RECOMB-CG 2026 Program

May 24, Sunday

8:30 - 9:30	Registration	
9:30 - 10:30	Keynote	**Pavlos Pavlidis**. At the Crossroads of the Mediterranean: Population Structure and Admixture History of Cretans
10:30 - 10:55	Proceedings talk	**Nicolae Sapoval**, Zejian Liu, Mehrdad Tamiji, Meng Li and Luay Nakhleh. Theoretical and Empirical Performance of Pseudo-likelihood-based Bayesian Inference of Species Trees under the Multispecies Coalescent
10:55 - 11:20	Proceedings talk	**David Sankoff**, Jiazhen Leng, Pratheesh Soman, Qiaoji Xu, Chunfang Zheng, Alexander Liu, Jim Leebens-Mack and Lingling Jin. Reconstructing the constituent genomes of the ancestral angiosperm pangenome.
11:20 - 13:00	Poster session	
11:20 - 13:30	Lunch (in parallel with poster session)	
13:30 - 13:55	Proceedings talk	Victor de Moraes and **Joao Meidanis**. Time complexity and relaxation gap for the rank median of three genomes
13:55 - 14:20	Proceedings talk	**Leonard Bohnenkämper** and Jens Stoye. Quantifying the Rearrangement Complexity of Pangenomes
14:20 - 14:45	Proceedings talk	Poly H da Silva, Arash Jamshidpey and **David Sankoff**. Breakpoint medians and anti-medians for signed genomes
14:45 - 15:05	Coffee break	
15:05 - 15:30	Proceedings talk	**Alan Mayer**, Shayesteh Arasti and Siavash Mirarab. Detecting Outlier Subtrees of Gene Trees Using SPR Moves and Machine Learning
15:30 - 15:55	Proceedings talk	Abdur Rafi, **Ahmed Mahir Sultan Rumi**, Sheikh Azizul Hakim and Md. Shamsuzzoha Bayzid. wQFM-GDL Enables Accurate Quartet-based Genome-scale Species Tree Inference Under Gene Duplication and Loss
15:55 - 16:10	Coffee break	
16:10 - 16:35	Proceedings talk	**Aleksandr Koshkarov** and Nadia Tahiri. k-Nearest Common Leaves Algorithm for Phylogenetic Tree Completion
16:35 - 17:00	Proceedings talk	**Bertrand Marchand**, Nadia Tahiri, Olivier Tremblay-Savard and Manuel Lafond. On the Comparison of LGT networks and Tree-based Networks

May 25, Monday

9:30 - 10:30	Keynote	**Simona Georgieva**. Convergent Evolution of Parasitism: From Ecology to Comparative Genomics
10:30 - 10:55	Proceedings talk	**Gabriele Di Palma**, Catherine Matias and Blerina Sinaimeri. Similarities, differences and biases in cophylogenetic models for host-symbiont coevolution
10:55 - 11:20	Coffee break	
11:20 - 11:45	Proceedings talk	**Mathieu Gascon**, Mattéo Delabre and Nadia El-Mabrouk. Gene repertoire evolution minimizing episodes of gains and losses
11:45 - 12:10	Proceedings talk	**Nicolae Sapoval** and Luay Nakhleh. On the consistency of duplication, loss, and deep coalescence gene tree parsimony costs under the multispecies coalescent
12:10 - 12:35	Proceedings talk	Manuel Lafond, **Kaari Landry**, Olivier Tremblay-Savard, Hamza Wahed, Chris Whidden and Norbert Zeh. Cherry-Picking Distance Between Binary Orchards Parameterized by Level
12:35 - 14:30	Lunch	
14:30 - 14:55	Proceedings talk	Meijun Gao, Byungho Lee and **Kevin Liu**. FIREFLY: PHYlogeny-informed REpresentation Learning to Estimate PHyLogenetic dIstances
14:55 - 15:20	Proceedings talk	**Victor Epain**, Aniket Mane, Gianluca Della Vedova, Paola Bonizzoni and Cédric Chauve. A multi-flow approach for binning circular plasmids from short-reads assembly graphs
15:20 - 15:45	Proceedings talk	**Martin Schmitz**, Lovro Vrcek, Kenji Kawaguchi and Mile Sikic. GNNome-Decision: Enhancing GNN training for de novo genome assembly by targeting decision nodes
15:45 - 16:05	Coffee break	
16:05 - 16:30	Proceedings talk	**Amos Onn**, Tzipy Marx, Liming Tao, Tamir Biezuner, Ehud Shapiro, Christoph A. Klein and Peter F. Stadler. Modeling the Mutational Dynamics of Very Short Tandem Repeats
16:30 - 16:55	Proceedings talk	**Martin Schmitz**, Lovro Vrcek, Kenji Kawaguchi and Mile Sikic. DipGNNome: Diploid de novo genome assembly with geometric deep learning and beam-search
16:55 - 17:20	Proceedings talk	Mark Maher Ebeid, Ali Tugrul Balci, Maria Chikina, Panayiotis Benos and Dennis Kostka. "Frustratingly Easy"' Domain Adaptation for Cross-Species Transcription Factor Binding Prediction
17:30 - 19:00	Poster session II	