Day 1 : Tuesday July 3

Time	Event
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*

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

Day 2 : Wednesday, July 4

Time	Event
8h45	Welcome Coffee
	Auditorium JOBIM | Plenary session

Session 2: *New Bioinformatic Challenges in the Personalized Medicine Era - Part 1*

Time	Event
9h00 10h00	**KEYNOTE: PIERRE-ANTOINE GOURRAUD**
10h00 10h20	*Bayesian Genome-Wide Association Study to discover novel lifespan-associated loci* **NINON MOUNIER**
10h20 10h40	*Aggregation of rare family-specific variants associated with Rheumatoid Arthritis* **MAËVA VEYSSIERE**
10h40 11h10	Coffee Break	**Booths in Exhibition Zone**

Time	Auditorium	DNA Room	Protein Room
	Methods for Variant analyses **Maxime Garcia** *Sarek, a portable workflow for WGS analysis of germline and somatic mutations*	**New solutions to methodological challenges** **Danesh Gonché** *A new rapid, flexible and intuitive software to simulate phylogenies of infections*	**Structural Bioinformatics for diseases** **Georges Bedran** *Assessing the functional impact of genomic alterations using proteogenomics*
11h10 11h30			
11h30 11h50	**Pierre-Julien Viailly** *I-LowVarFreq: improving low-frequency variant detection using a new UMI-based variant calling approach for paired-end sequencing NGS libraries*	**Tristan Cordier** *Combining eDNA metabarcoding and supervised machine learning for routine environmental applications: an example with marine aquaculture*	**Charline Fagnen** *Structural and dynamics studies of a potassium channel and disease-associated mutants*
11h50 12h10	**Tania Cuppens** *From individual genetic variations towards haplotype: GEMPROT a new way of reading VCF files*	**Raluca Uricaru** *On improving the approximation ratio of the r-shortest common superstring problem*	**Manon Réau** *NR-DBIND : A database dedicated to nuclear receptor binding data including negative data and pharmacological profile*
12h10 13h30	Lunch	**Cambridge2Marseilles Chat**	**Booths in Exhibition Zone**

	Auditorium JOBIM | Plenary session

Session 3: *New Bioinformatic Challenges in the Personalized Medicine Era - Part 2*

Time	Event
13h30 14h30	**KEYNOTE: ELEFTHERIA ZEGGINI**
14h30 14h50	*Unravelling human preimplantation development by single-cell RNA-Seq: from experiment design to cell fate trajectories* **DIMITRI MEISTERMANN**
14h50 15h10	*Proteomic and phosphoproteomic analysis of medulloblastoma reveals distinct activated pathways between subgroups* **LOREDANA MARTIGNETTI**
15h10 15h30	*Flash Poster Presentations Even numbers 4x5'*
15h30 16h00	Coffee Break	**Booths in Exhibition Zone**
16h00 17h00	*Poster Session Even numbers - Poster Zone*

Time	Auditorium	DNA Room	Protein Room
17h00 17h20	**Session 1 - Part 2** **Microbial Communities** **Eléonore Frouin** *Comparative metagenomics highlighted a core of metabolic capabilities in multiple serpentinizing ecosystems*	**Disease-associated genomics** **Christian Dina** *Fine-scale genetic population structure in western France*	**Demo** **Sébastien Légaré** *Biocuration and rule-based modelling of protein interaction networks in KAMI*
17h20 17h40	**Léo d'Agata** *Single-cell genome study of marine protists in the framework of the Tara Oceans project*	**Jeremy Tournayre** *Identification de marques épigénétiques marqueurs de prédisposition aux maladies métaboliques*	**Christophe Becavin** *Build your own multi-omics website with BACNET*
17h40 18h00	**Malo Le Boulch** *MACADAM a user-friendly MetAboliC pAthway DAtabase for complex Microbial community function analysis*	**Andreas Zanzoni** *Perturbed human sub-networks by Fusobacterium nucleatum candidate virulence proteins*	**Pierre Larmande** *Gigwa - Genotype Investigator for Genome-Wide Analyses*
18h00 19h30	**SOCIAL EVENTS**	**Booths in Exhibition Zone**	
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 MATHELIER**	
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** *RSAT 2018: regulatory sequence analysis tools 20th anniversary*	**Dynamic Modelling** **Firas Hammami** *Mathematical modeling of Fe-S biogenesis shows strong links between iron homeostasis and oxidative stress response*	**Functional genomics** **Diogo Ribeiro** *Predicting 3'UTR's regulation of protein multifunctionality*
11h30 11h50	**Jeanne Chèneby** *ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments*	**Aurélien Naldi** *Logical modelling and analysis of cellular regulatory networks with GINsim 3.0*	**Audrey Defosset** *Prediction of new multiciliogenesis genes using a fine-grained comparative genomic approach*
11h50 12h10	**Yves Clement** *Enhancer-gene associations in complete genomes unravel ancestral vertebrate regulation and key principles of enhancer function*	**Swann Floc'hlay** *Multilevel logical modelling of the regulatory network governing dorsal-ventral axis specification in the sea urchin P. lividus*	**Javier Diego Zea** *PhyloSofS: PHYLOgenies of Splicing isOForms Structures*
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 ZYTNICKI**
11h45 12h15	**CONFERENCE CLOSING SFBI awards Presentation JOBIM 2019**
12h15 13h00	Lunch-box **END OF THE CONFERENCE**