platform for the French SARS-CoV-2 genomic surveillance and research program,* **Thomas Denecker** *Metagenomics & microbial ecosystems - Amphi B* • *Genomic adaptation of the picoeukaryote Pelagomonas calceolata to iron-poor oceans revealed by a chromosome-scale genome sequence,* **Nina Guérin** • *Biosynthetic potential of the global ocean microbiome,* **Lucas Paoli** *Algorithms & data structures for sequences - Amphi C* • *Optimal Scaffolding for Chloroplasts' Inverted Repeats,* **Victor Epain** • *Findere: fast and precise approximate membership query,* **Lucas Robidou**
16:20 - 16:50	Coffee break
16:50 - 18:05	*Functional and integrative genomics - Amphi A* • *GC content but not nucleosome positioning directly contributes to intron-splicing efficiency in Paramecium,* **Chun-Long Chen** • *Gene Expression prediction using Deep Learning,* **Camille Kergal** • *Exploring variability of machine learning methods : first step towards biomarker consensus signatures,* **Raluca Uricaru** *Knowledge representation, databases & visualization - Amphi B* • *FORUM: Knowledge Graph (KG) for semantic representation and inference of relations between chemicals and biomedical concepts,* **Maxime Delmas** • *Detection and correction of non-conformities and redundancies in complexes of molecules in BioPAX,* **Camille Juigné** • *VOCAL: An early warning system to detect concerning new SARS-CoV-2 variants from sequencing data,* **Hugues Richard** *Statistics, machine learning, AI & image analysis - Amphi C* • *TopoFun: a machine learning method to improve the functional similarity of gene co-expression modules,* **Laurent Journot** • *GraphGONet: a self-explaining neural network encapsulating the Gene Ontology graph for phenotype prediction on gene expression,* **Victoria Bourgeais** • *Adaptive splines-based logistic regression with a ReLU neural network,* **Marie Guyomard**
18:05 - 18:30	**Denis Bourguet** ***Peer Community In: A free alternative to evaluate, validate (and publish) preprints*** *Amphi A+B*
18:30 - 20:00	Opening cocktail

DAY 2 - WEDNESDAY JULY 6TH

09:00 - 09:55	Keynote: **Pierre Peterlongo** ***Swim in the data tsunami*** *Amphi A+B*
09:55 - 10:15	Coffee break
10:15 - 11:30	*Algorithms & data structures for sequences - Amphi A* • *kmtricks: creating bloom filters for indexing large sequencing data collections*, **Téo Lemane** • *Genotyping multiscale variation with genome graphs*, **Brice Letcher** • *Assessing conservation of alternative splicing with evolutionary splicing graphs*, **Hugues Richard** *Structural bioinformatics & proteomics - Amphi B* • *Conformational variability in proteins bound to single-stranded DNA: A new benchmark for new docking perspectives*, **Dominique Mias-Lucquin** • *Tree Diet: Reducing the Treewidth to Unlock FPT Algorithms in RNA Bioinformatics*, **Bertrand Marchand** • *Analysis of SARS-CoV-2 and human protein interactions: a CA-PRI-COVID Round*, **Théo Mauri** *Systems biology & metabolomics - Amphi C* • *Inference of an Integrative, Executable Network for Rheumatoid Arthritis Combining Data-Driven Machine Learning Approaches and a State-of-the-Art Mechanistic Disease Map*, **Anna Niarakis** • *Calcium signaling is impaired in PTEN-deficient T cell acute lymphoblastic leukemia*, **Saran Pankaew** • *Comprehensive multi-omics integration of major depressive disorder*, **Amazigh Mokhtari**
11:30 - 12:30	Poster and demo presentations *(even numbers)*
12:30 - 14:00	Lunch
14:00 - 15:00	Keynote: **Hélène Morlon** ***Analyzing the evolution of the microbiome using meta-barcoding data*** *Amphi A+B*
15:00 - 16:00	AG SFBI *Amphi A+B*
16:00 - 16:30	Coffee break
16:30 - 17:00	GDR BIM meeting *Amphi A+B*
17:00 - 17:30	IFB meeting *Amphi A+B*
17:30 - 20:00	Social events

DAY 3 - THURSDAY JULY 7TH

09:00 - 09:55	Keynote: **Anne-Laure Boulesteix** ***A replication crisis in methodological computational research?*** *Amphi A+B*
09:55 - 10:15	Coffee break
10:15 - 11:30	*Statistics, machine learning, AI & image analysis - Amphi A* • *Computing disease progression scores using multimodal variational autoencoders trained with neuroimaging and microRNA data*, **Virgilio Kmetzsch** • *Improving the accuracy of small variant calling with ensemble machine learning methods*, **Guillaume Rizk** • *LowKi: Efficient estimation of kinship and fraternity coefficients from low-depth sequencing data*, **Anthony Herzig** *Functional and integrative genomics - Amphi B* • *Single-cell RNA sequencing reveals aberrant megakaryocyte-erythroid progenitor and megakaryocyte populations in thrombocytopenic ETV6 variant carriers*, **Timothée Bigot** • *Uncovering specific alterations of ribosomal RNA 2'O-ribose methylation in glioma subtypes using the latest improvements of RiboMethSeq technology*, **Hermes Paraqindes** • *Condition-specific and recurrent perturbation-communities in multiple differential co-expression networks*, **Galadriel Brière** *Workflows, reproducibility & open science - Amphi C* • *Bioinformatics platforms and data management : the GenOuest experience*, **Konogan Bourhy** • *Linda: an interactive framework for experimental design and management of metadata*, **Benjamin Dartigues** • *Improving clinical diagnosis using Nanopore Adaptive Sampling and NanoCliD*, **Eléonore Frouin**
11:30 - 12:30	Poster and demo presentations *(odd numbers)*
12:30 - 14:00	Lunch
14:00 - 15:00	Keynote: **Guillaume Bourque** ***Transposable elements are a source of innovation and variability in our response to infection*** *Amphi A+B*
15:00 - 18:00	**Mini-symposia in parallel:** *(coffee break 16h15-16h45)* • *Amphi A:* Indexing and query large collections of sequencing data • *Amphi B:* Management and integration of agronomical, phenotypical and environmental data • *Amphi C:* Bioinformatics of metabolic pathways, from sequences to molecules • *Amphi D:* Simulation of biological sequences and evolutionary processes • *Amphi E:* Structural characterization of macro-assemblies by integrative techniques
18:00	Gala dinner & more

DAY 4 - FRIDAY JULY 8TH

09:15 - 10:30	*Structural bioinformatics & proteomics - Amphi A* • *KinDock 2.0: A robust protein-kinases virtual screening tool enhanced by machine learning predictors,* **Victor Reys** • *Effect of quercetin on lipid membrane rigidity: assessment by atomic force microscopy and molecular dynamics simulations,* **Jad Eid** • *Pseudoquantifying hundreds of proteins in millions of single cells,* **Etienne Becht** *Integrative genomics & evolution - Amphi B* • *Overcoming small and incomplete datasets limitations in multi-omic integration,* **Pauline Brochet** • *Interaction between gene expression and chromatin environment: application to the study of H3K79me2 and its methyltransferase DOT1L during spermatogenesis,* **Manon Coulée** • *Insertion of Alu elements impacts sequence-mediated nucleosome positioning,* **Benjamin Audit** *Knowledge representation, databases & visualization - Amphi C* • *Discovery of potential functional paths by integration of phospho-proteomics data in the PPI network using a RWR framework,* **Jérémie Perrin** • *Semantic Web technologies are effective to remove redundancies from protein-protein interaction databases and define reproducible interactomes,* **Olivier Dameron** • *Investigating ADR mechanisms with Explainable AI: a feasibility study with knowledge graph mining,* **Adrien Coulet**
10:30 - 11:00	Coffee break
11:00 - 12:00	Keynote: **Raphaël Guérois** ***Exploring interactomes in 3D under the lens of coevolution*** *Amphi A+B*
12:00 - 12:30	JOBIM23, SFBI awards & closing remarks *Amphi A+B*
12:30	Lunch box

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EDUROAM :
To use in priority with your usual login/password. À utiliser en priorité avec votre identifiant/mot de passe.

EDUSPOT
With login/password given on request at the reception. Avec identifiant/mot de passe remis sur demande à l'accueil.

Please refrain from using your phone as a 4G hotspot.

Veuillez vous abstenir d'utiliser votre téléphone comme un hotspot 4G (pas de partage de connexion svp).

JULY 5, 18:30

Opening cocktail:
Université de Rennes 1, Campus de Beaulieu.

JULY 6, 17:30

Social events:
17h35 : Rdv dans le grand hall, pour un départ groupé en transports en commun (bus).

Pour les personnes qui souhaitent se rendre aux visites par leurs propres moyens :
- Visite couplée : la ville et le Parlement de Bretagne : rdv à 18h30 sous les arcades, bas de la place du parlement, rue de Brilhac.
- Le parc du Thabor, parenthèse enchantée : rdv à 18h30 place St Melaine, devant les grilles de l'entrée du Thabor.
- La folle aventure sonore : rdv à 18h30 sur le parvis du couvent des Jacobins, place Ste Anne.
- Séance d'escalade à la maison de l'escalade «The Roof» : rdv à 18h30 au 2 rue de l'Hôtel Dieu.
- Jeux et détente « à l'armoricaine », Immersion dans le cliché Breton : activités sur le campus de Beaulieu.

JULY 7, 18:00

Gala dinner:
Le MeM
Accès route de Sainte-Foix
La Piverdière
35000 Rennes

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