

# RECOMB-CG 2026 Program

May 24, Sunday

8:30 - 9:30	Registration	
9:30 - 10:30	Keynote	<b>Pavlos Pavlidis</b> . At the Crossroads of the Mediterranean: Population Structure and Admixture History of Cretans
10:30 - 10:55	Proceedings talk Chair: Kevin Liu	<b>Nicolae Sapoval</b> , 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	<b>David Sankoff</b> , 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 Chair: Maribel Hernandez-Rosales	Victor de Moraes and <b>Joao Meidanis</b> . Time complexity and relaxation gap for the rank median of three genomes
13:55 - 14:20	Proceedings talk	<b>Leonard Bohnenkämper</b> and Jens Stoye. Quantifying the Rearrangement Complexity of Pangenomes
14:20 - 14:45	Proceedings talk	Poly H da Silva, Arash Jamshidpey and <b>David Sankoff</b> . Breakpoint medians and anti-medians for signed genomes
14:45 - 15:05	Coffee break	
15:05 - 15:30	Proceedings talk Chair: Kaari Landry	<b>Alan Mayer</b> , Shayesteh Arasti and Siavash Mirarab. Detecting Outlier Subtrees of Gene Trees Using SPR Moves and Machine Learning
15:30 - 15:55	Proceedings talk	Mark Maher Ebeid, Ali Tugrul Balci, Maria Chikina, Panayiotis Benos and <b>Dennis Kostka</b> . "Frustratingly Easy" Domain Adaptation for Cross-Species Transcription Factor Binding Prediction
15:55 - 16:10	Coffee break	
16:10 - 16:35	Proceedings talk Chair: Paweł Górecki	<b>Aleksandr Koshkarov</b> and Nadia Tahiri. k-Nearest Common Leaves Algorithm for Phylogenetic Tree Completion
16:35 - 17:00	Proceedings talk	<b>Bertrand Marchand</b> , Nadia Tahiri, Olivier Tremblay-Savard and Manuel Lafond. On the Comparison of LGT networks and Tree-based Networks

## May 25, Monday

9:30 - 10:00	Special guest talk I	<b>Maribel Hernandez-Rosales</b>
10:00 - 10:30	Special guest talk II	<b>Paweł Górecki</b>
10:30 - 10:55	Proceedings talk	<b>Gabriele Di Palma</b> , Catherine Matias and Blerina Sinimeri. Similarities, differences and biases in cophylogenetic models for host-symbiont coevolution
10:55 - 11:20	Coffee break	
11:20 - 11:45	Proceedings talk Chair: Bertrand Marchand	<b>Mathieu Gascon</b> , Mattéo Delabre and Nadia El-Mabrouk. Gene repertoire evolution minimizing episodes of gains and losses
11:45 - 12:10	Proceedings talk	<b>Nicolae Sapoval</b> 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, <b>Kaari Landry</b> , 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 Chair: Joao Meidanis	Meijun Gao, Byungho Lee and <b>Kevin Liu</b> . FIREFLY: PHYlogeny-informed REpresentation Learning to Estimate PHyLogenetic dIstances
14:55 - 15:20	Proceedings talk	<b>Victor Epain</b> , 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	<b>Martin Schmitz</b> , 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 Chair: Jens Stoye	<b>Amos Onn</b> , 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	<b>Martin Schmitz</b> , 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	Abdur Rafi, <b>Ahmed Mahir Sultan Rumi</b> , Sheikh Azizul Hakim and Md. Shamsuzzoha Bayzid. wQFM-GDL Enables Accurate Quartet-based Genome-scale Species Tree Inference Under Gene Duplication and Loss
17:30 - 19:00	Poster session II	