Programme – RECOMB 2016 sur la génomique comparative

Mardi 11 octobre

18:00 – 20:00   Cocktail de bienvenue et inscription

Mercredi 12 octobre

08:00 – 08:50   Petit-déjeuner et inscription

08:50 – 09:00   Mots de bienvenue

Président: David Sankoff

09:00 – 09:50   **Conférencier principal - Edward Marcotte**
Comparative proteomics: Insights into protein function from deeply conserved gene modules

Président: Abdoulaye Banire Diallo

09:50 – 10:15   **Nam-Phuong Nguyen**
HIPPI: Highly Accurate Protein Family Classification with Ensembles of HMMs

10h15 – 10h40   **Olivier Tremblay-Savard**
Reconstruction of ancestral RNA sequences under multiple structural constraints

10:40 – 11:10   Pause-café

11:10 – 11:35   **Luay Nakhleh**
Exploring phylogenetic hypotheses via Gibbs sampling on evolutionary networks

11:35 – 12:00   **Kevin Liu**
A performance study of the impact of recombination on species tree analysis

12:00 – 12:25   **Jiafan Zhu**
In the Light of Deep Coalescence: Revisiting Trees Within Networks

12:30 – 14:00   Déjeuner

Président: Tandy Warnow

14:00 – 14:50   **Conférencier principal - Rebekah Rogers**
Chromosomal rearrangements as barriers to genetic homogenization between archaic and modern humans

14:50 – 15:15   **Guillaume Fertin**
Genome rearrangements with indels in intergenes restrict the scenario space

15:15 – 15:40   **Ashok Rajaraman**
Reconstructing ancestral gene orders with duplications guided by synteny level genome reconstruction

15:40 – 16:05   **Pedro Feijao**
Fast ancestral gene order reconstruction of genomes with unequal gene content

16:05 – 17:00   Session d'affiches et café

Jeudi 13 octobre

08:00 – 09:00   Petit-déjeuner

Président: Jens Lagergren

09:00 – 09:50   **Conférencier principal - Josée Dostie**
The reciprocity of genome architecture and gene expression

09:50 – 10:15	**Maureen Stolzer**
	Xenolog Classification
10h15 – 10h40	**Mark Jones**
	On the consistency of orthology relationships
10:40 – 11:10	Pause-café
11:10 – 11:35	**Nikita Alexeev**
	Comparative Genomics Meets Topology: a Novel View on Genome Median and Halving Problems
11:35 – 12:00	**Zhe Nicole Yu**
	A continuous analog of run length distributions reflecting accumulated fractionation events
12:00 – 12:25	**Lars Arvestad**
	Probabilistic inference of lateral gene transfer events
12:30 – 14:00	Déjeuner

Président: Luis Barreiro

14:00 – 14:50	**Conférencier principal - Guillaume Bourque**
	Comparative epigenomic resources to better understand non-coding DNA
14:50 – 15:15	**Tandy Warnow**
	Scaling Statistical Multiple Sequence Alignment to Large Datasets
15:15 – 15:40	**Geneviève Vallée**
	Economic importance, taxonomic representation and scientific priority as drivers of genome sequencing projects
15:40 – 17:00	Session d'affiches et café
19H	Banquet

Vendredi 14 octobre

08:00 – 09:00	Petit-déjeuner

Président: Dannie Durand

09:00 – 09:25	**Pranjal Vachaspati**
	FastRFS: Fast and Accurate Robinson-Foulds Supertrees using Constrained Exact Optimization
09h25 – 09h50	**Siavash Mirarab**
	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction
09:50 – 10:15	**Lawrence Uricchio**
	An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees
10:15 – 10:45	Pause-café
10:45 – 11:35	**Conférencier principal – Sohrab Shah**
	Evolutionary dynamics of cancer: a spatio-temporal analysis
11:35 – 12:00	**Adriana Muñoz**
	Evolution of transcriptional networks in yeast: alternative teams of transcriptional factors for different species
12:00 – 12:25	**Anne Bergeron**
	Assisted transcriptome reconstruction and splicing orthology
12:25 – 12:35	Conclusion
12:35	Déjeuner