

Program – RECOMB Comparative Genomics 2016

Tuesday October 11

18:00 – 20:00 Welcome Cocktail and Registration

Wednesday October 12

08:00 – 08:50 Continental Breakfast and Registration

08:50 – 09:00 Opening Remarks

Chair: David Sankoff

09:00 – 09:50 **Keynote Speaker - Edward Marcotte**

Comparative proteomics: Insights into protein function from deeply conserved gene modules

Chair: Abdoulaye Banire Diallo

09:50 – 10:15 **Nam-Phuong Nguyen**

HIPPI: Highly Accurate Protein Family Classification with Ensembles of HMMs

10:15 – 10:40 **Olivier Tremblay-Savard**

Reconstruction of ancestral RNA sequences under multiple structural constraints

10:40 – 11:10 Coffee Break

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 Lunch

Chair: Tandy Warnow

14:00 – 14:50 **Keynote Speaker - 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 Poster Session and Coffee

Thursday October 13

08:00 – 09:00 Continental Breakfast

Chair: Jens Lagergren

09:00 – 09:50 **Keynote Speaker - Josée Dostie**

The reciprocity of genome architecture and gene expression

09:50 – 10:15	Maureen Stolzer <i>Xenolog Classification</i>
10h15 – 10h40	Mark Jones <i>On the consistency of orthology relationships</i>
10:40 – 11:10	Coffee Break
11:10 – 11:35	Nikita Alexeev <i>Comparative Genomics Meets Topology: a Novel View on Genome Median and Halving Problems</i>
11:35 – 12:00	Zhe Nicole Yu <i>A continuous analog of run length distributions reflecting accumulated fractionation events</i>
12:00 – 12:25	Lars Arvestad <i>Probabilistic inference of lateral gene transfer events</i>
12:30 – 14:00	Lunch
	Chair: Luis Barreiro
14:00 – 14:50	Keynote Speaker - Guillaume Bourque <i>Comparative epigenomic resources to better understand non-coding DNA</i>
14:50 – 15:15	Tandy Warnow <i>Scaling Statistical Multiple Sequence Alignment to Large Datasets</i>
15:15 – 15:40	Geneviève Vallée <i>Economic importance, taxonomic representation and scientific priority as drivers of genome sequencing projects</i>
15:40 – 17:00	Poster Session and Coffee
19H	Banquet

Friday October 14

08:00 – 09:00	Continental Breakfast
	Chair: Dannie Durand
09:00 – 09:25	Pranjal Vachaspati <i>FastRFS: Fast and Accurate Robinson-Foulds Supertrees using Constrained Exact Optimization</i>
09h25 – 09h50	Siavash Mirarab <i>Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction</i>
09:50 – 10:15	Lawrence Urichio <i>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</i>
10:15 – 10:45	Coffee Break
10:45 – 11:35	Keynote Speaker – Sohrab Shah <i>Evolutionary dynamics of cancer: a spatio-temporal analysis</i>
11:35 – 12:00	Adriana Muñoz <i>Evolution of transcriptional networks in yeast: alternative teams of transcriptional factors for different species</i>
12:00 – 12:25	Anne Bergeron <i>Assisted transcriptome reconstruction and splicing orthology</i>
12:25 – 12:35	Closing Remarks
12:35	Lunch