

# RECOMB-Seq 2014 – TENTATIVE PROGRAM

## *Rangos Hall Carnegie Mellon University*

### Day 1 (March 31st)

9:00-9:10                      Opening Remarks

#### **Assembly Session**

9:10-9:30                      Paper 1- Romeo Rizzi, Alexandru I. Tomescu and Veli Mäkinen. *On the Complexity of Minimum Path Cover with Subpath Constraints for Multi-assembly*

9:30-9:50                      Paper 2 - Jintao Meng and Yanjie Wei. *SWAP-Assembler: Scalable and Efficient Genome Assembly towards Thousands of Cores*

9:50-10:10                    Paper 3 - Ka-Kit Lam, Asif Khalak and David Tse. *Near-optimal Assembly for Shotgun Sequencing with Noisy Reads*

10:10-10:30                   Paper 4 - James Lindsay, Hamed Salooti, Alex Zelikovsky and Ion Mandoiu. *ILP-based Maximum Likelihood Genome Scaffolding*

10:30-11:00                   Coffee break

#### **Emerging Trends Part 1**

11:00-11:20                   Paper 5 - Roye Rozov, Ron Shamir and Eran Halperin. *Fast Lossless Compression via Cascading Bloom Filters*

11:20-11:40                   Select Abstract 2

11:40-12:10                   ET discussion

12:10-2:00                    Lunch/posters

#### **2:00-3:00                      Keynote 1: Cecilia Lo, PhD**

Professor and Chair  
F. Sargent Cheever Chair  
Department of Developmental Biology  
University of Pittsburgh

3:00-3:30                      Coffee break

#### **RNA-Seq and Technology**

3:30-3:50                      Paper 6 - Jingua Gu, Xiao Wang, Leena Hilakivi-Clarke, Robert Clarke and Jianhua Xuan. *BADGE: A novel Bayesian model for accurate abundance quantification and differential analysis of RNA-seq data*

3:50-4:10                      Paper 7 - Yan Huang, Yin Hu and Jinze Liu. *Piecing the puzzle together: a revisit to transcript reconstruction problem in RNA-Seq*

4:10-4:30                      Paper 8 - Zeinab Taghavi. *Adaptive Compressed Genome Sequencing Using Depth First Search Strategy*

4:30-6:00                      Poster session

## Day 2 (April 1st)

### Alignment Session

9:10-9:30	Paper 9 - Matteo Comin and Michele Schimd. <i>Assembly-free Genome Comparison based on Next-Generation Sequencing Reads and Variable Length Patterns</i>
9:30-9:50	Paper 10 - Milad Gholami, Aryan Arbabi, Ali Sharifi-Zarchi, Hamidreza Chitsaz and Mehdi Sadeghi. <i>ARYANA: Aligning Reads by Yet Another Approach</i>
9:50-10:10	Paper 11 - Ping Ge, Cuncong Zhong and Shaojie Zhang. <i>ProbeAlign: Incorporating high-throughput sequencing-based structure probing information into ncRNA homology search</i>
10:10-10:30	Paper 12 - Sunyoung Kwon, Byunghan Lee and Sungroh Yoon. <i>CASPER: Context-Aware Scheme for Paired-End Read from high-throughput amplicon sequencing</i>
10:30-11:00	Coffee break

### Emerging Trends Part 2

11:00-11:20	Paper 13 - Anton Polishko, Evelien Bunnik, Karine Le Roch and Stefano Lonardi. <i>PuFFIN - A Parameter-free Method to Build Nucleosome Maps from Paired-end Reads</i>
11:20-11:40	Selected Abstract Talk 2
11:40-12:10	ET discussion
12:10-2:00	Lunch/posters
2:00-3:00	<b>Keynote 2: Ben Raphael, PhD</b> Associate Professor Department of Computer Science Director of the Center for Computational Molecular Biology Brown University
3:00-3:30	Coffee break

### Metagenomics

3:30-3:50	Paper 14 - Noam D. Beckmann, Sashank Karri, Ali Bashir and Gang Fang. <i>Detecting Epigenetic Motifs in Low Coverage and Metagenomics Settings</i>
3:50-4:10	Paper 15 - Stephen Johnson, Brett Trost, Jeffrey Long, Vanessa Pittet and Anthony Kusalik. <i>A better sequence-read simulator program for metagenomics</i>
4:10-4:30	Paper 16 - Wazim Mohammed Ismail, Yuzhen Ye and Haixu Tang. <i>Gene finding in metatranscriptomic sequences</i>
4:30-4:50	Closing Remarks
4:50-6:00	Poster session