



DAY 1 - TUESDAY JULY 2ND

12:00 - 14:00	Registration
Auditorium 450	
14:00 - 14:30	Welcome speech and JOBIM opening
14:30 - 15:30	Keynote: Olivier Delaneau, <i>Chromatin three-dimensional interactions mediate genetic effects on gene expression</i>
15:30 - 15:50	Genotyping Structural Variations using Long Reads data, <i>Lolita Lecomppte</i>
15:50 - 16:10	Sequana coverage: detection and characterization of genomic variations using running median and mixture models, <i>Thomas Cokelaer</i>
16:10 - 16:30	mCNA : a new methodology to improve high-resolution copy number variation analysis from next generation sequencing using unique molecular identifiers, <i>Pierre-Julien Viailly</i>
16:30 - 17:00	Coffee Break
17:00 - 17:20	How to build up soil bacterial co-occurrence networks from wide spatial scale sampling?, <i>Battle Karimi</i>
17:20 - 17:40	Reference-guided genome assembly in metagenomic samples, <i>Cervin Guyomar</i>
17:40 - 18:00	Deciphering intra-species bacterial diversity of meat and seafood spoilage microbiota using gyrB amplicon sequencing: A comparative analysis with 16S rDNA V3-V4 amplicon sequencing, <i>Olivier Rué</i>
18:00 - 18:35	Bioinformatics associations overview
18:35 - 20:15	Opening cocktail

DAY 2 - WEDNESDAY JULY 3RD

Auditorium 450	
09:00 - 10:00	Keynote: Alessandra Carbone, <i>Evolutionary conservation</i>
10:00 - 10:20	Flash poster presentation odd numbers (4x5')
10:20 - 10:40	Coffee Break
Auditorium 450	
10:40	A review of different ways to insert known RNA modules into RNA secondary structures, <i>Louis Becquey</i>
11:00	Allele-specific analysis of epigenetic and transcriptomic data to study Drosophila developmental cis-regulatory architecture, <i>Swann Floc'Hlay</i>
11:20	SPiP: Splicing Prediction Pipeline addressing the diversity of splice alterations, validated on a curated diagnostic set of 2,784 exonic and intronic variants, <i>Raphael Leman</i>
Room 200	
10:40	Signature analysis of Structural Variants reveals a new subclass of hepatocellular carcinoma characterized by Cyclin A2/E1 alterations, <i>Quentin Bayard</i>
11:00	Adaptation to animal sources of Salmonella enterica subsp. enterica deciphered by Genome Wide Association Study and Gene Ontology Enrichment Analysis at the pangenomic scale, <i>Vila Nova Meryl</i>
11:20	Merging of phenotypic information from cytometric profiles at the single-cell resolution, <i>Nicolas Tchitchek</i>
Auditorium 450	
11:40 - 12:40	Poster and Demo session odd numbers
12:40 - 14:00	Lunch
Auditorium 450	
14:00 - 15:00	Keynote: Christophe Dessimoz, <i>Big Data: opportunities, pitfalls, and remedies</i>
Thematic workshops:	
15:00 - 16:30	1 Bioimage informatique : la generation de phenomique en bioimagerie Room H
	2 Methods for single-cell omics data analysis Room 200
	3 Omics dark matter Auditorium 450
	4 Predictive approaches for biological systems engineering Room G
	5 Protein structure and design: from sequence to function Room I
16:30 - 17:00	Coffee Break

17:00 - 18:00	Thematic workshops (second part)
18:00 - 20:20	Social events

DAY 3 - THURSDAY JULY 4TH

Auditorium 450	
09:00 - 10:00	Keynote: Alexander Bockmayr, <i>Understanding cellular behaviours through mathematical optimization</i>
10:00 - 10:20	Flash poster presentation even numbers (4x5')
10:20 - 10:40	Coffee Break
Auditorium 450	
10:40	Architecture and evolution of blade assembly in β -propeller lectins, <i>François Bonnardel</i>
11:00	Novel insight on molecular dynamics trajectories: local equilibrium viewed by kappa-segmentation, <i>Sharad Goulam</i>
Room 200	
10:40	CISPER: Computational Identification of Switch Points (in a Metabolic Network) within an Environmental Range, <i>Francis Mairat</i>
11:00	A new method for evaluating the impacts of semantic similarity measures on the annotation of gene sets, <i>Aarón Ayllón-Benítez</i>
Auditorium 450	
11:20 - 12:20	Poster and Demo session even numbers
12:20 - 13:30	Lunch
Auditorium 450	
13:30 - 14:30	Keynote: Chloe-Agathe Azencott, <i>Structured feature selection for biomarker discovery in precision medicine</i>
14:30 - 15:10	IFB invited speaker: Guy Cochrane, <i>European Nucleotide Archive: connectivity and community</i>
Auditorium 450	
Parallel session	
15:10 - 15:25	AskOmics: a user-friendly interface to Semantic Web technologies for integrating local datasets with reference resources, <i>Xavier Garnier</i>
15:25 - 15:40	WAVES: a Web Application for Versatile Enhanced bioinformatic Services, <i>Vincent Lefort</i>
15:40 - 15:55	DevOps bioinformatics services with Docker, GitLab CI, and Kubernetes, <i>Bryan Brancotte</i>

15:55 - 16:10	Shiny and Galaxy interactive software for multi-source data analysis, <i>Etienne Camenen</i>
16:10 - 16:30	NNCR IFB : Les ressources Core Cluster et Cloud de l'IFB, <i>Nicole Charrière, David Benaben</i>
Room 200	
Parallel session	
15:10 - 15:30	Exploring the uncharacterized human proteome using neXtProt, <i>Lydie Lane</i>
15:30 - 15:50	Redesign of iPPI-DB, a database for modulators of Protein-Protein Interactions, <i>Rachel Torchet</i>
15:50 - 16:10	ProteoRE, a Galaxy-based platform for the annotation and the interpretation of proteomics data in biomedical research, <i>David Christiany</i>
16:10 - 16:30	UniFIRE: the UniProt Functional annotation Inference Rule Engine, <i>Rabie Saïdi</i>
16:30 - 17:00	Coffee Break
Auditorium 450	
17:00 - 18:00	AG SFBI
18:00 - 18:30	Meeting GDR BIM
18:30 - 19:00	Meeting IFB
19:30 - 02:00	Gala dinner and more

DAY 4 - FRIDAY JULY 5TH

Auditorium 450	
09:30 - 10:30	Keynote: Juliette Martin, <i>Protein-protein interactions: the tip of the iceberg</i>
10:30 - 11:00	Coffee Break
11:00 - 11:20	eIPrep 4: A high-performance tool for sequence analysis, <i>Roel Wuylts</i>
11:20 - 11:40	CONSENT: Scalable self-correction of long reads with multiple sequence alignment, <i>Pierre Morisse</i>
11:40 - 12:00	A De Novo Robust Clustering Approach for Amplicon-Based Sequence Data, <i>Alexandre Bazin</i>
12:00 - 12:30	Closing and farewell JOBIM 2019 Presentation of JOBIM 2020