

PROGRAMME

24th November, Thursday (forenoon)

- 10:00-10:10 Welcome speech
10:10-10:20 *Gábor Kardos*: Opening speech

MODELING, STATISTICAL ANALYSES, MACHINE LEARNING, BIG DATA I.

Chairperson: *Gábor Kardos*

Keynote presentation (30 minutes + 15 minutes discussion)

- 10:25-11:10 *Katalin Gombos*: Synthesis of molecular genetics and bioinformatics to develop clinical diagnostics and surveillance

Short presentations (15 minutes + 5 minutes discussion)

- 11:10-11:30 *Zoltán Rádai*: Complex effects of Next Generation Sequencing error sources on the quality of *de novo* genome assembly
11:30-11:50 *Alex Váradi*: Effects of genome size and composition and duplicate removal on the results of *de novo* transcriptome assembly and DGE analysis: an *in silico* study
11:50-12:10 *Otília Menyhart*: Preserved correlations identify extracellular matrix organization as a critical factor in pancreatic ductal adenocarcinoma

24th November, Thursday (afternoon)

MODELING, STATISTICAL ANALYSES, MACHINE LEARNING, BIG DATA II.

Chairperson: *Péter Takács*

Keynote presentation (30 minutes + 15 minutes discussion)

- 13:15-14:00 *Serhii Vakal*: Why protein folding is not yet solved, and you should be careful when using AlphaFold as a "black box"

Short presentations (15 minutes + 5 minutes discussion)

- 14:00-14:20 *Szonja Anna Kovács*: Investigation of predictive biomarkers in cancer patients treated with immune-checkpoint inhibitors
14:20-14:40 *János Tibor Fekete*: Predictive biomarkers in cancer cell lines
14:40-15:00 *Zoltán Pethő*: Protein homology modeling as a tool to study intra- and interprotein interactions

PROGRAMME

25th November, Friday (forenoon)

GENOME, PANGENOME, METAGENOME, POPULATION GENETICS, PHYLOGENETICS, PHYLOGENOMICS

Chairperson: *Eszter Virág*

Keynote presentation (30 minutes + 15 minutes discussion)

10:00-10:45 *Péter Oláh*: Analysis of whole-genome and marker gene-based cutaneous microbiome signatures in autoimmunity and allergy

Short presentations (15 minutes + 5 minutes discussion)

10:45-11:05 *Levente Laczkó*: Assessment of the accuracy of plasmid prediction tools using draft genome sequences

11:05-11:25 *Valter Péter Pfliegler*: Phylogenomics of *Saccharomyces* yeasts infecting and colonizing humans

11:25-11:45 *Eszter Ari*: Global map of evolutionary dependencies between antibiotic resistance and virulence genes in *E. coli*

25th November, Friday (afternoon)

TRANSCRIPTOME, PROTEOME, METABOLOME, FUNCTIONAL GENOMICS

Chairperson: *Nikoletta Andrea Nagy*

Keynote presentation (30 minutes + 15 minutes discussion)

13:00-13:45 *Eszter Virág*: Time-course gene expression analysis of the effect of SC-CO₂ garlic extract encapsulated in nanoscale liposomes

Short presentations (15 minutes + 5 minutes discussion)

13:45-14:05 *William Jayasekara Kothalawala*: Transcriptomic and cell type enrichment analysis of colorectal cancer by combining multiple independent cohorts

14:05-14:25 *Eszter Kaszab*: Genetic characterization of probiotic candidate microbial strains

14:25-14:45 *Gergely Nagy*: Dissecting the cistromes determining bone marrow-derived macrophage identity

14:45-15:05 *Gyula Hoffka*: Structural analysis of the binding of nirmatrelvir to the SARS-CoV-2 main protease

15:05-15:15 Concluding remarks