

Day 1 : 06 July

From 09:00	Connection tests		
10:00 - 11:00	Opening remarks		Main room
11:00 - 11:55	<p>Opening Keynote Sarah Teichmann <i>TBAMultiMAP: Dimensionality Reduction of Multiple Datasets by Manifold Approximation and Projection</i> Chairwoman: Emmanuelle Becker</p>		Main room
12:00 - 12:15	<p>Sponsor - Plan France Médecine Génomique <i>Le Collecteur analyseur de données du Plan France médecine génomique</i> Yves Vandenbrouck</p>		Main room
Lunch			
13:30 - 14:00	<p>GDR Bioinformatique Moléculaire (BIM) Hélène Touzet</p>		Main room
14:00 - 15:20	<p>Session 1 <i>Room 1</i> Structural Bioinformatics I Chairwoman: Christine Gaspin</p>	<p>Session 2 <i>Room 2</i> Statistics, machine learning & artificial intelligence I Chairwoman: Laura Cantini</p>	<p>Session 3 <i>Room 3</i> Functional Genomics Chairman: Nicolas Thierry-Mieg</p>
	<p>Jean-Christophe Gelly <i>Flexible protein structural alignment for non trivial comparisons</i></p>	<p>Nicolas Scalzitti <i>Spliceator: A new strategy for genome annotation using deep learning algorithm</i></p>	<p>Lucile Massenet-Regad <i>Dissection of intercellular communication using the transcriptome-based framework ICELLNET</i></p>
	<p>Tatiana Galochkina <i>MEDUSA: deep learning based protein flexibility prediction</i></p>	<p>Thomas Weber <i>MISTIC: A prediction tool to reveal disease-relevant deleterious missense variants</i></p>	<p>Yaqun Liu <i>Topoisomerase I prevents transcription-replication conflicts at transcription termination sites</i></p>
	<p>Coline Gianfrotta <i>A graph-based similarity approach to classify recurrent complex motifs from their context in RNA structures</i></p>	<p>Mathys Grapotte <i>Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network</i></p>	<p>Jean Fontaine <i>Automated quality control of NGS data using machine learning</i></p>
	<p>Alix Delannoy <i>Feature extraction for the clustering of small 3D structures: application to RNA fragments</i></p>	<p>Camille Roquencourt <i>Processing of Proton Transfer Reaction Time-of Flight Mass Spectrometry (PTR-TOF-MS) data for untargeted biomarker discovery in exhaled breath: application to COVID-19 intubated ventilated patient</i></p>	<p>Clémentine Decamps <i>PenDA, a rank-based method for personalized differential analysis: application to lung cancer</i></p>
Coffee break			
15:30 - 17:00	Posters session 1 (Even numbers)		Poster room
17:00 - 17:30	<p>Institut Français de Bioinformatique (IFB) Claudine Médigue & Jacques van Helden</p>		Main room

Day 2 : 07 July

09:00 - 09:55	<p>Keynote Main room Jean-Philippe Vert <i>Deep learning for biological sequences</i> Chairman: Mahendra Mariadassou</p>	
10:00 - 10:40	<p>Session 4 Room 1 Databases & data visualisation Chairwoman: Sophie Schbath</p>	<p>Session 5 Room 2 Evolution & phylogenetics Chairman: Etienne Danchin</p>
	<p>Alexandre G. De Brevern <i>CALR-ETdb, the database of calreticulin variants diversity in essential thrombocythemia</i></p>	<p>Georgios Koutsovoulos <i>AvP: a software package for automatic phylogenetic detection of candidate horizontal gene transfers.</i></p>
	<p>Sandra Dérozier <i>Genoscapist: online exploration of quantitative profiles along genomes via interactively customized graphical representations</i></p>	<p>Marie Morel <i>ConDor: Site-wise convergence detector in large protein alignments</i></p>
<p>Session 6 Room 3 Computational Systems Biology Chairwoman: Elisabeth Remy</p>		
<p>Athénaïs Vaginay <i>Automatic Synthesis of Boolean Networks from Biological Knowledge and Data</i></p>		
<p>Sébastien Légaré <i>Distinguishing context dependent events in quotients of causal stories</i></p>		
<p>Coffee break</p>		
11:00 - 12:30	<p>Posters session 2 (Odd numbers) Poster room</p>	
<p>Lunch</p>		
14:00 - 14:55	<p>Keynote Main room Julie Reveillaud <i>Wolbachia population genomes from individual Culex pipiens ovaries reveal a plasmid-like extrachromosomal circular element</i> Chairwoman: Claudine Médigue</p>	
15:00 - 15:15	<p>Sponsor - Illumina Main room David Townley</p>	
<p>Coffee break</p>		
15:30 - 18:00	<p>Symposium Room 1 Bioinformatics for microbiomes</p>	<p>Symposium Room 2 Symposium Post selection inference: valid double-dipping</p>
	<p>Rob Fin <i>Translating microbiome research outputs into main stream services in MGnify</i></p>	<p>Yuval Benjamini <i>Selective inference for region detection with high-throughput genomic assays</i></p>
	<p>Lisa Röttjers <i>Development of computational approaches for the prediction and analysis of species interaction networks from metagenomics data</i></p>	<p>Mitra Ebrahimpoor <i>Inflated False Discovery Rate due to Volcano Plots: Problem and Solutions</i></p>
<p>Raffaele Siano <i>Sedimentary ancient DNA revealed irreversible plankton shifts and toxic microalgae species invasion in relation to human impact in the Bay of Brest</i></p>		<p>Pause</p>
<p>Flash presentations</p>		<p>Antoine Villié <i>Post-Selection Inference for Sequence Motifs</i></p>
<p>Flash presentations</p>		<p>Lucy Gao <i>Valid Differential Analysis for Groups Defined via Clustering</i></p>

Day 3 : 08 July (Morning)

<p>09:00 - 09:55</p>	<p style="text-align: center;">Keynote Thomas Schiex <i>Computer-aided protein design</i> Chairwoman: Gwenaëlle André-Leroux</p> <p style="text-align: right;"><i>Main room</i></p>		
<p>10:00 - 11:00</p>	<p style="text-align: center;">Session 7 Room 1 Algorithms & sequence data structures I Chairwoman: Raluca Uricaru</p>	<p style="text-align: center;">Session 8 Room 2 Meta-omics & microbial genomics Chairman: Damien Eveillard</p>	<p style="text-align: center;">Session 9 Room 3 Platform services and activities Chairman: Erwan Corre</p>
	<p style="text-align: center;">Vincent Sater <i>UMI-Gen: a UMI-based read simulator for variant calling evaluation</i></p>	<p style="text-align: center;">Clémence Frioux <i>No microbe is an island: metabolic complementarity in the microbiota and identification of key players</i></p>	<p style="text-align: center;">Fabrice Allain <i>Best practices of software development with Nextflow to support daily production in oncology</i></p>
	<p style="text-align: center;">Frederic Jarlier <i>QUARTIC: QUick pArallel algoRithms for high-Throughput sequenCing data proCessing</i></p>	<p style="text-align: center;">Benoit Goutorbe <i>Shallow Shotgun Metagenomics as a cost-effective and accurate alternative to WGS for taxonomic profiling and clinical diagnosis</i></p>	<p style="text-align: center;">Laurent Jourden <i>ToulligQC 2: fast and comprehensive quality control for Oxford Nanopore sequencing data</i></p>
<p style="text-align: center;">Roland Faure <i>GraphUnzip: unzipping assembly graphs with long reads and Hi-C</i></p>	<p style="text-align: center;">Adelme Bazin <i>panRGP: a pangenome-based method to predict genomic islands and explore their diversity</i></p>	<p style="text-align: center;">Romain Dallet <i>Galaxy Genome Annotation (GGA) environment in the cloud</i></p> <p style="text-align: center;">Jacques van Helden <i>A digital space for EMERGEN, the French plan for SARS-CoV-2 genomic surveillance and research</i></p>	
<p>Coffee break</p>			
<p>11:15 - 11:30</p>	<p style="text-align: center;">Association des Jeunes Bioinformaticiens de France (JeBiF) Victor Grentzinger</p> <p style="text-align: right;"><i>Main room</i></p>		
<p>11:30 - 12:30</p>	<p style="text-align: center;">Assemblée Générale de la Société Française de Bioinformatique (SFBI) Julien Fumey, Anna-Sophie Fiston-Lavier & Matthias Zytnicki</p> <p style="text-align: right;"><i>Main room</i></p>		
<p>Lunch</p>			

Day 3 : 08 July (Afternoon)

14:00 - 14:55	<p>Keynote Carole Goble <i>FAIR Computational Workflows</i> Chairwoman: Sarah Cohen-Boulakia</p>	<i>Main room</i>
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15:00 - 15:15	<p>Sponsor - Génopole d'Evry <i>Genomics in Genopole : A second wind</i> Christophe Lanneau</p>	<i>Main room</i>
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Coffee break

	Symposium Open Science and Interoperability in Bioinformatics <i>Room 1</i>	Symposium Where are we in the search for DNA motifs involved in transcriptional regulation? <i>Room 2</i>	Symposium Integrative structural modeling in the era of big data and artificial intelligence <i>Room 3</i>
15:30 - 18:00	<p>Sarah Cohen-Boulakia <i>Introduction aux concepts de la Science Ouverte et de l'Interopérabilité appliqués à la Bioinformatique</i></p> <p>Frank Michel <i>Annoter les pages web liées à la biodiversité avec des informations structurées pour les rendre plus découvrables et réutilisables</i></p> <p>Philippe Rocca-Serra <i>Operating Fair principles: the FAIR cookbook project</i></p> <p>Cyril Pommier <i>Standards d'échanges et concepts FAIR pour la Communauté Plantes</i></p> <p>Laura Furlong <i>The DisGeNET knowledge platform: facilitating the access and use of disease genomics data</i></p> <p>Oliver Collin & Konogan Bouhry <i>maDMP: vers un écosystème intégré pour la gestion des données de la Recherche</i></p> <p style="text-align: center;">Pause</p> <p>Flash presentations: T.Rosnet, J. Seiler, P.Poulain, H. Chiapello</p> <p style="text-align: center;">Round Table</p>	<p>François Parcy <i>Confronting in vitro genomics to real life data reveals properties of floral transcription factors</i></p> <p>Morgane Thomas-Chollier <i>Motif discovery in epigenomics datasets with RSAT peak-motifs2</i></p> <p>Anthony Mathelier <i>Combining TF binding profiles with ChIP-seq data to predict high quality direct TF-DNA interaction</i></p> <p style="text-align: center;">Pause</p> <p>Laurent Bréhélin <i>Identification of long regulatory elements in the genome of Plasmodium falciparum and other eukaryotes</i></p> <p>Julien Rozière <i>Genome-wide de novo detection of preferentially located motifs in 5'- and 3'-proximal regions from Arabidopsis and maize</i></p>	<p style="text-align: center;"><i>Introduction: Current challenges in 3D modeling of proteins and complexes</i></p> <p>Riccardo Pellarin <i>Bayesian modeling in integrative structural biology</i></p> <p>Ezgi Karaca <i>Dynamic Integrative Modeling of Molecular Machines</i></p> <p style="text-align: center;">Pause</p> <p>Sergei Grudinin <i>Entering the post-protein structure prediction era</i></p> <p>Slavica Jonic <i>Cryo-EM studies of continuous conformational variability of biomolecules in vitro and in situ based on image analysis, simulation and deep learning</i></p>

Day 4 : 09 July

09:00 - 09:55

Keynote
Roderic Guigó Serra
The epigenetic logic of gene activation
Chairman: Charles Lecellier

Main room

10:00 - 10:15

Sponsor - **France Génomique**
France Génomique : a distributed Infrastructure for Genomic Projects
Patrick Wincker

Main room

Coffee break

10:30 - 11:50

Session 10 *Room 1*
Structural Bioinformatics II
Chairman: Benjamin Bardiaux

Victor Reys
SLiMAN - a webserver to analyze protein-protein interaction mediated by short linear motifs

Gautier Peyrat
Discovery of macrocyclic inhibitors of ALK using Frags2Drugs, a fragment-based drug design in silico tool

Sarah Naceri
Structural analysis of interaction between SARS-CoV-2 spike protein and the human ACE2 receptor

Anastasia Croitoru
Cyclodipeptide synthases of the NYH subfamily recognize tRNA using an α -helix enriched with positive residues

Session 11 *Room 2*
Statistics, machine learning & artificial intelligence II
Chairman: Nicolas Vergne

Nicolas Enjalbert-Courrech
IIDEA: Interactive Inference for Differential Expression Analyses

Laura Cantini
Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer

Charles-Elie Rabier
The SgenoLasso and its cousins for selective genotyping and extreme sampling

Raphaël Romero
A systematic analysis of the genomic features involved in cellular specificities of transcription factor binding

Session 12 *Room 3*
Algorithms & sequence data structures II
Chairman: Rayan Chikhi

Anne Guichard
MTG-Link: filling gaps in draft genome assemblies with linked read data

Pierre Morisse
LEVIATHAN: efficient discovery of large structural variants by leveraging long-range information from Linked-Reads data

Cedric Chauve
Freddie: annotation-independent detection and Ddscovery of transcriptomic alternative splicing isoforms using long-read sequencing

11:50 - 12:30

Présentation JOBIM 2022
Prix SFBI
Clôture de JOBIM 2021

Main room