

08h50-09h00	Accueil et mot de bienvenue	
09h00-09h45	Invité 1	Laurent Jacob : Simulation-based inference for molecular evolution
09h45-10h05	Génétique et génomique	Guyomar et al. : Genotyping a thousand animals using low coverage sequencing and imputation
10h05-10h25	Génétique et génomique	Foissac et al. : Chromatin Compartment Detection and Comparison from Hi-C Data
10h25-10h45	Génétique et génomique	Durante et al. : Environmental and genetic influences on whole-blood gene expression levels in Large-White/Creole backcross pigs
10h45-11h15	Pause café	
11h15-11h35	Statistique	Maigné et al. : ASTERICS: A Simple Tool for the ExploRation and Integration of omiCS data
11h35-11h55	Statistique	Mercadié et al. : Extension de la NMF supervisée pour l'intégration de données omiques
11h55-12h15	Statistique	Déjean et al. : localScore: an R package to highlight atypical segment in a sequence
12h15-14h00	Pause déjeuner	
14h00-14h45	Invité 2	Sarah Cohen-Boulakia
14h45-15h05	Bioinformatique	Cabanac et al. : P-GRe : a efficient pipeline to maximised pseudogene prediction in plants/eucaryotes
15h05-15h25	Bioinformatique	Caetano et al. : RNA sequencing, how quantifying the <i>in vivo</i> 5'-ends helps understanding RNA metabolism in <i>Staphylococcus aureus</i>
15h25-15h45	Bioinformatique	Rocher et al. : DeepG4: A deep learning approach to predict cell-type specific active G-quadruplex regions
15h45-16h15	Pause café	
16h15-16h35	RNA/cancer	Bessière et al. : Sequencing of circular RNAs in full-length identifies splice variants linked with resistance to ALK inhibition in pediatric cancers
16h35-16h55	RNA/cancer	Khajavi : Transcriptomics Profiling of the Non-Small Cell Lung Cancer (NSCLC) Microenvironment Across Disease Stages Reveals Dual Immune Cell-Type Behaviors