

Day 1 : Tuesday July 3

From 12:00		Registration Check-in Welcome Coffee	
14h00 Auditorium JOBIM Plenary session Welcome opening speech JOBIM 2018			
Session 1: Bioinformatics for Bugs, Beasts and Greens - Part 1			
14h30		KEYNOTE: LUDOVIC ORLANDO	
15h30		Co-option of complex molecular system in bacterial and archaeal membrane	
15h30		REMI DENISE	
15h50		The evolution of large and giant viruses and their relationships with Eukaryotes	
15h50 16h10		JULIEN GUGLIELMINI	
16h10 16h30		Probabilistic PCA for count data in microbial ecology	
16h30		MAHENDRA MARIADASSOU	
16h30		Coffee Break	Booths in Exhibition Zone
17h00		Presentation of the "Groupement de Recherche Génomique Environnementale"	
17h05		PPanGGOLiN: Depicting microbial diversity via a Partitioned Pangenome Graph	
17h05		GUILLAUME GAUTREAU	
17h25		CARNAC-LR: Clustering coefficient-based Acquisition of RNA Communities in Long Reads	
17h25 17h45		CAMILLE MARCHET	
17h45		Assembling the genome of the desert ant and uncovering structural rearrangements with instaGRAAL, a fast and scalable scaffolder based on Hi-C data	
18h05		LYAM BAUDRY	
18h05		Presentations JeBiF / bioinfo-fr.net / Bioinfuse	
18h35		OPENING DINNER COCKTAIL	
22h00			

Day 2 : Wednesday, July 4

8h45		Welcome Coffee	
Auditorium JOBIM Plenary session			
Session 2: New Bioinformatic Challenges in the Personalized Medicine Era - Part 1			
9h00		KEYNOTE: PIERRE-ANTOINE GOURRAUD	
10h00		Bayesian Genome-Wide Association Study to discover novel lifespan-associated loci	
10h00		NINON MOUNIER	
10h20		Aggregation of rare family-specific variants associated with Rheumatoid Arthritis	
10h20		MAËVA VEYSSIERE	
10h40		Coffee Break	Booths in Exhibition Zone
11h10		Auditorium	DNA Room
11h10		Methods for Variant analyses	New solutions to methodological challenges
11h30		Maxime Garcia	Danesh Gonché
11h30		Sarek, a portable workflow for WGS analysis of germline and somatic mutations	A new rapid, flexible and intuitive software to simulate phylogenies of infections
11h30		Pierre-Julien Vially	Tristan Cordier
11h50		I-LowVarFreq: improving low-frequency variant detection using a new UMI-based variant calling approach for paired-end sequencing NGS libraries	Combining eDNA metabarcoding and supervised machine learning for routine environmental applications: an example with marine aquaculture
11h50		Tania Cuppens	Raluca Uricaru
12h10		From individual genetic variations towards haplotype: GEMPROT a new way of reading VCF files	On improving the approximation ratio of the r-shortest common superstring problem
12h10		Lunch	Cambridge2Marseilles Chat
13h30		Auditorium JOBIM Plenary session	
Session 3: New Bioinformatic Challenges in the Personalized Medicine Era - Part 2			
13h30		KEYNOTE: ELEFThERIA ZEGGINI	
14h30		Unravelling human preimplantation development by single-cell RNA-Seq: from experiment design to cell fate trajectories	
14h30		DIMITRI MEISTERMANN	
14h50		Proteomic and phosphoproteomic analysis of medulloblastoma reveals distinct activated pathways between subgroups	
15h10		LOREDANA MARTIGNETTI	
15h10		Flash Poster Presentations Even numbers 4x5'	
15h30		Coffee Break	Booths in Exhibition Zone
16h00		Poster Session Even numbers - Poster Zone	
17h00		Auditorium	DNA Room
17h00		Session 1 - Part 2 Microbial Communities	Disease-associated genomics
17h20		Eléonore Frouin	Christian Dina
17h20		Comparative metagenomics highlighted a core of metabolic capabilities in multiple serpentinizing ecosystems	Fine-scale genetic population structure in western France
17h20		Léo d'Agata	Jeremy Tournayre
17h40		Single-cell genome study of marine protists in the framework of the Tara Oceans project	Identification de marques épigénétiques marqueurs de prédisposition aux maladies métaboliques
17h40		Malo Le Boulch	Andreas Zanzoni
18h00		MACADAM a user-friendly MetAboliC pPathway DAtabase for complex Microbial community function analysis	Perturbed human sub-networks by Fusobacterium nucleatum candidate virulence proteins
18h00		Booths in Exhibition Zone	
19h30		SOCIAL EVENTS	
20h30		FREE EVENING	
Evening			

Day 3 : Thursday, July 5

8h20	Welcome Coffee		
Auditorium JOBIM Plenary session			
Session 4: Systems Biology and Functional Genomics			
8h40 9h40	KEYNOTE: EDDA KLIPP		
9h40 10h00	Statistical modeling of bacterial promoter sequences for regulatory motif discovery using expression data IBRAHIM SULTAN		
10h00 10h20	A map of direct TF-DNA interactions in the human genome ANTHONY MATHÉLIER		
10h20 10h40	Multiple probabilistic models resolve the functional organization of the cryptochrome/photolyase protein family RICCARDO VICEDOMINI		
10h40 11h10	Coffee Break	Booths in Exhibition Zone	
	Auditorium	DNA Room	Protein Room
11h10 11h30	Cis-regulation Morgane Thomas-Chollier <i>RSAT 2018: regulatory sequence analysis tools 20th anniversary</i>	Dynamic Modelling Firas Hammami <i>Mathematical modeling of Fe-S biogenesis shows strong links between iron homeostasis and oxidative stress response</i>	Functional genomics Diogo Ribeiro <i>Predicting 3'UTR's regulation of protein multifunctionality</i>
11h30 11h50	Jeanne Chèneby <i>ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments</i>	Aurélien Naldi <i>Logical modelling and analysis of cellular regulatory networks with GINSim 3.0</i>	Audrey Defosset <i>Prediction of new multiciliogenesis genes using a fine-grained comparative genomic approach</i>
11h50 12h10	Yves Clement <i>Enhancer-gene associations in complete genomes unravel ancestral vertebrate regulation and key principles of enhancer function</i>	Swann Floc'hlay <i>Multilevel logical modelling of the regulatory network governing dorsal-ventral axis specification in the sea urchin <i>P. lividus</i></i>	Javier Diego Zea <i>PhyloSofS: PHYLOgenies of Splicing isoForms Structures</i>
12h10 13h30	Lunch	Booths in Exhibition Zone	
Auditorium JOBIM Plenary session			
Session 5: Structural Biology			
13h30 14h30	KEYNOTE: EMMANUEL LEVY		
14h30 14h50	Protein interaction energy landscapes are shaped by functional and also non-functional partners HUGO SCHWEKE		
14h50 15h10	A hybrid combinatorial method for docking a single-stranded RNA in a protein pocket at the thermodynamic equilibrium ISAURE CHAUVOT DE BEAUCHENE		
15h10 15h30	Flash Poster Presentations Odd numbers 4x5'		
15h30 16h00	Coffee Break	Booths in Exhibition Zone	
16h00 17h00	Poster Session Odd numbers - Poster Zone		
17h00 18h00	AG SFBI		
18h00 18h30	AG IFB		
18h30 19h00	AG GdR BIM		
19h00 01h00	GALA DINNER & CONCERT		

Day 4 : Friday, July 6

8h45	Welcome Coffee		
Auditorium JOBIM Plenary session			
Session 6: Data Science			
9h00 10h00	KEYNOTE: ELIZABETH PURDOM		
10h00 10h20	Protein domain sequence analyses using Long-Short Term Memory Recurrent Neural Networks TRISTAN BITARD FEILDEL		
10h20 10h40	RNA complex prediction as a constrained maximum clique problem AUDREY LEGENDRE		
10h40 11h05	Coffee Break		
11h05 11h25	Latent Tree based Inference of Ecological Network using the Poisson Log-Normal Model RAPHAËLLE MOMAL		
11h25 11h45	mmquant and mmannot: How to handle multiple-mapping reads in (s)RNA-Seq MATTHIAS ZYTNIKI		
11h45 12h15	CONFERENCE CLOSING SFBI awards Presentation JOBIM 2019		
12h15 13h00	Lunch-box END OF THE CONFERENCE		

