

ORAL PRESENTATION SCHEDULE
INTERNATIONAL CONFERENCE ON BIOINFORMATICS (INCOB) 2019
UNIVERSITAS YARSI, JAKARTA, INDONESIA
SEPTEMBER 10-12, 2019

DAY/DATE	TIME	Workshop Room 1	Workshop Room 2	Workshop Room 3
Tue, Sept 10, 2019	1:45-2:45 PM	Theme I: Sequencing and NGS data analysis	Theme II: Protein structure, function and interaction	Theme III: Immuno informatics and host pathogen interactions
	1:45-2:00 PM	O-02: Angana Chakraborty: conLSH: Context based Locality Sensitive Hashing for Mapping of noisy SMRT Reads	O-01: Abel Avitesh: Bigram-PGK: phosphoglycerylation prediction using the technique of bigram probabilities of position specific scoring matrix	O-05: Fransiskus Xaverius Ivan: Rule-based meta-analysis reveals the major role of PB2 in influencing influenza A virus virulence in mice
	2:00-2:15 PM	O-06: Gareth Price: Galaxy Australia - a truly national open-source bioinformatics platform	O-07: Hui Liu: MADOKA: An Ultra-fast Approach for Large-Scale Protein Structure Similarity Searching	O-22: Sataruda Prakash Singh: Design of precise vaccine construct against visceral leishmaniasis through predicted ensemble epitope: a contemporary approach
	2:15-2:30 PM	O-31: Yasubumi Sakakibara: An improved de novo genome assembly of the common marmoset genome yields improved contiguity and increased mapping rates of sequence data	O-45: Alhadi Bustamam: Performance of Rotation Forest Ensemble Classifier and Feature Extractor in Predicting Protein Interactions Using Amino Acid Sequences	O-44: Asif M Khan: Identification of highly conserved, serotype-specific dengue virus sequences: implications for vaccine design
	2:30-2:45 PM	O-32: Younghi Lee: Differential alternative splicing regulation among hepatocellular		O-47: Shoba Ranganathan: Prediction of novel mouseTLR9 agonists using a random forest approach

		carcinoma with different risk factors		
	3:00-4:30 PM	Theme IV: Genomics and Evolutionary Biology	Theme V: Tools, databases and web services in Bioinformatics	Theme VI: Network biology and interaction networks
	3:00-3:15 PM	O-10: Jing Li: Genome-wide identification, phylogeny, and expression analysis of the SBP-box gene family in Euphorbiaceae	O-23: Sheng-Yao Su: EpiMOLAS: An Intuitive Web-based Framework for Genome-wide DNA Methylation Analysis	O-20: Rama Kalia: A module refinement approach to find functionally significant communities in molecular networks
	3:15-3:30 PM	O-48: Reeki Emirzal: Phylogenetic analysis of Type IX Secretion System (T9SS) protein components revealed that PorR undergoes horizontal gene transfer	O-28: Tsukasa Fukunaga: Logicome Profiler: Exhaustive detection of statistically significant logic relationships from comparative omics data	O-30: Xiaoshi Zhong: GO2Vec: Transforming GO Terms and Proteins to Vector Representations Using Graph Embeddings
	3:30-3:45 PM	O-41: Yen-Jung Chiu: Deconvolution of bulk gene expression profiles from complex tissues to quantify subsets of immune cells	O-39: Xuan Zhang: JCDB: a comprehensive knowledge database for <i>Jatropha curcas</i> , an emerging model for woody energy plants	O-33: Young-Rae Cho: LePrimAlign: local entropy-based alignment of PPI networks to predict conserved modules
	3:45-4:00 PM	O-18: Rajith Vidanaarachchi: IMPARO: Inferring Microbial Interactions through Parameter Optimisation	O-13: Yue Cao: scDC: Single cell differential composition analysis	O-04: Binh Phu Nguyen: Classification of Adaptor Proteins using Recurrent Neural Networks and PSSM Profiles
	4:00-4:15 PM	O-35: Yung-Keun Kwon: Effects of ordered mutations on dynamics in signaling networks	O-16: Taiyun Kim: scReClassify: post hoc cell type classification of single-cell RNA-seq data	O-27: Binh Phu Nguyen: Enhancer Identification and Classification using One-Hot Encoding and Ensemble Convolutional Neural Networks

	4:15-4:30 PM	O-49: Sean Chun-Chang Chen: RNA editing-based classification of diffuse gliomas: predicting isocitrate dehydrogenase (IDH) mutation and chromosome 1p/19q codeletion		
Wed, Sept 11, 2019	11:45-12:45 PM	Theme VII: Mass spectrometry and nano-bioinformatics	Theme VIII: Genome wide association studies (GWAS) and Biomarker discovery	Theme IX: Machine learning, AI and novel algorithms-I
	11:45-12:00 PM	O-03: Zaved Hazarika: Computational analysis of Silver nanoparticle - human serum albumin complex	O-14: Kyungsook Han: Finding prognostic gene pairs for cancer from patient-specific gene networks	O-11: Md. Sarwar Kamal: Instance-Based Learning for Personalized Cancer Diagnosis and Treatment Planning
	12:00-12.15 PM	O-08: Jang-Jih Lu: Statistical Considerations and Machine Learning Approaches for Rapid Strain Typing of Staphylococcus haemolyticus based on Matrix-Assisted Laser Desorption Ionization-Time-of Flight Mass Spectrometry	O-25: Srinivasulu YS: Characterization of risk genes of autism spectrum disorders using gene expression profiles	O-12: Yi Zheng: DDI-PULearn: a novel positive-unlabeled learning method for large-scale prediction of drug-drug interactions
	12:15-12:30 PM	O-09: Yang Ming Lin: MS2CNN: Predicting MS/MS spectrum based on protein sequence by Deep	O-34: Yun Zheng: The transcriptome variations of Panax notoginseng roots treated with different forms of nitrogen fertilizers	O-15: Fan Lu: Predicting Synthetic Lethal Interactions in Human Cancers using Graph Regularized Self-Representative Matrix Factorization

		Convolutional Neural Networks		
	12:30-12:45 PM	O-42: Tzong-Yi Lee: Rapid Classification of Group B Streptococcus Serotypes based on Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry and Machine Learning Techniques	O-36: Zhixun Zhao: Identification of Lung Cancer Gene Markers through kernel Maximum Mean Discrepancy and Information Entropy	O-17: Thomas Geddes: Autoencoder-based cluster ensembles for single-cell RNA-seq data analysis
Thu, Sept 12, 2019	11:00-12:00 PM	Theme X: Machine learning, AI and novel algorithms-II	NA	NA
	11:00-11:15 AM	O-38: Jacob Bradford: Improving CRISPR guide design with consensus approaches		
	11:15-11:30 AM	O-40: Ling Zou: Predicting synergistic drugs using gradient tree boosting based on features extracted from drug-protein heterogeneous network		
	11:30-11:45 AM	O-43: Kuo-Ching Liang: MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenomics assembly		

	1:00-1:45 PM	Theme XI: Machine learning, AI and novel algorithms-III	Theme XII: Disease data modeling and integrative Biology	NA
	1:00-1:15 PM	O-21: Lun Li: A novel constrained reconstruction model towards high-resolution sub-tomogram averaging	O-24: Shobana Sundar: Rv0807, a putative phospholipase A2 of Mycobacterium tuberculosis; Elucidation through sequence analysis, homology modeling, molecular docking and molecular dynamics studies of potential substrates and inhibitors	
	1:15-1:30 PM	O-37: Dhillon Sarinder Kaur: An Automated 3D Modelling Pipeline for Constructing 3D Models of Monogenean Hardpart Using Machine Learning Techniques	O-26: Sudipto Saha: Computational approach to target USP28 for regulating Myc	
	1:30-1:45 PM		O-29: Vivitri Dewi Prasastry: Structure-based Discovery of Novel Inhibitors of Mycobacterium tuberculosis CYP121 from Indonesian Natural Products	
	1:45-2:00 PM		O-51: Asif M. Khan: A systematic bioinformatics approach for large-scale identification and characterization of host-pathogen shared sequences	