

	<b>Dimanche, 24 septembre</b>	<b>Lundi, 25 septembre</b>	<b>Mardi, 26 septembre</b>
08:30-09:00			
09:00-09:30	<b>Inscription et bienvenue</b>	<b>Conférencier invité: Tao Jiang</b> <i>A Parsimony Approach to Genome-Wide Ortholog Assignment</i>	<b>Conférencier invité: Liqing Zhang</b> <i>A Roadmap of Tandemly Arrayed Genes in the Mammalian Genomes</i>
09:30-10:00			
10:00-10:30	<b>Conférencier invité: Thomas J. Hudson</b> <i>Influence of Human Genome Polymorphism on Gene Expression</i>	<i>How Pseudo-Boolean Programming can help Genome Rearrangement Distance Computation</i> S. Angibaud, G. Fertin, I. Rusu, S. Vialette	<i>Common Intervals and Symmetric Difference in a Model-free Phylogenomics, with an Application to Streptophyte Evolution</i> Z. Adam, M. Turmel, C. Lemieux, D. Sankoff
10:30-11:00	pause-café	pause-café	pause-café
11:00-11:30	<i>Reconstructing Domain Compositions of Ancestral Multi-domain Proteins</i> B. Behzadi and M. Vingron	<i>Sorting by translocations via reversals theory</i> M. Ozery-Flato, R. Shamir	<i>Finding Maximum Likelihood Indel Scenarios</i> A. Banière Diallo, V. Makarenkov, and M. Blanchette
11:30-12:00	<i>Domain Architecture in Homolog Identification</i> N. Song, R. Sedgewick, D. Durand	<i>Inferring gene orders from gene maps using the breakpoint distance</i> G. Blin, E. Blais, P. Guillon, M. Blanchette, N. El-Mabrouk	<i>On genome evolution with accumulated change and innovation</i> D. Wojtowicz and J. Tiuryn
12:00-12:30	<i>Inferring positional homologs with common intervals of sequences</i> G. Blin, A. Chateau, C. Chauve, Y. Gingras	<i>Ordering Partially Assembled Genomes Using Gene Arrangements</i> É. Gaul, M. Blanchette	<i>Transcription Factor Centric Discovery of Regulatory Elements in Mammalian Genomes Using Alignment- Independent Conservation Maps</i> N. Banerjee and A. Califano
12:30-14:00	déjeuner	déjeuner	déjeuner
14:00-15:00	<b>Conférencier invité: Lars Feuk</b> <i>Identification of structural variation in the human genome</i>	<b>Conférencier invité: Fiona Brinkman</b> <i>Evolution of microbial cellular networks: Insights from improved genome-wide prediction of orthologs and protein subcellular localization</i>	
15:00-15:30	pause-café	pause-café	
15:30-16:00	<i>Conservation Patterns in Cis-elements Reveal Compensatory Mutations</i> P. Evans, G. Donahue, S. Hannenhalli	<i>Evolution of Tandemly Repeated Sequences through Duplication and Inversion</i> D. Bertrand, M. Lajoie, N. El-Mabrouk, O. Gascuel	
16:00-16:30	<i>Paths and Cycles in Breakpoint Graphs of Random Multichromosomal Genomes</i> W. Xu, C. Zheng, D. Sankoff	<i>A PQ Framework for Reconstructions of Common Ancestors &amp; Phylogeny</i> L. Parida	
16:30-17:00	<i>Identifiability Issues in Phylogeny-based Detection of Horizontal Gene Transfer</i> C. Than, D. Ruths, H. Innan, L. Nakhleh	<i>Intron Loss Dynamics in Mammals</i> J. Coulombe-Huntington and J. Majewski	
	<b>17:00:</b> Session d'affichage	<b>19:00:</b> Cocktail et banquet	