General information:

WIFI connection: *network:* NH / *password:* WIFI

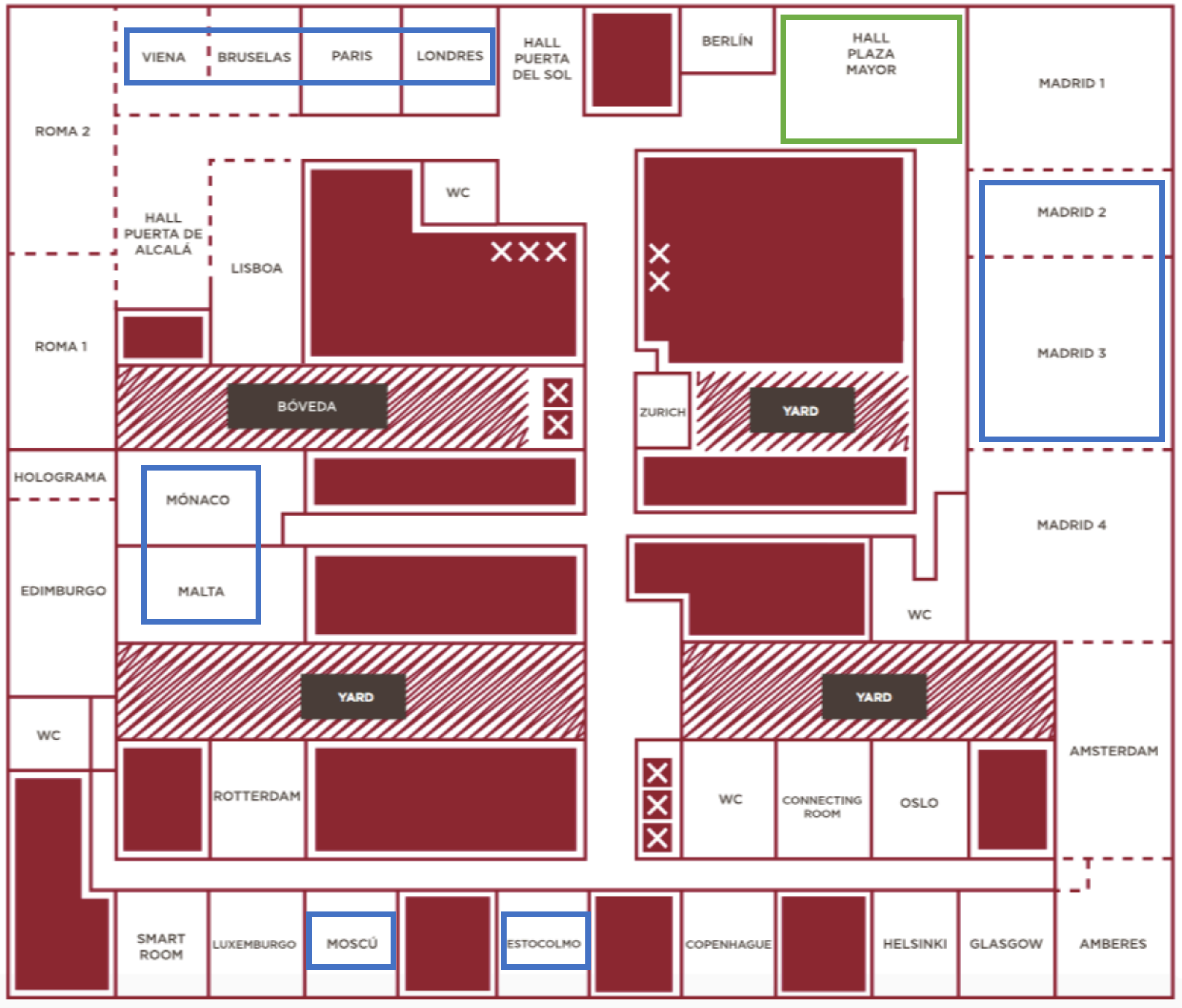
Keynote Lecture: 60 minutes (about 45 minutes for talk and 15 minutes for Q&A)
Regular Paper: 20 minutes (about 15 minutes for talk and 5 minutes for Q&A)
Short Paper: 15 minutes (about 12 minutes for talk and 3 minutes for Q&A)

PROGRAM AT A GLANCE

	Sun, Dec 2	**Mon, Dec 3 Workshops**	**Tue, Dec 4**	**Wed, Dec 5**	**Thu, Dec 6**
		Registration, *Hall Plaza Mayor* (08:30 – 18:00)			**Registration** (08:30 – 10:30)
08:45 – 9:00		**Workshops** *(Starting at 8:00)*	**Welcome and opening** *Room Madrid 2&3*		
09:00 – 10:00			**Keynote: Jan Baumbach** *Room Madrid 2&3*	**Keynote: Harald Schmidt** *Room Madrid 2&3*	**Sessions 33 to 37**
10:00 – 10:30		**Coffee break** (10:00 to 10:30) *Room Florencia*			
10:30 –13:00		**Workshops**	**Sessions 1 to 7** (10:30 to 11:45)	**Sessions 22 to 27** (10:30 to 11:45)	**Sessions 38 to 42** (10:30 to 12:00)
			Sessions 8 to 14 (12:00 to 13:30)	**Sessions 28 to 32** (12:00 to 13:30)	**Sessions 43 to 46** (12:15 to 13:35)
13:00 – 14:30		**Lunch (on own)**	**Lunch (provided by the conference)** (13:30 to 14:30) *Room Florencia*		
14:30 – 15:00		**Workshops**	**Sessions 15 to 21** (14:30 to 16:00)	**Awards ceremony**	
15:00 - 16:00	**Registration** **(15:00 to 20:00)** *Hall Plaza Mayor*			**Keynote: Xuegong Zhang** *Room Madrid 2&3*	
16:00 – 16:30		**Coffee break** (16:00 to 16:30) *Room Florencia*			
16:30 - 17:30		**Workshops** *(Ending at 18:30)*	**Poster session I** *Hall Plaza Mayor*	**Poster session II** *Hall Plaza Mayor*	
19:00 – 21:00				**Banquet** *Real Academia de Bellas Artes de San Fernando*	

FLOOR PLAN

Floor PC (1) (Rooms for workshops and sessions)



FLOOR PS (2)

Room Florencia

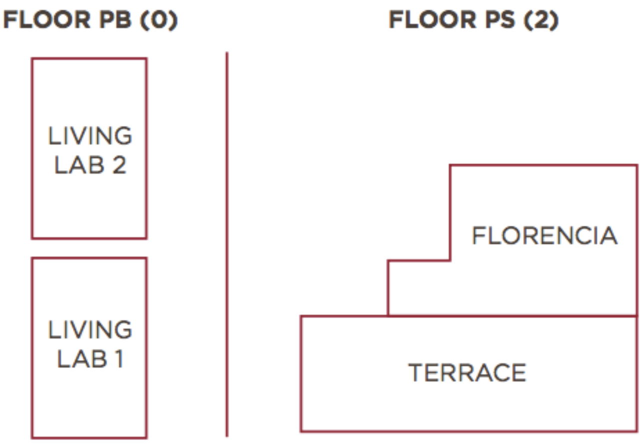
(Coffee and Lunch)

FLOOR PB (0)

Living Lab 1

Living Lab 2

(Rooms for workshops)



SCHEDULE

SUNDAY 2nd DECEMBER

REGISTRATION

16:00 to 21:00, *Hall Plaza Mayor*
Registration

MONDAY 3rd DECEMBER

WORKSHOPS

08:30 to 18:00	**Registration**, *Hall Plaza Mayor*		
08:00 to 10:00	**Workshop**	Workshop Chair	Location
	[1]MADMMLBE (session 1/2)	Xiaohua Douglas Zhang	Bruselas
	[3]DMGA (session 1/2)	Taesung Park	Estocolmo
	CBPBL (session 1/2)	Pierangelo Veltri	Londres
	CMISF 2018 (session 1/4)	Francesco Pappalardo	Malta
	MLESP 2018 (session 1/3)	Larbi Boubchir	Monaco
	SEPDA 2018 (session 1/3)	Zhe He	Moscu
	[4]AMTSC(session 1/2)	Mikhail Gelfand	Madrid 2+3
	IDASB 2018 (session 1/2)	Huiriu Zheng	Paris
	HPCB 2018 (Session 1/1)	Che-Lun Hung	Viena
	BHI 2018 (session 1/6)	Illhoi Yoo	Living Lab 1
	MABM(session 1/4)	Haiying Wang	Living Lab 2
10:00 to 10:30	**Coffee break**, *Sala Florencia*		
10:30 to 13:00	**Workshop**	Workshop Chair	Location
	MADMMLBE[1] (session 2/2)	Xiaohua Douglas Zhang	Bruselas
	[3]DMGA (session 2/2)	Taesung Park	Estocolmo
	CBPBL (session 2/2)	Pierangelo Veltri	Londres
	CMISF 2018(session 2/4)	Francesco Pappalardo	Malta
	MLESP 2018 (session 2/3)	Larbi Boubchir	Monaco
	SEPDA 2018 (session 2/3)	Zhe He	Moscu
	[4]AMTSC(session 2/2)	Mikhail Gelfand	Madrid 2+3
	IDASB 2018 (session 2/2)	Huiriu Zheng	Paris
	[6]QABBOT + [7]LSNASB (session 1/1)	Ankur Agrawal	Viena
	BHI 2018 (session 2/6)	Illhoi Yoo	Living Lab 1
	MABM(session 2/4)	Haiying Wang	Living Lab 2
13:00 to 14:30	**Lunch** **(on own)**		

	Workshop	Workshop Chair	Location
14:30 to 16:00	HiBB 2018 (session 1/2)	Mario Cannataro	Bruselas
	ACBH&DAM 2018 (session 1/2)	Huiru Zheng	Estocolmo
	AIBH 2018 (session 1/2)	Pierangelo Veltri	Londres
	CMISF 2018 (session 3/4)	Francesco Pappalardo	Malta
	MLESP 2018 (session 3/3)	Larbi Boubchir	Monaco
	SEPDA 2018 (session 3/3)	Zhe He	Moscu
	IWBNA & DLB2H 2018 (session 1/2)	Mingon Kang	Madrid 2+3
	[5]AMLSP (1/2)	Sheida Nabavi	Paris
	BiOK (session 1/2)	Jiajie Peng	Viena
	BHI 2018 (session 3/6)	Illhoi Yoo	Living Lab 1
	MABM 2018 (session 3/4)	Haiying Wang	Living Lab 2
16:00 to 16:30	**Coffee break**, *Sala Florencia*		
16:30 to 18:30	**Workshop**	Workshop Chair	Location
	HiBB 2018 (session 2/2)	Mario Cannataro	Bruselas
	ACBH &DAM 2018 (session 2/2)	Huiru Zheng	Estocolmo
	AIBH 2018 (session 2/2)	Pierangelo Veltri	Londres
	CMISF 2018 (session 4/4)	Francesco Pappalardo	Malta
	[2]MLAHRMI+[8]MBB(session 1/1) – Starts at 16:00	Ilker Ersoy	Monaco
	KDTBI +BigDataNetAnalysis (session 1/1)	Pietro Hiram Guzzi	Moscu
	IWBNA & DLB2H 2018 (session 2/2)	Mingon Kang	Madrid 2+3
	[5]AMLSP (2/2)	Sheida Nabavi	Paris
	BiOK (session 2/2)	Jiajie Peng	Viena
	BHI 2018 (session 4/6)	Illhoi Yoo	Living Lab 1
	MABM 2018 (session 4/4)	Haiying Wang	Living Lab 2

The BHI 2018 workshop continues on 4th December in the room *Living Lab 1 (see next pages*)

The meetings of the OpenMultiMed COST Action WG3/4 Workshop will take place on 5th December (room *Madrid2&3*) and 6th December (room *Viena*)

[1] Methods and Applications of Data Mining and Machine Learning for Biomedical Engineering (MADMMLBE)
[2] Machine Learning Approaches in High Resolution Microscopy Imaging (MLAHRMI)
[3] Data Mining from Genomic Variants and Its Application to Genome-wide Analysis 2018 (DMGV)
[4] Analysis and Modeling of the Three-dimensional Structure of Chromatin (AMTSC)
[5] Application of Machine Learning and Signal Processing in Biomedical Informatics and Computational Genomics (AMLSP)
[6] Quality Assurance of Biological and Biomedical Ontologies and Terminologies (QABBOT)
[7] Workshop on challenges and opportunities in Large Scale Network Analysis in Systems Biology(LSNASB)
[8] 1st International Workshop on Metaheuristics in Bioinformatics and Biomedicine (MBB)

TUESDAY 4th DECEMBER

08:30 to 18:00	**Registration**, *Hall Plaza Mayor*		
08:45 to 09:00	**Welcome and opening**, *Room Madrid 2&3*		
09:00 to 10:00	**Keynote: Jan Baumbach** From gene panels to systems medicine *Room Madrid 2&3 / Chair: Xiaohu Hu*		
10:00 to 10:30	**Coffee break**, *Room Florencia*		
10:30 to 11:45	**Session**	Session Chair	Room
	Session 1: Genomics I	Sheida Nabavi	Malta
	Session 2: Genomics II	Yang C. Fann	Monaco
	Session 3: Proteins I	Xuefeng Cui	Bruselas
	Session 4: Microbes and virus	Usama Bakry	Viena
	Session 5: Cheminformatics, drug representation and interaction I	Spiwok Vojtech	Madrid 2&3
	Session 6: Analysis of medical images and graphs I	Paolo Soda	Paris
	Session 7: Biomedical text processing I	Chen Li	Londres
	Special session: medical informatics and engineering (session 1/2)	Hanshu Cai	Living Lab 1
12:00 to 13:30	**Session**	Session Chair	Room
	Session 8: Proteins II	Fiona Brown	Bruselas
	Session 9: Biomedical text processing II	Sunghwan Sohn	Londres
	Session 10: Stress and depression	Eva K. Lee	Malta
	Session 11: Analysis of medical images and graphs II	Lei Du	Paris
	Session 12: Acceleration, optimization, scalability and computability I	Mozhgan Kabiri Chimeh	Madrid 2&3
	Session 13: Cancer I	Tianhai Tian	Monaco
	Session 14: Biology	Da Zhang	Viena
	Special session: medical informatics and engineering (session 2/2)	Hanshu Cai	Living Lab 1
13:30 to 14:30	**Lunch**, *Room Florencia*		
14:30 to 16:00	**Session**	Session Chair	Room
	Session 15: Analysis of medical images and graphs III	Truong Tran	Londres
	Session 16: Genomics III	Sheida Nabavi	Madrid 2&3

14:30 to 16:00	Session 17: Cheminformatics, drug representation and interaction II	Jan Baumbach	Monaco
	Session 18: Diagnosis, clinical procedures, progression and recovery I	Martin Macaš	Bruselas
	Session 19: Monitoring, sensors and devices I	Vladimir Brusic	Viena
	Session 20: Cancer II	Iman Hajirasouliha	Paris
	Session 21: Industry track I	Mario Guarracino	Malta
	BHI 2018 Workshop (session 5/6)	Illhoi Yoo	Living Lab 1
16:00 to 16:30	**Coffee break**, *Room Florencia*		
16:30 to 17:30	**Session**	Session Chair	Room
	Poster session I	-	Hall Plaza Mayor
	BHI 2018 Workshop (session 6/6)	Illhoi Yoo	Living Lab 1

WEDNESDAY 5th DECEMBER

08:30 to 18:00	**Registration**, *Hall Plaza Mayor*		
09:00 to 10:00	**Keynote: Harald Schmidt** REPO-TRIAL: Common mechanism-based drug repurposing and endophenotyping *Room Madrid 2&3 / Chair: Huiru (Jane) Zheng*		
10:00 to 10:30	**Coffee break**, *Room Florencia*		
10:30 to 11:45	**Session**	Session Chair	Location
	Session 22: Genomics IV	James Green	Malta
	Session 23: Genomics V	Ekaterina Khrameeva	Monaco
	Session 24: Biomedical text processing III	Chunlei Tang	Bruselas
	Session 25: Analysis of medical images and graphs IV	WonSook Lee	Viena
	Session 26: Cheminformatics, drug representation and interaction III	Yang C. Fann	Paris
	Session 27: Proteins III	Xuefeng Cui	Londres
	OpenMultiMed COST Action WG3/4 Workshop	Huiru Zheng	Madrid 2&3

	Session	Session Chair	Location
12:00 to 13:30	Session 28: Genomics VI	Lingling Jin	Malta
	Session 29: Descriptive languages, transcription and annotation	Chen Li	Paris
	Session 30: Biomedical text processing IV	Chunlei Tang	Bruselas
	Session 31: Biomedical text processing V	David Sankoff	Viena
	Session 32: Analysis of medical images and graphs V	Truong Tran	Monaco
	OpenMultiMed COST Action WG3/4 Workshop	Tatjana Loncar Turukalo	Madrid 2&3
13:30 to 14:30	**Lunch**, *Room Florencia*		
14:30 to 15:00	**Awards Ceremony** Best paper and Best Student Paper *Room Madrid 2&3*		
15:00 to 16:00	**Keynote: Xuegong Zhang** An Overview of Bioinformatics Challenges for Human Cell Atlas *Room Madrid 2&3 / Chair: Zoraida Callejas*		
16:00 to 16:30	**Coffee break**, *Room Florencia*		
16:30 to 17:30	**Session**	Session Chair	Location
	Poster session II	-	Hall Plaza Mayor
19:00 to 21:00	**Banquet (ticket required)** *Real Academia de Bellas Artes de San Fernando* *Calle de Alcalá 13 (instructions to reach it in the bag)*		

THURSDAY 6th DECEMBER

	Session	Session Chair	Location
08:30 to 10:30	**Registration**, *Hall Plaza Mayor*		
09:00 to 10:00	Session 33: Genomics VII	Mario Guarracino	Malta
	Session 34: Acceleration, optimization, scalability and computability II	Mozhgan Kabiri Chimeh	Monaco
	Session 35: Diagnosis, clinical procedures, progression and recovery II	Lixia Yao	Bruselas
	Session 36: Cancer III	Usama Bakry	Paris
	Session 37: Industry track II	Paul Walsh	Londres

09:00 to 10:00	OpenMultiMed COST Action WG3/4 Workshop	Mihnea Alexandru Moisescu	Viena
10:00 to 10:30	**Coffee break**, *Room Florencia*		
10:30 to 12:00	**Session**	Session Chair	Location
	Session 38: Biomedical text processing VI	Sunghwan Sohn	Malta
	Session 39: Analysis of medical images and graphs VII	Kumaradevan Punithakumar	Monaco
	Session 40: Patient adaptation and representation	Adam Craig	Bruselas
	Session 41: Heterogeneous and large data analysis	Marina Bendersky	Londres
	OpenMultiMed COST Action WG3/4 Workshop	Massimiliano Zanin	Viena
12:15 to 13:35	**Session**	Session Chair	Location
	Session 42: Genomics VIII	Brianna Sierra Chrisman	Paris
	Session 43: Brain and EEG	Taghi Mostafavi	Malta
	Session 44: Microbiome	Haiying Wang	Monaco
	Session 45: Obstetrics and fetal studies	Trupti Joshi	Bruselas
	Session 46: Diagnosis, clinical procedures, progression and recovery III	Lixia Yao	Londres
	OpenMultiMed COST Action WG3/4 Workshop	Ivan Chorbey	Viena

WORKSHOPS

Methods and Applications of Data Mining and Machine Learning for Biomedical Engineering (MADMMLBE)

Date: 3rd Dec, 8:00-13:00; Room: Bruselas

Workshop Chairs: Zhirong Sun, Xiaohua Douglas Zhang, Le Zhang, Yan Shi, Quan Zou

Time	Title	Presenter/Author
8:00-8:15	*Continuous Monitoring of Human Physiological Signals for Health and Disease*	Xiaohua Douglas Zhang
8:15-8:30	*An approach on discretizing time series using recurrent neural network*	Kuan-Cheok Lei
8:30-8:45	*An Improved Method for Using Sample Entropy to Reveal Medical Information in Data from Continuously Monitored Physiological Signals*	Chang Chen
8:45-9:00	*Comparison of Ocular Biomechanical Machine Learning Classifiers for Glaucoma Diagnosis*	Shu-Hao LU
9:00-9:15	*Complexity pattern of Physiological Dynamics for Allergic Asthma and Rhinitis*	Dandan Wang
9:15-9:30	*A new type of wavelet de-noising algorithm for lung sound signals*	Fei Meng
9:30-9:45	*Analysis of Impact Factors of Multiscale Entropy*	Teng Zhang
9:45-10:00	*Q & A*	
10:00-10:30	**Coffee Break**	
10:30-10:45	*K-mer Counting: memory-efficient strategy, parallel computing and field of application for Bioinformatics*	Ming Xiao
10:45-11:00	*Transcriptome analysis of human peripheral blood reveals key circRNAs implicated in Allergic bronchopulmonary aspergillosis*	Chen Huang
11:00-11:15	*Context-Aware U-Net for Biomedical Image Segmentation*	Jiaxu Leng
11:15-11:30	*Prediction Indicators for Acute Exacerbations of Chronic Obstructive Pulmonary Disease By Combining Non-linear analyses and Machine Learning*	Yu Jin
11:30-11:45	*Unsupervised clustering of DVT Ultrasound Images using High Order Statistics*	Thibaud Berthomier
11:45-12:00	*Exploration of dysregulated lncRNA-mRNA network from the RNA-seq data of rats induced by three different synthetic cytotoxic compounds*	Dongliang Leng
12:00-12:15	*Application of Arrayed CRISPR/Cas9 Screen and its Data Analysis: a Systematic Review*	Shixue Sun
12:15-12:30	*Systems Analysis of Dopaminergic Neurons Specific Dynamic Transcriptome in Drosophila Reveals New Insights into Pathogenesis and Progression of Parkinson's Disease*	Zhirong Sun
12:30-12:45	*Q & A*	

Data Mining from Genomic Variants and Its Application to Genome-wide Analysis (DMGA)

Organizer: Prof. Taesung Park / Monday 3rd December, Room Estocolmo

Time	Title	Presenter/Author
08:00-10:00	**Session 1: Advanced Transcriptomics Data Analysis** **(15 minutes for each talk, 2 minutes Q and A)** *Session Chair: Prof. Seungyoon Nam*	
08:00-08:50	Gene expression based prediction of prognostic outcome in ovarian cancer	TaeJin Ahn, Nayeon Kang, **Yonggab Kim**, and Taesung Park
	sleBioRepo: a curated database of gene expression levels, in systematic lupus erythematosus	Sungjin Park and **Seungyoon Nam**
	Deep Learning-based Identification of Cancer or Normal Tissue using Gene Expression Data	**TaeJin Ahn**, Taewan Goo, Sungmin Kim, Kyullhee Han, Saigick Park, and Taesung Park
08:50-10:00	Cluster Switches in Gene Expression Data	**Tal Shay**, Guy Shani, and Maayan Hassidim
	CLIPSeed: Achieving High Precision miRNA Binding Sites Prediction using PAR-CLIP Data	**Mingzhu Lu** and Yufei Huang
	Correcting genomic deletion calls with complex boundaries from next generation sequencing data	**Zhongmeng Zhao**, Zewen Tian, Yu Geng, Siyu He, Xuanping Zhang, and Jiayin Wang
	Detecting Outliers in segmented genomes of Flu virus using an alignment-free approach	**Mosaab Daoud**
10:00-10:30	**Coffee Break,** *Sala Florencia*	
10:30-13:00	**Session 2: Advanced Genomics Data Analysis** **(15 minutes for each talk, 2 minutes for Q and A)** *Session Chair: Prof. Taesung Park*	
10:30-10:50	**Invited talk:** Prediction of Platinum Resistance in High Grade Serous Ovarian Cancer Using Hybrid Ensemble Deep Learning	**TaeJin Ahn**
10:50-12:00	An approximation method of extremely low p-values using permutation test	**Sangseob Leem** and Taesung Park
	Practical fast on-line exact pattern matching algorithms for highly similar sequences	**Nadia Ben Nsira**, Thierry Lecroq, and Elise Prieur-Gaston
	Insights of Window-Based Mechanism Approach to Visualize Composite BioData Point in Feature Spaces	Mosaab Daoud
	DITGOssi: a two-stage invasive tumor growth optimization algorithm for the detection of SNP-SNP interactions	**Kaiwen Tan**, Shoubin Dong, Jing Zhou, and Jinlong Hu
12:00-12:50	Detecting population structures by independent component analysis	**Mira Park**, Eunbin Choi, Yongkang Kim, and Taesung Park
	Comparing Four Genome-Wide Association Study (GWAS) Programs with Varied Input Data Quantity	**Yan Yan**, Connor Burbridg, Jinhong Shi, Juxin Liu, and Anthony Kusalik
	Topological data analysis can extract subgroups with high incidence rates of Type 2 diabetes	Hyung Sun Kim, Changwoo Yi, Yongkang Kim, Uhnmee Park, Woong Woong, Hyuk Kim, and **Taesung Park**
12:50	**Closing Remarks**	

Workshop on Computer Based Processes and Algorithms for Biomedicine and Life Quality Improvement (CBPBL)

3 December 2018, 08:00-13:00: Room: Londres

Workshop Chair: Pierangelo Veltri

Time	Title	Presenter/Author
09:00 – 09:10	Workshop Introduction	Pierangelo Veltri
09:10-09:30	"Cross-topic Rumour Detection in the Health Domain	Rosa Sicilia, Mario Merone, Roberto Valenti, Ermanno Cordelli, Federico D'Antoni, Vincenzo De Ruvo, Patrizia Benedetta Dragone, Sara Esposito, and Paolo Sod
09:30-9:50	"On the use of mining techniques to analyse human papilloma virus dataset"	Domenico Mirarchi, Patrizia Vizza, Giuseppe Tradigo, Giuseppe Di Fatta, and Pierangelo Veltri
9:50-10:10	"Graph Cuts-based Segmentation of Alveolar Bone in Ultrasound Imaging"	Kim Cuong Nguyen, Danni Shi, Neelambar Kaipatur, Edmond Lou, Paul Major, Kumaradevan Punithakumar, and Lawrence Le
10:10-10:30	**Coffee Break**	
10:30-10:50	"Modeling and application of aorta coarctation: support system for pre-operative decision"	Lina T. Gaudio, Pierangelo Veltri, and Gionata Fragomeni,
10:50-11:10	"Tracking agricultural products for wellness care"	Patrizia Vizza, Giuseppe Tradigo, Pierangelo Veltri, Pasquale Lambardi, Claudia Garofalo, Fulvia Michela Caligiuri, Gianmichele Caligiuri, and Pietro H. Guzzi,
11:10-11:30	"A Comparison of PAR-CLIP Peak Calling Approaches on Noisy Data"	Oier Echaniz and Manuel Graña,
11:30-11:50	"Artificial Neural Networks Classification of Patients with Parkinsonism based on Gait"	Carlos Fernandes, Luís Fonseca, Flora Ferreira, Miguel Gago, Luís Costa, Nuno Sousa, Carlos Ferreira, João Gama, Wolfram Erlhagen, and Estela Bicho,
11:50-12:10	"Agent-based modeling of mesenchymal stem cells on a 3D-printed bio-device for the regenerative treatment of the infarcted myocardium"	Diana V. Ramírez López, Carlos Peña-Reyes, and Álvaro J. Rojas
12:10-12:30	Closing Remarks and Discussion	Pierangelo Veltri

Computational Methods for the Immune System Function (CMISF)

Dec, 3rd 2018 – 9:15; Room: Malta

Workshop Chairs: Francesco Pappalardo, Marzio Pennisi, Pedro Reche

Time	Title	Presenter/Author
09:15	**Welcome message**	
09:20	*Agent based modeling of relapsing multiple sclerosis: a possible approach to predict treatment outcome*	Giulia Russo
09:40	*A WED Method for Evaluating the Performance of Change-Point Detection Algorithms*	Ping Zhang
10:00-10:30	**Coffee Break**	
10:30	*Combination of Principal Component Analysis and Genetic Algorithm for Microbial Biomarker Identification in Obesity*	Ping Zhang
10:50	*Computational design of a legacy-based epitope vaccine against Human Cytomegalovirus*	Pedro Reche
11:10	*Optimal control in a mathematical model for tumor escape*	Marzio Pennisi
11:30	*Parallel Pair-Wise Interaction for Multi-Agent Immune Systems Modelling*	Mozhgan Kabiri chimeh
11:50	*Correlation-based network analysis for biomarkers in obesity*	Pin-Yen (Fiona) Chen
12:10	*Single Cell Transcriptomics Reveals Summary Patterns Specific for PBMCs and Other Cell Types*	Vladimir Brusic
13:00-14:30	**Lunch**	
15:00	*Estimating Daclizumab effects in Multiple Sclerosis using Stochastic Symmetric Nets*	Marzio Pennisi
15:20	*An Hydro-Mechanical Model of Edema Formation Applied to Bacterial Myocarditis*	Marcelo Lobosco
15:40	*A mathematical model of Chagas disease infection predicts inhibition of the immune system*	Leandro Martins de Freitas
16:00-16:30	**Coffee Break**	
16:30	*A mathematical model of murine macrophage infected with Leishmania sp*	Henrique de Assis Lopes Ribeiro
16:50	*Evolutionary Game Theory Can Explain the Choice between Apoptotic and Necrotic Pathways in Neutrophils*	Alva Presbitero
17:10	*Computational modeling approach to suggest possible therapeutic interventions in spinal muscular atrophy*	Giulia Russo
17:30	*An agent based modeling approach for the analysis of tuberculosis – immune system dynamics*	Francesco Pappalardo
17:50	**Closing Remarks**	

1st International Workshop on Machine Learning for EEG Signal Processing (MLESP)

December 3th (8:30am – 4pm); Room: Monaco / *Workshop Chair: Larbi Boubchir*

Time	Title	Presenter/Authors
8:30	**Opening Workshop**	
8:40-9:00	Active Learning for Semiautomatic Sleep Staging and Transitional EEG Segments	Martin Macas, Nela Grimova, Vaclav Gerla, Lenka Lhotska, and Elisaveta Saifutdinova
9:00-9:20	Detection of sleep spindles in NREM 2 sleep stages: Preliminary study & benchmarking of algorithms	Olivier Pallanca, Sammy Khalife, and Jesse Read
9:20-9:40	Expert-in-the-loop Learning for Sleep EEG Data	Vaclav Gerla, Vaclav Kremen, Martin Macas, Elizaveta Saifutdinova, Arnost Mladek, and Lenka Lhotska
9:40-10:00	Deep Convolutional Autoencoder for EEG Noise Filtering	Niago Leite, Eanes Pereira, Edmar Gurjão, and Luciana Veloso
10:00-10:30	**Coffee Break** (Room Florencia)	
10:30-10:50	Heuristic Active Learning for the Prediction of Epileptic Seizures Using Single EEG Channel	Joao Marcos Correia Marques, Hilda A. Cerdeira, Edgar Tanaka, Conrado de Vitor, and Paula Gomez
10:50-11:10	Convolutional Neural Networks for Epileptic Seizure Prediction	Matthias Eberlein, Raphael Hildebrand, Ronald Tetzlaff, Nico Hoffmann, Levin Kuhlmann, Benjamin Brinkmann, and Jens Müller
11:10-11:30	Machine learning for EEG-based biomarkers in Parkinson's disease	M. Isabel Vanegas, M. Felice Ghilardi, Simon P. Kelly, and Annabelle Blangero
11:30-11:50	Localizing Current Dipoles from EEG Data Using a Birth–Death Process	Keita Nakamura, Sho Sonoda, Hideitsu Hino, Masahiro Kawasaki, Shotaro Akaho, and Noboru Murata
11:50-12:10	Resting state EEG based depression recognition research using voting strategy method	Jing Yang, Junhong Niu, Shuai Zeng, Ying Wang, Rong La, Wandeng Mao, and Hanshu Cai
12:10-12:30	Focal EEG signal detection based on constant-bandwidth TQWT filter-banks	Vipin Gupta, Anurag Nishad, and Ram Bilas Pachori
12:30-12:50	EEG Signal Classification for BCI based on Neural Network	Kathia Chenane and Youcef Touati
13:00-14:30	**Lunch Break** (on own)	
14:00-14:20	Mutual Information-Based Electrode Selection Extended With Prior Knowledge For Use in Brain-Computer Interfacing	Ruben Moermans, Benjamin Wittevrongel, and Marc Van Hulle
14:20-14:40	Comparison between Single, Dual and Triple Rapid Serial Visual Presentation Paradigms for P300 Speller	Amir Mohamad Mijani, Mohammad Bagher Shamsollahi, Mohsen Sheikh Hassani, and Shayan Jalilpour
14:40-15:00	Correlated Attention Networks for Multimodal Emotion Recognition	Jie-Lin Qiu, Xiao-Yu Li, and Kai Hu
15:00-15:20	Single-Trial EEG Predicts Memory Retrieval Using Leave-One-Subject-Out Classification	Kueida Liao, Matthew Mollison, Tim Curran, and Virginia de Sa
15:20-15:40	Spatial Correlation Preserving EEG Dimensionality Reduction Using Machine Learning	Haymanot Gebre-Amlak, Hoang (Mark) Nguyen, Jesse Lowe, Ala-Addin Nabulsi, and Narisa Chu
15:40	**Closing Remarks**	
16:00	**Coffee Break** (Room Florencia)	

The 3rd International Workshop on Semantics-Powered Data Analytics (SEPDA)

December 3, 2018, 8:00 am – 4:40 pm; Room: Moscu

Workshop Chairs: Zhe He, Jiang Bian, Cui Tao, and Rui Zhang

Time	Title	Presenter/Author
8:00 am – 8:05 am	Opening Remarks	Zhe He
8:05 am – 8:50 am	Keynote: TBA	
8:50 am – 9:00 am	**Short Break**	
9:00 am – 10:00 am	**Session 1: Natural Language Processing & Text Mining**	
	Analyzing Early Signals of Older Adult Cognitive Impairment in Electronic Health Records	Somaieh Goudarzvand, Jennifer St. Sauver, Michelle Mielke, Paul Takahashi, and Sunghwan Sohn
	Representing Knowledge for Radiation Therapy Planning with Markov Logic Networks	Yi Zhen, Saugat Karki, Lulin Yuan, Jackie Wu, and Yaorong Ge
	Automatic Relationship Verification in Online Medical Knowledge Base: a Large Scale Study in SemMedDB	Danchen Zhang, Daqing He, Ning Zou, Xin Zhou, and Fen Pei
10:00 am -10:30 pm	**Coffee Break**	
10:30 am – 12:10 pm	**Session 2: Ontology and Knowledgebase**	
	Extended Analysis of Topological-Pattern-Based Ontology Enrichment	Zhe He, Vipina Kuttichi Keloth, Yan Chen, and James Geller
	A Methodology for Extracting Knowledge about Controlled Vocabularies from Textual Data using FCA-Based Ontology Engineering	Simin Jabbari and Kilian Stoffel
	OntoKeeper: A Semiotic-driven Ontology Evaluation Tool For Biomedical Ontologists	Muhammad Amith, Frank Manion, Chen Liang, Marcelline Harris, Dennis Wang, Yongqun He, and Cui Tao
	Prototyping an Interactive Visualization of Dietary Supplement Knowledge Graph	Xing He, Rui Zhang, Rubina Rizvi, Jake Vasilakes, Xi Yang, Yi Guo, Zhe He, and Jiang Bian
	Constructing Biomedical Knowledge Graph based on SemMedDB and Linked Open Data	Qing Cong, Zhiyong Feng, Fang Li, Li Zhang, Guozheng Rao, and Cui Tao
12:10 pm – 2:00pm	**Lunch Break**	
2:00 pm – 3:00pm	**Session 3: Ontology-Based Data Analytics**	
	Ontology-based Venous Thromboembolism Risk Factors Mining and Model Developing from Medical Records	Yuqing Yang, Xin Wang, Yu Huang, Ning Chen, Juhong Shi, and Ting Chen
	Comparing adverse effects of Hepatitis C drugs using FAERS data	Jing Huang, Xinyuan Zhang, Jingcheng Du, Rui Duan, Liu Yang, Jason Moore, Yong Chen, and Cui Tao
	Gene Family-led Meta-Analysis of Drug Target Data	Qiong Cheng, Saurabh Mehta, Tudor Oprea, and Stephan Schurer
3:00 pm - 3:30 pm	**Break**	
3:30 pm - 4:30 pm	**Session 4: Deep Learning and Data Mining**	
	Deep Convolution Neural Networks for Drug-Drug Interaction Extraction	Xia Sun, Long Ma, Xiaodong Du, Jun Feng, and Ke Dong
	X-A-BiLSTM: a Combinational Deep Learning Approach for Depression Detection in Imbalanced Data	Qing Cong, Zhiyong Feng, Fang Li, Yang Xiang, Guozheng Rao, and Cui Tao
	Formulation of FAIR Metrics for Primary Research Articles	Adam Craig and Carl Taswell
4:30 pm – 4:40pm	**Closing Remarks and Feedback**	

Analysis and Modeling of the Three-dimensional Structure of Chromatin (AMTSC)

Dec. 3rd 8:00-13:00; Room: Madrid 2+3

Workshop Chairs: Mikhail Gelfand, Leonid Mirny, Sergei Razin

Time	Title	Presenter/Author
8:00	**Opening Remarks (none)**	
8:00-8:30	*The study of Dictyostelium discoideum chromatin structure*	Olga Tsoy
8:30-8:50	*Nuclear lamina maintains global spatial organization of chromatin in Drosophila*	Sergei Ulyanov
8:50-9:00	*Recognizing Patterns of Nucleosome and DNA Structures Positioning*	Elen Tevanyan
9:00-9:30	*Large-scale analysis of RNA-DNA interactions*	Alexandra Galitsyna
9:30-10:00	*Single-cell Hi-C demonstrates that TADs are stable units of Drosophila genome folding that persist in individual cells*	Sergei Razin
10:00 – 10:30	**Coffee Break**	
10:30-11:00	*Interplay of Loop Extrusion, Compartmentalization and Global Chromosome Dynamics Across Conditions and the Cell Cycle*	Johannes Nuebler
11:00-11:30	*Gaussian network approach to the description of topological constraints in the chromatin*	Mikhail Tamm
12:10-12:20	*Homopolymer with intrachain reversible bonds as a model of large-scale chromatin organization and dynamics*	Artem Petrov
11:50-12:10	*Reconstruction of the chromatin 3D conformation from single cell Hi-C data*	Pavel Kos
11:30-11:50	*Optimal Modularity Method (OMM) for unbiased TADs detection in chromatin contact maps of single cells*	Kirill Polovnikov
12:20-12:30	*Algorithms for Clustering and the Comparison of Hierarchies within the Spatial Organization of Chromatin*	Olga Pushkareva
12:30-12:40	*Prediction of 3D Chromatin Structure with Recurrent Neural Networks*	Michal Rozenwald
12:40-12:50	*Prediction of chromatin spatial structure characteristics using machine learning methods*	Sergei Starikov
12:50-13:00	*Inferring chromatin states with stochastic autoencoder*	Roman Kudrin
13:00	**Closing Remarks (none)**	

9th Integrative Data Analysis in Systems Biology (IDASB 2018)

3rd December 2018; Room: Paris

*Workshop Chairs: **Huiru Zheng**, Zhongming Zhao, Rui Jiang*

Time	Title	Presenter/Author
8:45 – 9:00	**Welcome and Opening Remarks (Chair)**	
9:00 – 9:20	*Asymmetric Integration of Single-Cell Transcriptomic Data using Latent Dirichlet Allocation and Procrustes Analysis (S16201)*	Mitsuhiro Eto, Wataru Hirota, **Shigeto Seno**, and Hideo Matsuda
9:20 – 9:40	*A computational method for detecting the associations between multiple loci and phenotypes (B730)*	Zhongmeng Zhao, Jiali Huang, Ruoyu Liu, Mingzhe Xu, Siyu He, Xuanping Zhang, and **Jiayin Wang**
9:40 – 10:00	*Inference of protein-protein networks for triple-negative breast cancer using single-patient proteomic data (S16205)*	Yan Yan, Jiangyong Wei, Xiaohua Hu, and **Tianhai Tian**
10:00-10:30	**Coffee Break**	
10:30 – 10:50	*VIA-QMI: A visualized data analytic tool for Quantitative Multiplex Co-Immunoprecipitation(QMI) Platform (S16207)*	**Feiping Li,** Stephen Smith, and Wooyoung Kim
10:50 – 11:10	*Multiscale Computing in Systems Medicine: a Brief Reflection (S16208)*	Huiru Zheng, Jyotsna Wassan, **Mihnea Moisescu**, Lacramioara Stoicu-Tivadar, João Miranda, Mihaela Crisan-Vida, Almir Badnjevic, Ioan Sacala, Ivan Chorbev, and Boro Jakimovski
11:10 – 11:30	*Wavelet Based Compressed Sensing Sampling and Estimation of N-States Random Evolution Model Parameters in Microtubule Signal (B338)*	Vineetha Menon and **Shantia Yarahmadian**
11:30 – 11:50	*A Tissue-aware Gene Selection Approach for Analyzing Multi-tissue Gene Expression Data (B427)*	**Cindy Perscheid**, Lukas Faber, Milena Kraus, Paul Arndt, Michael Janke, Sebastian Rehfeldt, Antje Schubotz, Tamara Slosarek, and Matthias Uflacker
11:50 – 12:10	*Mathematical Modelling of Genetic Network for Regulating the Fate Determination of Hematopoietic Stem Cells (B538)*	**Siyuan Wu**, Tiangang Cui, and Tianhai Tian
12:10 – 12 30	*Weighted gene co-expression network analysis of microarray mRNA expression profiling in response to electroacupuncture*	**Afsaneh Mohammadnejad**, Shuxia Li, Hongmei Duan, Jesper Lund, Weilong Li, Jan Baumbach, and Qihua Tan
12:30 – 12:50	*Type 2 Diabetes Gene Identification Using an Integrated Approach from Single-Cell RNA Sequencing Data (S16202)*	Sushmita Paul and Sonu Bansal
12:50 – 1:00pm	**Closing Remarks**	

5th International Workshop on High Performance Computing on Bioinformatics (HPCB)

3rd, December, 8:00-10:00; Room: Viena

Workshop Chairs: Che-Lun Hung, Huiru Zheng, Chuan Yi Tang, Chun-Yuan Lin

Time	Title	Presenter/Author
8:00-8:20	*Using Deep Learning to Identify Cell and Particle in Live-Cell Time-lapse Images*	Hui-Jun Cheng, Cheng-Xian Wu, Wei-Hsiang Chen, Chun-Yuan Lin, Che-Lun Hung, and Chuan-Yi Tang
8:20-8:40	*Job Allocation schemes for Mobile Service Robots in Hospitals*	Bikram Kumar Basaba, Lokesh Sharma, and Shih-Lin Wu
8:40-9:00	*Chronic Kidney Disease Survival Prediction with Artificial Neural Networks*	Hanyu Zhang, Che-Lun Hung, William Cheng-Chung Chu, Ping-Fang Chiu, and Chuan-Yi Tang
9:00-9:20	*An Overview of Machine Learning and HPC in Open Sources for Bioinformatics*	Yin Te Tsai
9:20-9:40	*Sparse Orthogonal Nonnegative Matrix Factorization for Identifying Differentially Expressed Genes and Clustering Tumor Samples*	Ling-Yun Dai, Jin-Xing Liu, Rong Zhu, Xiang-Zhen Kong, Mi-Xiao Hou, and Sha-Sha Yuan
9:40-10:00	*CloudGT: A High Performance Genome Analysis Toolkit Leveraging Pipeline Optimization on Spark*	Anghong Xiao, Shoubin Dong, Cheng Liu, Lingqi Zhang, and Zongze Wu
10:00-10:30	**Coffee Break**	

Biomedical and Health Informatics (BHI) Workshop

December **3**-4 (First Day); Room: Living Lab 1

Workshop Chairs: Illhoi Yoo

Time	Title	Presenter/Author
9:00-9:05	**Welcome (Chair)**	
9:05	*Estimating New York Heart Association Classification for Heart Failure Patients from Information in the Electronic Health Record*	Sisi Ma, Rui Zhang, Jessica Munroe, Lindsey Shanahan, Sarah Horn, and Stuart Speedie
9:25	*Does music help to be more attentive while performing a task? A brain activity analysis*	Ana Rita Teixeira, Ana Tomé, Luís Roseiro, and Anabela Gomes
9:40	*Improve Chinese Clinical Named Entity Recognition Performance by Using the Graphical and Phonetic Feature*	Yifei Wang, Sophia Ananiadou, and Jun'ichi Tsujii
10:00-10:30	Coffee Break	
10:30	*Mapping Common Data Elements to a Domain Model Using an Artificial Neural Network*	Robinette Renner, Shengyu Li, Yulong Huang, Shaobo Tan, Dongqi Li, Ada Chaeli van der Zijp-Tan, Ryan Benton, Glen M. Borchert, Jingshan Huang, and Guoqian Jiang
10:50	*Automated Clinical Documentation Improvement*	Vatsal Shah, Raxit Goswami, Vivek Kumar, Binni Shah, and Helly Shah
11:05	*Deep Medical Entity Recognition for Swedish and Spanish*	Rebecka Weegar, Alicia Pérez, Arantza Casillas, and Maite Oronoz
11:25	*Can Existing Guideline Languages Meet the Requirements of Computerized Checklist Systems?*	Leixing Lu, Shan Nan, Sicui Zhang, Xudong Lu, and Huilong Duan

11:40	*Design and Application of Mental Fatigue Detection System Using Non-Contact ECG and BCG Measurement*	Yonghao Ma, Fuze Tian, Qinglin Zhao, and Bin Hu
12:00	*An Unobtrusive Sensing Solution for home based Post-Stroke Rehabilitation*	Idongesit Ekerete, Chris Nugent, and Jim McLaughlin
12:15	*Biomechanical Parameters of Muscles, Objective Assessment Using MyotonPRO*	Iva Milerská, Martin Macas, and Lenka Lhotská
12:30-2:00	Lunch (on your own)	
2:00-3:00	***Keynote: Innovation in Big Data Analytics and Applications to Biomedicine*** *Abstract: Risk and decision models and predictive analytics have long been cornerstones for advancement in industrial, government, and military applications. In particular, multi-source data system modeling and big data analytics and technologies play an increasingly important role in modern business enterprise. Many problems arising in these domains can be formulated into mathematical models and can be analyzed using sophisticated optimization, decision analysis, and computational techniques. In this talk, we will share some of our successes in medicine and healthcare through innovation in predictive and big data analytics.* **Eva K Lee, PhD** Director, NSF-Whitaker Center for Operations Research in Medicine and HealthCare Co-Director, NSF I/UCRC Center for Health Organization Transformation Distinguished Scholar in Health Systems, Health System Institute, Georgia Tech/Emory University Virginia C. and Joseph C. Mello Chair and Professor, School of Industrial and Systems Engineering Professor, College of Computing, Georgia Institute of Technology	
3:00-4:00	***Keynote: The Role of Big Data & A.I. in Mental Health Research*** *Abstract: In recent years, big data resources have attracted significant interest across health and healthcare, including monitoring personal health and wellness to creating risk prediction algorithms that can facilitate minimization of hospital re-admissions. Yet when it comes to big data science in mental health care and research, the successes have remained relatively limited to date. We continue to use primitive ways to identify and measure mental illness, lack organizational capacity for building and maintaining large and longitudinal data repositories, and have yet to define a robust model for turning individual data into collective knowledge that can benefit patient care. Our research is an attempt to address these challenges by developing and applying novel big data analytics methods in understanding effective ways to diagnose, treat and manage patients suffering from mental health issues, such as major depression.* **Jyotishman Pathak, PhD** Frances and John L. Loeb Professor of Medical Informatics and Chief of Division of Health Informatics, Department of Healthcare Policy & Research, Weill Cornell Medical College, Cornell University	
4:00-4:30	Coffee Break	
4:30	*Attention and concentration in normal and deaf gamers*	Ana Rita Teixeira, Ana Tomé, Luís Roseiro, and Anabela Gomes
4:50	*Bootstrapping analysis of crowdsourced non-expert estimates of the number of calories in photographs of meals*	Raymond Bond, Anne Moorhead, Huiru Zheng, and Patrick McAllister
5:05	*Nanopore SimulatION – a raw data simulator for Nanopore Sequencing*	Christian Rohrandt, Nadine Kraft, Pay Gießelmann, Björn Brändl, Bernhard M. Schuldt, Ulrich Jetzek, and Franz-Josef Müller
5:25	*ImmunoAdept – bringing blood microbiome profiling to the clinical practice*	Paul Walsh, Bruno Andrade, Jason Wu, Brendan Lawlor, Matthias Hemmje, Brain Kelly, Cintia Palu, and Michael Kramer

5:40	*Construction of DNA methylation analysis platform based on high-throughput sequencing*	Jiangyu Li, Jiakuan Li, Xiaolei Wang, Dongsheng Zhao, and Siqing Zhao
5:55	*A Practical Algorithm for DNA Pattern Searching using Database-Based Approach*	FREESON Kaniwa and Mpho Phuthego
6:15	*A Fast Quantum Clustering Approach for Cancer Gene Clustering*	Rong Zhu, Guangshun Li, Jin-Xing Liu, Ling-Yun Dai, Sha-Sha Yuan, and Ying Guo
6:30	End of the first day	

Biomedical and Health Informatics (BHI) Workshop

December 3-**4** (Second Day); Room: Living Lab 1

Workshop Chairs: Illhoi Yoo

Time	Title	Presenter/Author
1:00-2:30	Lunch (provided)	
2:30	*An Effective Standardization Method for the Lab Indicators in Regional Medical Health Platform*	Jiaying Zhang, Qi Wang, Zhixing Zhang, Yangming Zhou, Qi Ye, Huanhuan Zhang, Jiahui Qiu, and Ping He
2:50	*Classification of radiology reports by modality and anatomy: A comparative study*	Marina Bendersky, Joy Wu, and Tanveer Syeda-Mahmood
3:10	*Using multi-anchors to identify patients suffering from multimorbidities*	Karl Øyvind Mikalsen, Cristina Soguero-Ruiz, Inmaculada Mora-Jiménez, Isabel Caballero López Fando, and Robert Jenssen,
3:30	*Recurrent Capsule Network for Relation Extraction: A Practical Application to the Severity Classification of Coronary Artery Disease*	Qi Wang, Jiahui Qiu, Yangming Zhou, Tong Ruan, Daqi Gao, and Ju Gao
4:00	Coffee Break	
4:30	*A New Optimized Queue Model with Compensation and Buffer*	Tianyou Bao, Jingsong Li, Hanxing Hu, Shiang Li, Yu Meng, and Changjiang Zhang
4:50	*Body Composition and Biochemical Characteristics of Normal Weight Obesity in Japanese Young Women with Different Physical Activities*	Jingshan Huang, Keisuke Fukuo, Gen Yoshino, Tsutomu Kazumi, Chandan Basetty, Yulong Huang, Shaobo Tan, Dongqi Li, Ada Chaeli van der Zijp-Tan, Ada Fong, Glen M. Borchert, and Bin Wu
5:05	*An Efficient Method for Attractor Observability in Boolean Networks*	Yushan Qiu, Yulong Huang, Shaobo Tan, Dongqi Li, Ada Chaeli van der Zijp-Tan, Ada Fong, Glen M. Borchert, and Jingshan Huang
5:25	*Singling out ischemic lesion zones and transplanted mesenchymal stem cells in the rat brain MRI*	Olga Anokhina, Vitaly Fralenko, Mikhail Khachumov, Vyacheslav Khachumov, and Maria Shustova
5:45	*Analysis of Sex and Recurrence Ratios in Simplex and Multiplex Autism Spectrum Disorder Implicates Female-Specific Alleles as Inheritance Mechanism*	Brianna Chrisman, Maya Varma, Peter Washington, Kelley Paskov, Nate Stockham, Jae-Yoon Jung, and Dennis Wall
6:00	*An inside look at the Opioid Crisis over Twitter*	Juan Antonio Lossio-Ventura and Jiang Bian
6:15	*A Pulmonary Vascular Segmentation Algorithm of Chest CT Images Based on Fast Marching Method*	Wenjun Tan
6:35	*An Extracting Method of Symmetry Plane from Head CT images for Surgery Based on OBB and Image Mutual Information*	Wenjun Tan
	Closing Remarks	

Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM)

3rd Dec; Room: Living Lab 2 / *Workshop Chair: Haiying Wang*

Time	Title	Presenter/Author
8:30 8:45	**Welcome and Opening Remarks (Chair)**	
8:45 9:10	*Fully Automated Left Atrial Segmentation from MR Image Sequences Using Deep Convolutional Neural Network and Unscented Kalman Filter*	Xiaoran Zhang, Glynn Martin, Michelle Noga, and Kumaradevan Punithakumar
9:10 9: 35	*Utilizing Mask R-CNN for Detection and Segmentation of Oral Diseases*	Rajaram Anantharaman, Matthew Velazquez, and Yugyung Lee
9:35 10:00	*Using deep neural network to recognize mutation entities in biomedical literature*	Dongsheng Zhao, Fan Tong, and Zheheng Luo
10:00	**Coffee Break**	
10:30 10:55	*Hypertension Warning Model Based on Random Forest and Distance Metrics*	Yiyuan Ma, Bo Yang, Guixia Kang, and Beibei Hou
10:55 11:20	*Attention-Based Multi-Task Learning in Pharmacovigilance*	Shinan Zhang, Shantanu Dev, Joseph Voyles, and Anand Rao
11:20 11:45	*eZiGait: Toward an AI gait analysis and assistant system*	Graham McCalmont, Philip Morrow, Huiru Zheng, Anas Samara, Haiying Wang, and Sally McClean
11:45 12:10	*Detection of functional state after alcohol consumption by classification and machine learning technics*	Morgane Evin, Joffrey Taillard, Hugo Loeches De la Fuente, Edith Galy, and Catherine Berthelon
12:10 12:30	*Heterogeneous Hi-C data super-resolution with a conditional generative adversarial network*	Yifeng Chen, Wei Sun, and Haohan Wang
Lunch break (on your own) – From 13:00 to 14:30		
2:30 2:55	*Discovery of Sets and Representatives of Variables in Co-nonlinear Relationships by Neural Network Regression and Group Lasso*	Miho Ohsaki, Hayato Sasaki, Naoya Kishimoto, Shigeru Katagiri, and Patrick Hang Hui Then,
2:55 3:20	*Addressing the Cold Start Problem in Active Learning Approach Used For Semi-automated Sleep Stages Classification*	Nela Grimova, Martin Macas, and Vaclav Gerla
3:20 3:45	*Evaluation of using a collective approach when selecting biomarker features from machine learning models*	Carly Bobak and Jane Hill
3:45 4:00	*A Statistical Approach To Correlating Environmental and Demographic Factors to Cancer Incidences Across U.S. Counties*	Kaushik Shivakumar
4:00	**Coffee Break**	
4:30 4:55	*Else-Tree Classifier for Minimizing Misclassification of Biological Data*	Truong Tran, Marc Pusey, and Ramazan Aygun
4:55 5:20	*A novel ensemble method for high-dimensional genomic data classification*	Alexandra Espichan and Edwin Villanueva
5:20 5:45	*Toward data-driven identification of Kingdom-specific protein sequence motifs*	Corrine Elliott, Kristin Linscott, Satrio Husodo, Joseph Chappell, and Jinze Liu
5:45 6:10	*Analysis of hot regions prediction in PPI with different amino acid mutation using machine learning algorithm*	Jing Hu, Haomin Gan, Xiaolong Zhang, and Nansheng Chen
6:10 6:30	*A New Model based on Fuzzy integral for Cancer Prediction*	Jinfeng Wang, Jiajie Chen, and Hui Wang
	Closing Remarks	

Quality Assurance of Biological and Biomedical Ontologies and Terminologies (QABBOT)

Monday Dec 3, 2018, 10:30-13:00; Room: Viena

Workshop Chairs: Ankur Agrawal, Licong Cui

Time	Title	Presenter/Author
10:30-10:50	Enrichment of SNOMED CT Ophthalmology Component to Support EHR Coding	Hao Liu, P. Lloyd Hildebrand, Yehoshua Perl, and **James Geller**
10:50-11:10	A Lexical Approach to Identifying Subtype Inconsistencies in Biomedical Terminologies	**Rashmie Abeysinghe**, Fengbo Zheng, Eugene Hinderer, Hunter Moseley, and Licong Cui
11:10-11:30	Quality Assurance of Concept Roles in the National Cancer Institute thesaurus	Ling Zheng, Yan Chen, Yehoshua Perl, Michael Halper, **James Geller**, and Sherri de Coronado
11:30-11:50	Mapping of MalaCards Maladies to UMLS Concepts	**C Paul Morrey**
11:50-12:10	An Efficient Implementation of a Subgraph Isomorphism Algorithm for GPUs	**Vincenzo Bonnici**, Rosalba Giugno, and Nicola Bombieri

9th International Workshop on High Performance Bioinformatics and Biomedicine (HiBB-2018)

Workshop Chair: Mario Cannataro, Location: Room Bruselas

Time	Title	Presenter/Author
14.00	**Opening Remarks**	**Mario Cannataro**
14.20-14.40	S08205: MULTI-X, a state-of-the-art cloud-based ecosystem for biomedical research	**Milton Hoz de Vila**, Rahman Attar, Marco Pereanez, and Alejandro Frangi,
14.40 - 15.00	S08203: Cost and Time Prediction for Efficient Execution of Bioinformatics Workflows in Federated Cloud	Michel Rosa, **Aletéia Araújo**, and Felipe Souza
15.00 - 15.20	S08202: Using Quartets to Compare the NCD and MCMC Methods for Constructing Phylogenetic Trees	**John Rogers**
15.20 - 15.40	B678: S4S: RESTful Services to Collect, Integrate and Analyze SNPs and Clinical Data on the Web	**Giuseppe Agapito**, Pietro H. Guzzi, and Mario Cannataro
15.40 - 16.00	S08204: Predicting abandonment in telehomecare programs using Sentiment Analysis: a system proposal	**Chiara Zucco**, Sergio Bella, Clarissa Paglia, Paola Tabarini, and Mario Cannataro
16.00	**Coffee Break**	
16.30-16.50	B736: Random Subspace Projection for Predicting Biogeographical Ancestry	Tanjin Toma, Tayo Obafemi-Ajayi, Jeremy Dawson, and **Donald Adjeroh**
16.50-17.10	B423: p-SCNAClonal: Somatic copy number alterations based tumor subclonal population inferring method	Yanshuo Chu, **Chenxi Nie**, and Yadong Wang
17.10-17.30	S08207: Explainable Sentiment Analysis with Applications in Medicine	**Chiara Zucco**, Huizhi Liang, Giuseppe Di Fatta, and Mario Cannataro
17.30-17.50	S08206: Survey of main tools for querying and analyzing TCGA Data	**Marzia Settino** and Mario Cannataro
17.50	**Closing Remarks**	**Mario Cannataro**

The 3rd International Workshop on Affective Computing in Biomedicine and Healthcare (ACBH 2018)
Data Analytics in Metagenomics (DAM 2018)

3rd Dec.2018; Room: Estocolmo

Workshop Chairs: Huiru (Jane) Zheng, Paul Walsh, Haiying Wang

Time	Title	Presenter/Author
2:30 – 2:40	**Welcome and Opening remarks (Chairs)**	
2:40 – 3:00	A Machine Learning Emotion Detection Platform to Support Affective Well Being	Michael Healy, Ryan Donovan, Paul Walsh, and Huiru Zheng
3:00 – 3:20	The SenseCare System: Using Automatic Emotional Analysis to Provide Effective Tools for Supporting Wellbein	Ryan Donovan, Michael Healy, Huiru Zheng, Felix Engel, Binh Vu, Michael Fuchs, Paul Walsh, Matthias Hemmje, and Paul Mc Kevitt
3:20 – 3:40	Exploration of Multiclass and One-class Learning Methods for Prediction of Phage-bacteria Interaction at Strain Level	Diogo Manuel Carvalho Leite, Juan Fernando Lopez, Xavier Brochet, Miguel Barreto-Sanz, Yok-Ai Que, Gréegory Resch, and Carlos Peña-Reyes
3:40 – 4:00	An Integrative Framework for Functional Analysis of Cattle Rumen Microbiome	Jyotsna Talreja Wassan, Huiru Zheng, Fiona Browne, Jenna Bowen, Paul Walsh, Rainer Roehe, Richard Dewhurst, Cintia Palu, Brain Kelly, and Haiying Wang,
4:00-4:30	**Coffee Break**	
4:30 – 4:50	Effects from structure of Metabarcode Sequences on Lossy Analysis of Microbiome Data	David Molik, Michael Pfrender, and Scott Emrich
4:50 – 5:10	An Interface to Heterogeneous Data Sources Based on the Mediator/Wrapper Architecture in the Hadoop Ecosystem	Klaus-Dieter Schmatz, Kevin Berwind, Felix Engel, and Matthias L. Hemmje
5:10 – 5:30	Phylogeny-Aware Deep 1-Dimensional Convolutional Neural Network for the Classification of Metagenomes	Tim Manning, Jyotsna Wassan, Cintia Palu, Haiying Wang, Fiona Browne, Huiru Zheng, Brain Kelly, and Paul Walsh
5:30-5:50	Correlation Model Analysis of Nitrogen Addition and Tan Sheep Grazing Effects on Soil Bacterial Community in the Loess Plateau , China	Mengyuan Wang, Fujiang Hou, Huiru Zheng, and Haiying Wang
5:50 - 6:00	**Closing Remarks**	

Workshop in Artificial Intelligence Techniques for BioMedicine and HealthCare (AIBH)

December 3, 13:30; Location: Room Londres

Workshop Chairs: Ester Zumpano, Pierangelo Veltri, Luciano Caroprese

Time	Title	Presenter/Author
13:30	**Workshop Introduction**	
13:40	*Can I find information about rare diseases in some other language?*	Mikel Laburu, Alicia Pérez, Arantza Casillas, Iakes Goenaga, and Maite Oronoz,
14:00	*Convolutional Neural Networks Learning from Respiratory data*	Diego Perna
14:20	*Guiding Exploration of Antimicrobial Peptide Space with a Deep Neural Network*	Manpriya Dua, Daniel Veltri, Barney Bishop, and Amarda Shehu
14:40	*An Integrative Framework for the Construction of Big Functional Networks*	Claudia Giallombardo, Salvatore Morfea, and Simona E. Rombo
15:00	*SIMPATICO 3D: A Medical Information System for Diagnostic Procedures*	Ester Zumpano, Luciano Caroprese, Giuseppe Lucio Cascini, Pierangelo Veltri, Francesco Dattola, Pasquale Iaquinta, Miriam Iusi, Eugenio Vocaturo, and Pasquale Franco
15:20	*Partial Parallel Error Correction of Pair-end Short Reads using GPU*	Umberto Ferraro Petrillo and Francesco Palini
15:40	*Image pre-processing in computer vision systems for melanoma detection*	Eugenio Vocaturo, Ester Zumpano, and Pierangelo Veltri
16:00-16:30	**Coffee Break**	
16:30	*Big Data and Health Care: a lesson learned*	Mario Ciampi, Angelo Esposito, Giuseppe De Pietro, Elio Masciari, and Mario Sicuranza
16:50	*A "big data oriented" and "complex network based" model supporting the uniform investigation of heterogeneous personalized medicine data*	Paolo Lo Giudice, Domenico Ursino, and Luca Virgili
17:10	*INTEGRO: an algorithm for data-integration and disease-gene association*	Pietro Cinaglia, Pietro H. Guzzi, and Pierangelo Veltri
17:30	**Closing Remarks**	

Joint workshops with International Workshop on Biological Network Analysis and Integrative Graph-Based Approaches (IWBNA 2018) and International Workshop on Deep Learning in Bioinformatics, Biomedicine and Healthcare Informatics (DLB2H 2018)

Dec, 3rd 2018 – 14:00 to 18:30; Room: Madrid 2+3

Workshop Chairs: Jung Hun Oh, Mingon Kang, Young-Rae Cho

Time	Title	Presenter/Author
14:00 – 14:20	Computer-Aided Diagnosis and Localization of Glaucoma Using Deep Learning	Mijung Kim, Ho-min Park, Jasper Zuallaert, Olivier Janssens, and Wesley De Neve
14:20 – 14:40	Using Deep Learning to classify X-ray images of potential Tuberculosis patients	Kalpdrum Passi, Ojasvi Yadav, and Chakresh Jain
14:40 – 15:00	Using transfer learning for classification of gait pathologies	Tanmay Verlekar, Paulo Correia, and Luís Soares
15:00 - 15:20	End-to-end prediction of protein-protein interaction based on embedding and recurrent neural networks	Francisco Gonzalez-Lopez, Juan A. Morales-Cordovilla, Amelia Villegas- Morcillo, Angel M. Gomez, and Victoria Sanchez
15:20 – 15:40	Analysis for Early Seizure Detection System Based on Deep Learning Algorithm	Fuxu Wang, Mingrui Sun, Tengfei Min, Yueying Wang, Chunpu Liu, Tianyi Zang, and Yadong Wang
15:40 – 16:00	Semi-supervised Deep Linear Discriminant Analysis	Lei Cui, Jun Feng, and Lin Yang
16:00 – 16:30	**Coffee break**	
16:30 – 16:50	Brain MRI Segmentation using efficient 3D Fully Convolutional Neural Networks	Ghazala Khan and Naimul Mefraz Khan
16:50 – 17:10	Protein Family Classification with Multi-Layer Graph Convolutional Networks	Da Zhang and Mansur Kabuka
17:10 – 17:30	Domain-Aware Abstractive Text Summarization for Medical Documents	Paul Gigioli, Nikhita Sagar, Joseph Voyles, and Anand Rao
17:40 – 17:50	L-FCN: A lightweight fully convolutional network for biomedical semantic segmentation	Kaiyue Li, Guangtai Ding, and Haitao Wang
17:50 – 18:10	A BCHC genetic algorithm model of cotemporal hierarchical Arabidopsis thaliana gene interactions	Bree LaPointe, David John, James Norris, Edward Allen, Alexandria Harkey, Joelle Muhlemann, and Gloria Muday
18:10 – 18:30	INDEED: R package for network based differential expression analysis	Zhenzhi Li, Yiming Zuo, Chaohui Xu, Rency Varghese, and Habtom Ressom
18:30	**Closing Remarks**	

Application of Machine Learning and Signal Processing in Biomedical Informatics and Computational Genomics (AMLSP)

3rd Dec, 14:30 to 18:30; Room: Paris

Workshop Chairs: Sheida Nabavi, Kayvan Najarian

Time	Title	Presenter/Author
2:00-2:20	*Use of Machine Learning for Diagnosis of Cancer in Ovarian Tissues with a Selected mRNA Panel*	Pourya Naderi Yeganeh and M. Taghi Mostafavi
2:20-2:40	*Supraventricular Tachycardia Detection via Machine Learning Algorithms*	Zhi Li, Harm Derksen, Jonathan Gryak, Mohsen Hooshmand, Alexander Wood, Hamid Ghanbari, Pujitha Gunaratne, and Kayvan Najarian
2:40-3:00	*Predictive Meta-analysis of Multiple Microarray Datasets: An Application to Classification of Malignant Gliomas*	Nurislam Tursynbek, Ghazal Ghahramany, Sheida Nabavi, and Amin Zollanvari
3:00-3:20	*Classifying Osteosarcoma Using Meta-Analysis of Gene Expression*	Olivia Alge, Jonathan Gryak, Yingqi Hua, and Kayvan Najarian
3:20-3:40	*AmpliconNet: Sequence based Multi-layer Perceptron For Amplicon Read Classification Using Real-time Data Augmentation*	Ali Kishk and Mohamed Elhadidi
3:40-:400	*Copy number variation detection using partial alignment information*	Fatima Zare, Sardar Ansari, Kayvan Najarian, and Sheida Nabavi
4:00-4:30	**Coffee Break**	
4:30-4:50	*Breast Cancer Histopathological Image Classification: A Deep Learning Approach*	Mahboubeh Jannesari, Mehdi Habibzadeh Motlagh, HamidReza Aboulkheyr, Pegah Khosravi, Olivier Elemento, Mehdi Totonchi, and Iman Hajirasouliha
4:50-5:10	*Deep neural network based body posture recognitions and fall detection from low resolution infrared array sensor*	Jindrich Adolf, Martin Macas, Lenka Lhotska, and Jaromir Dolezal
5:10	**Closing Remarks**	

BiOK

3rd December; 2pm to 6:30pm; Room: Viena

Workshop Chairs: Jiajie Peng, Jin Chen; Host: Tao Wang

Time	Title	Presenter/Author
2:00-2:20pm	*ProbPFP: A Multiple Sequence Alignment Algorithm Combining Partition Function and Hidden Markov Model with Particle Swarm Optimization*	Qing Zhan, Nan Wang, Shuilin Jin, Renjie Tan, Qinghua Jiang, and Yadong Wang
2:25-2:45pm	*Two-step Random Walk Algorithm to Identify Cancer Genes Based on Various Biological Data*	Wenxiang Zhang and Xiujuan Lei
2:50-3:10pm	*Automatic Acceptance Prediction for Answers in Online Healthcare Community*	Qianlong Liu, Kangenbei Liao, and Zhongyu Wei
3:15-3:35pm	*TSGOE: A web tool for tissue-specific gene ontology enrichment*	Jiajie Peng, Guilin Lu, Hansheng Xue, Tao Wang, and Xuequn Shang
3:40-4:00pm	*Speeding up Collective Cell Migration Using Deep Reinforcement Learning*	Gan Tian, Yaodong Yang, Hao Jianye, Xianglei Zhu, and Zhenyu Liao
4:00-4:30pm	**Coffee Break**	
4:30-4:50pm	*Exploring DNA Methylation Data of Lung Cancer Samples with Variational Autoencoders*	Zhenxing Wang and Yadong Wang
4:55-5:15pm	*Identification of lncRNA-disease association using bi-random walks*	Yiqun Gao, Jialu Hu, and Xuequn Shang
5:20-5:40pm	*A Novel Method for Identifying Alzheimer's Disease-related Proteins*	Yang Hu, Tianyi Zhao, Tianyi Zang, Jun Zhang, and Liang Cheng
5:45-6:05pm	*Attention-Based Recurrent Multi-Channel Neural Network for Influenza Epidemic Prediction*	Bofeng Fu, Yaodong Yang, Yu Ma, Siqi Chen, Shuang Liu, Tiegang Li, Zhenyu Liao, and Xianglei Zhu
6:10-6:30pm	*Creation of Unambiguous Centralized Knowledge Base from UMLS Metathesaurus*	Vatsal Shah, Binni Shah, Raxit Goswami, Saket Kumar, and Chetan Moradiya
6:30pm	**Closing Remarks**	

Machine Learning Approaches in High Resolution Microscopy Imaging (MLAHRMI)

3rd December, 4:00pm-6:30pm; Room: Monaco

Workshop Chairs: Tommi White, Filiz Bunyak, Ilker Ersoy

Time	Title	Presenter/Author
4:00-4:25	*Sparse Scanning Electron Microscopy for Imaging and Segmentation in Connectomics*	Pavel Potocek
4:25-4:50	*Feature Decomposition based Saliency Detection in Electron Cryo-Tomograms*	Min Xu
4:50-5:15	*Single-molecule Imaging of Metallic Nanostructures on a Plasmonic Metal Grating Superlens*	Shubhra Gangopadhyay
5:15-5:40	*Automated Particle Picking in Cryo-Electron Micrographs using Deep Regression*	Tommi White
5:40-6:05	*Single-Particle 3D Reconstruction beyond the Nyquist Frequency*	James Chen
6:05-6:30	*Estimating Probabilistic Context-Free Grammars for Proteins Using Contact Map Constraints*	Witold Dyrka
6:30	**Closing Remarks**	

KDTBI

3rd December, 16:30 to 18:30; Room: Moscu

Workshop Chairs: Pietro Hiram Guzzi

Time	Title	Presenter/Author
16:30 16 50	*Annotating Cohort Data Elements with OHDSI Common Data Model to Promote Research Reproducibility*	Yiqing Zhao
16:50 17:10	*Protein Regulating Network towards Tonifying Primal Qi Delivered by Ginseng*	Guang Zheng
17:10 17:30	*Leveraging Association Rule Mining to Detect Pathophysiological Mechanisms of Chronic Kidney Disease Complicated by Metabolic Syndrome*	Suyuan Peng
17:30 17:50	Ilaria Granata, Mario Rosario Guarracino, Valery Kalyagin, Lucia Maddalena, Ichcha Manipur, and Panos Pardalos, *Supervised Classification of Metabolic Networks*	Mario Rosario Guarracino
17:50 18:10	Ananda Mondal, Cornelia Schultz, Markea Sheppard, Jasmine Carson, Raihanul Tanvir, and Tasmia Aqila, *Graph Theoretic Concepts as the Building Blocks for Disease Initiation and Progression at Protein Network Level: Identification and Challenges*	Ananda Mondal
18:10 18:30	Antara Sengupta, Pabitra Pal Choudry, Hazel Nicolette Manners, Pietro H. Guzzi, and Swarup Roy, *Chemical Characterization of Interacting Genes in Few Subnetworks of Alzheimer's Disease*	Swarup Roy

DETAILED SESSION LIST

TUESDAY 4th DECEMBER

Session 1: Genomics I	
Regular	B387 "Analysis of gene expression data of RPL10 mutant T-cell leukemia by SEMsubPA" Daniele Pepe and Kim De Keersmaecker
Regular	B479 "Robust Hypergraph regularized Non-negative Matrix Factorization for Clustering and Com-abnormal Expression Genes Selection" Na Yu, Ying-Lian Gao, Jin-Xing Liu, Juan Wang, and Junliang Shang
Regular	B629 "Integrating Gene Expression Data and Pathway Knowledge for In Silico Hypothesis Generation with IMPRes v1.0" Yuexu Jiang, Duolin Wang, Dong Xu, and Trupti Joshi
Short	B261 “Finding a Center Tree of Phylogenetic Trees via Leaf Removal” Zhi-Zhong Chen, Shohei Ueta, Jingyu Li, and Lusheng Wang

Session 2: Genomics II	
Regular	B273 "rCANID: read Clustering and Assembly-based Novel Insertion Detection tool" Tao Jiang, Yilei Fu, Bo Liu, and Yadong Wang
Regular	B589 "Statistical Modeling of Short-Tandem Repeat Capillary Electrophoresis Profiles" Slim Karkar, Lauren Alfonse, Grgicak Catherine, and Desmond Lun
Regular	B329 "Fast variation-aware read alignment with deBGA-VARA" Hongzhe Guo, Bo Liu, Dengfeng Guan, Yilei Fu, and Yadong Wang
Short	B695 “Prediction of transposable elements evolution using tabu search” Lingling Jin and Ian McQuillan

Session 3: Proteins I	
Regular	B613 "Integrating Protein Localization with Automated Signaling Pathway Reconstruction" Ibrahim Youssef, Jeffrey Law, and Anna Ritz
Regular	B328 "DeepEP: a deep learning framework for identification of essential proteins" Min Zeng, Min Li, Zhihui Fei, Fang-Xiang Wu, Yaohang Li, and Yi Pan
Regular	B312 "Protein2Vec: Aligning Multiple PPI Networks by Representation Learning on Networks" Bo Song, Jianliang Gao, and Xiaohua Hu
Short	B483 "A Weak Supervised Learning Method for Essential Protein Detection Based on STRING Database and Learning Representation" Zhizheng Wang, Yuanyuan Sun, Yawen Guan, Yibin Zhang, Liang Yang, Kan Xu, Yijia Zhang, and Hongfei Lin

Session 4: Microbes and virus	
Regular	B506 "High-order Organization of Weighted Microbial Interaction Network" Xianjun Shen, Xue Gong, Xingpeng Jiang, Jincai Yang, Tingting He, and Xiaohua Hu
Regular	B508 "Inferring Microbial Communities for City Scale Metagenomics Using Neural Networks" Guangyu Zhou, Jyun-Yu Jiang, Chelsea J.-T. Ju, and Wei Wang
Regular	B372 "Virus-host Association Prediction by using Kernelized Logistic Matrix Factorization on Heterogeneous Networks" Dan Liu, Hu Xiaohua, He Tingting, and Xingpeng Jiang

Session 5: Cheminformatics, drug representation and interaction I	
Short	B663 "WarfarinSeer": a predictive tool based on SMOTE-random forest to improve warfarin dose prediction in Chinese patients" Yanyun Tao and Yuzhen zhang
Short	B511 "A System for Learning Atoms Based on Long Short-Term Memory Recurrent Neural Networks" Zhe Quan, Xuan Lin, Zhi-Jie Wang, Yan Liu, Fan Wang, and Kenli Li
Short *(Video)*	B365 "Calibration of Rule-Based Stochastic Biochemical Models using Statistical Model Checking" Arfeen Khalid and Sumit Jha
Short	B265 "Drug2Vec: Knowledge-aware Feature-driven Method for Drug Representation Learning" Ying SHEN, Kaiqi Yuan, Yaliang Li, Buzhou Tang, Min Yang, Nan Du, and Kai Lei

Session 6: Analysis of medical images and graphs I	
Regular	B336 "Automatic Hand Skeletal Shape Estimation from Radiographs" Radu Mihail and Nathan Jacobs
Regular	B432 "A Novel Radiogenomics Framework for Genomic and Image Feature Correlation using Deep Learning" Shuai Li, Hongze Han, Dong Sui, Aimin Hao, and Hong Qin
Regular	B484 "Inter/Intra-Constraints Optimization for Fast Vessel Enhancement in X-ray Angiographic Image Sequence" Chenbing Du, Shuang Song, Danni Ai, Hong Song, Yong Huang, Yongtian Wang, and Jian Yang
Short	B262 "An Adaptive Ray-Shooting Model for Terminations Detection: Applications in Neuron and Retinal Blood Vessel Images" WeiXun Chen, Min Liu, and Keran Liu

Session 7: Biomedical text processing I	
Regular	B497 "Hierarchical Multi-layer Transfer Learning Model for Biomedical Question Answering" Yongping Du, Bingbing Pei, Xiaozheng Zhao, and Junzhong Ji
Regular	B344 "Improve Diversity-oriented Biomedical Information Retrieval using Supervised Query Expansion" Bo Xu, Hongfei Lin, Liang Yang, Kan Xu, Yijia Zhang, Dongyu Zhang, Zhihao Yang, and Jian Wang

Regular	B526 "GrantExtractor: A Winning System for Extracting Grant Support Information from Biomedical Literature" Suyang Dai, Shanfeng Zhu, and Xiaodi Huang
Short	B720 "Exploring Deep Learning-based Approaches for Predicting Concept Names in SNOMED CT" Fengbo Zheng and Licong Cui

Session 8: Proteins II	
Regular	B472 "Multimodal Deep Representation Learning for Protein Protein Interaction Networks" Da Zhang and Mansur Kabuka
Regular	B486 "Protein-Protein Interaction Article Classification: A Knowledge-enriched Self-Attention Convolutional Neural Network Approach" Ling Luo, Zhihao Yang, Lei Wang, yin Zhang, Hongfei Lin, Jian Wang, Liang Yang, Kan Xu, and Yijia Zhang
Regular	B505 "HMNPPID: A Database of Protein-protein Interactions Associated with Human Malignant Neoplasms" Qingqing Li, Zhihao Yang, Zhehuan Zhao, Ling Luo, Zhiheng Li, Lei Wang, yin Zhang, Hongfei Lin, Jian Wang, and Yijia Zhang
Short	B228 "Reconstructing and Decomposing Protein Energy Landscapes to Organize Structure Spaces and Reveal Biologically-active States" Nasrin Akhter, Jing Lei, Wanli Qiao, and Amarda Shehu
Short	B474 “Regression Models and Ranking Method for p53 Inhibitor Candidates Using Machine Learning” Haruka Motohashi, Tatsuro Teraoka, Shin Aoki, and Hayato Ohwada

Session 9: Biomedical text processing II	
Regular	B682 "Capturing Central Venous Catheterization Events in Health Record Texts" Thomas Brox Røst, Christine Raaen Tvedt, Haldor Husby, Ingrid Andås Berg, and Øystein Nytrø
Regular	B298 "Implementing a Portable Clinical NLP System with a Common Data Model – a LISP Perspective" Yuan Luo and Peter Szolovits
Short	B515 "Understanding Markush Structures in Chemistry Documents with Deep Learning" Penghui Sun, Xiaoqing Lyu, Xin Li, Bei Wang, Xiaohan Yi, and Zhi Tang
Regular	B563 "Generation of Synthetic Electronic Medical Record Text" Jiaqi Guan, Runzhe Li, Sheng Yu, and Xuegong Zhang

Session 10: Stress and depression	
Regular	B422 "HTRgene: Integrating Multiple Heterogeneous Time-series Data to Investigate Cold and Heat Stress Response Signaling Genes in Arabidopsis" Sun Kim, Hongryul Ahn, Inuk Jung, Heejoon Chae, Dongwon Kang, and Woosuk Jung
Regular	B510 "Identifying stress-related genes and predicting stress types in Arabidopsis using logical correlation layer and CMCL loss through time-series data" Sun Kim, Dongwon Kang, Hongryul Ahn, Sangseon Lee, Jihye Hur, and Woosuk Jung
Regular	B400 "Genome-wide miRNA expression alterations in Nucleus Accumbens provide insights into chronic stress and treatment in depression" Weichen Song, Guan Ning Lin, Sufang Peng, Yanhua Zhang, Yifeng Shen, Huafang Li, and Shunying Yu
Short	B651 "Forecasting depressive relapse in Bipolar Disorder from clinical data" Renato Borges-Júnior, Rogerio Salvini, Andrew Nierenberg, Gary Sachs, Beny Lafer, and Rodrigo Dias
Short	B313 "A novel study for MDD detection through task-elicited facial cues" Jinlong Li, Zhenyu Liu, Zhijie Ding, and Gangping Wang

Session 11: Analysis of medical images and graphs II	
Regular	B742 "Determining Dose-Response Characteristics of Molecular Perturbations in Whole-Organism Assays Using Biological Imaging and Machine Learning" Daniel Asarnow and Rahul Singh
Regular	B609 "Optimizing U-Net to Segment Left Ventricle from Magnetic Resonance Imaging" Sadegh Charmchi, Kumaradevan Punithakumar, and Pierre Boulanger
Regular	B634 "Early Sepsis Recognition Based on Ear Localization using Infrared Thermography" Hasanin Al-Sadr, Mihail Popescu, and James Keller
Short	B598 "Leveraging Disease Progression Learning for Medical Image Recognition" Qicheng Lao, Thomas Fevens, and Boyu Wang
Short	B714 "IterVM: An Iterative Model for Single-Particle Cryo-EM Image Clustering Based on Variational Autoencoder and Multi-Reference Alignment" Guowei Ji, Yang Yang, and Hong-Bin Shen

Session 12: Acceleration, optimization, scalability and computability I	
Regular	B379 "Accelerated Super-resolution MR Image Reconstruction via a 3D Densely Connected Deep Convolutional Neural Network" Jinglong Du, Lulu Wang, Ali Gholipour, Zhongshi He, and Yuanyuan Jia
Regular	B404 "Virtual Grid Engine: Accelerating thousands of omics sample analyses using large-scale supercomputers" Satoshi Ito, Masaaki Yadome, Tatsuo Nishiki, Shigeru Ishiduki, Hikaru Inoue, Rui Yamaguchi, and Satoru Miyano
Regular	B440 "GPU-accelerated CellProfiler" Imen Chakroun, Nick Michiels, and Roel Wuyts
Short	B489 "Mmalloc: A Dynamic Memory Management on Many-core Coprocessor for the Acceleration of Storage-intensive Bioinformatics Application" Zihao Wang, Mingzhe Zhang, Jingrong Zhang, Rui Yan, Xiaohua Wan, Zhiyong Liu, and Fa Zhang
Short	B685 "Fast and accurate genome-scale identification of DNA-binding sites" David Martin, Vincent Maillol, and Eric Rivals

Session 13: Cancer I	
Regular	B712 "PASCL: Pathway-based Sparse Deep Clustering for Identifying Unknown Cancer Subtypes" Tejaswini Mallavarapu, Jie Hao, Youngsoon Kim, Jung Hun Oh, and Mingon Kang
Regular	B694 "Renall cell carcinoma classification: a case study of pitfalls associated with metabolic landscape analysis" Krzysztof Gogolewski, Marcin Kostecki, and Anna Gambin
Regular	B439 "Deep Subspace Similarity Fusion for the Prediction of Cancer Subtypes" Bo Yang, Shuhui Liu, Shanmin Pang, Chenpai Pang, and Xuequn Shang

Session 14: Biology	
Regular	B675 "Knowledge Base Commons (KBCommons) v1.0: A multi 'OMICS' web-based data integration framework for biological discoveries" Shuai Zeng, Zhen Lyu, Siva Ratna Kumari Narisetti, Dong Xu, Trupti Joshi
Regular	B593 "OLIVER: A Tool for Visual Data Analysis on Longitudinal Plant Phenomics Data" Oliver Tessmer, David Kramer, and Jin Chen
Regular	B530 "Identifying Representative Network Motifs for Inferring Higher-order Structure of Biological Networks" Tao Wang, Jiajie Peng, Yadong Wang, and Jin Chen
Short	B435 "A Multi-scale Pyramid of Fully Convolutional Networks for Automatic Cell Detection" Jiang Gu, Yichen Zhu, Bohong Yang, Jingkai Jia, Juanjuan Wang, Jian Yang, and Wen-Qiang Zhang
Short	B517 "Chrysanthemum Abnormal Petal Type Classification using Random Forest and Over-sampling" Peisen Yuan, Jin Chen, Shougang Ren, and Huanliang Xu

Session 15: Analysis of medical images and graphs III	
Regular	B478 "Cell Tracking Across Noisy Image Sequences Via Faster R-CNN and Dynamic Local Graph Matching" Min Liu, Lehui Wu, Weili Qian, and Yalan Liu
Regular	B572 "A Hybrid Convolutional and Recurrent Deep Neural Network for Breast Cancer Pathological Image Classification" Rui Yan, Fei Ren, Zihao Wang, Lihua Wang, Yubo Ren, Yudong Liu, Xiaosong Rao, Chunhou Zheng, and Fa Zhang
Regular	B664 "HMIML: Hierarchical Multi-Instance Multi-Label Learning of Drosophila Embryogenesis Images Using Convolutional Neural Networks" Tiange Li, Yang Yang, and Hong-Bin Shen
Regular	B681 "Radiomics and machine learning in the prediction of response to CyberKnife radiosurgery for acoustic neuroma: a pilot study" Natascha Claudia D'Amico, Rosa Sicilia, Ermanno Cordelli, Giovanni Valbusa, Isa Bossi Zanetti, Deborah Fazzini, Giuseppe Scotti, Giulio Iannello, and Paolo Soda

Session 16: Genomics III	
Regular	B267 "Weighted matrix factorization based data fusion for predicting lncRNA-disease associations" Guoxian Yu, Yuehui Wang, Jun Wang, Guangyuan Fu, Maozu Guo, and Carlotta Domeniconi
Regular	B464 "Active Learning for microRNA Prediction" Mohsen Sheikh Hassani and James Green
Regular	B620 "ParLECH: Parallel Long-read Error Correction with Hadoop" Arghya Kusum Das, Kisung Lee, and Seung-Jong Park
Regular	B680 "Discovering COPD phenotyping via simultaneous feature selection and clustering" Mario Merone, Panaiotis Finamore, Claudio Pedone, Raffaele Antonelli Incalzi, Giulio Iannello, and Paolo Soda

Session 17: Cheminformatics, drug representation and interaction II	
Regular	B429 "Drug-Protein-Disease Association Prediction and Drug Repositioning Based on Tensor Decomposition" Ran Wang, Shuai Li, Man Hon Wong, and Kwong Sak Leung
Regular	B605 "Toxicity Prediction Using Pre-trained Autoencoder" Mykola Galushka, Fiona Browne, Maurice Mulvenna, Raymond Bond, and Gaye Lightbody
Regular	B528 "New visualization of dynamical flexibility of N-Glycans: Umbrella Visualization in UnityMol." Camille Besançon, Alexandre Guillot, Sébastien Blaise, Manuel Dauchez, Nicolas Belloy, Jessica Prévoteau-Jonquet, and Stéphanie Baud
Short	B637 "Prediction of DTIs for high-dimensional and class-imbalanced data based on CGAN" Kang Yang, Song He, Zhongnan Zhang, and Xiaochen Bo

Session 18: Diagnosis, clinical procedures, progression and recovery I	
Regular	B743 "Factors Influencing Epidural Anesthesia for Cesarean Section Outcome" Eva Lee, Haozheng Tian, Jinha Lee, Xin Wei, John Neeld Jr, Doug Smith, and Alan Kaplan
Regular	B295 "A Deep Learning Approach to Handling Temporal Variation in Chronic Obstructive Pulmonary Disease Progression" Chunlei Tang, Joseph Plasek, Haohan Zhang, Yun Xiong, David Bates, and Li Zhou
Regular *(Vídeo)*	B351 "A General Framework for Diagnosis Prediction via Incorporating Medical Code Descriptions" Fenglong Ma, Yaqing Wang, Houping Xiao, Ye Yuan, Radha Chitta, Jing Zhou, and Jing Gao

Session 19: Monitoring, sensors and devices I	
Short	B227 "The LookAfterRisk Project: Dynamic Cardiovascular Risk Assessment based on Remote Monitoring Solutions" Simão Paredes, Jorge Henriques, Teresa Rocha, Paulo de Carvalho, João Morais, Luís Santos, and Rita Carvalho
Short	B731 "VicoVR-based Wireless Daily Activity Recognition and Assessment System for Stroke Rehabilitation" Mengxuan Ma, Benjamin Meyer, Le Lin, Rachel Proffitt, and Marjorie Skubic
Short	B390 "A Wearable Sensor Design for Cardiorespiratory Signals Acquisition Based on PVDF Sensors" Mourad Adnane and Zhongwei Jiang
Short	B624 "Configurable Pulmonary-Tuned Privacy Preservation Algorithm for Mobile Devices" Sujee Lee, Ebrahim Nemati, and Jilong Kuang
Short	B342 "Intelligent Walk Authentication: Implicit Authentication When You Walk with Smartphone" Huiyong Li and Jiannan Yu
Short	B289 "Effect of UX Design Guideline on the information accessibility for the visually impaired in the mobile health apps" Woo Jin Kim, Min Ji Kim, Eun Joo Lee, and Il Kon Kim

Session 20: Cancer II	
Short	B369 "Autoencoders as Weight Initialization of Deep Classification Networks Applied to Papillary Thyroid Carcinoma" Mafalda Falcão Ferreira, Rui Camacho, and Luís Filipe Teixeira
Regular	B580 "Examining Tumor Phylogeny Inference in Noisy Sequencing Data" Kiran Tomlinson and Layla Oesper
Regular	B711 "Cox-PASNet: Pathway-based Sparse Deep Neural Network for Survival Analysis" Jie Hao, Youngsoon Kim, Tejaswini Mallavarapu, Jung Hun Oh, and Mingon Kang

Session 21: Industry track I (60 minutes)	
Regular	N207 "Improving Coding Efficiency of MPEG-G Standard Using Context-Based Arithmetic Coding" Wenxian Yang, Yating Lin, Shiyao Wu, and Rongshan Yu
Regular	N208 "Optimization of Genomics Analysis Pipeline for Scalable Performance in a Cloud Environment" Carlos Costa, Claudia Misale, Frank Liu, Marcio Silva, Hubertus Franke, Paul Crumley, and Bruce D'Amora,
Regular	N206 "Performance Evaluation of IMP: a Rapid Secondary Analysis Pipeline for NGS Data" Shun Wang, Wenxian Yang, Xiang Zhang, and Rongshan Yu

Poster session I	
P203	Matej Lexa, Radovan Lapar, Pavel Jedlicka, Ivan Vanat, Michal Cervenansky, and Eduard Kejnovsky *TE-nester: a recursive software tool for structure-based discovery of nested transposable elements*
P204	Slim Karkar, Yann Le Guen, Cathy Philippe, Claire Dandine-Roulland, Morgane Pierre-Jean, Jean-Francois Mangin, Edith Le Floch, and Vincent Frouin *A study of feasibility for genome-wide haplotype association of complex traits in genetic imaging*
P208	Elen Tevanyan and Maria Poptsova *Recognizing Patterns of Nucleosome and DNA Structures Positioning*
P211	Elise Larsonneur, Jonathan Mercier, Nicolas Wiart, Edith Le Floch, Olivier Delhomme, and Vincent Meyer *Evaluating Workflow Management Systems: A Bioinformatics Use Case*
P212	Namjin Koo, Sangho Oh, and Yong-Min Kim *Inter-kingdom Comparative Analysis of Translationally Controlled Tumor Protein (TCTP) Provides Clues for Their Lineage-specific Evolution*
P213	Hongwei Ge, Keyi Sun, Liang Sun, Mingde Zhao, and Chunguo Wu *A Selective Ensemble Learning Framework for ECG-Based Heartbeat Classification with Imbalanced Data*
P216	Giulia Fiscon, Emanuel Weitschek, Maria Cristina De Cola, Giovanni Felici, and Paola Bertolazzi *An integrated approach based on EEG signals processing combined with supervised methods to classify Alzheimer's disease patients*
P217	Konosuke Asano, Naoaki Ono, Chika Iwamoto, Kenoki Ohuchida, Koji Shindo, and Shigehiko Kanaya *Feature extraction and Cluster analysis of Pancreatic Pathological Image Based on Unsupervised Convolutional Neural Network*
P218	Abdurrahman Elbasir, Balasubramanian Moovarkumudalvan, Khalid Kunji, Prasanna Kolatkar, Raghvendra Mall, and Halima Bensmail *DeepCrystal: A Deep Learning Framework for sequence-based Protein*

	Crystallization Prediction
P219	Adam Zhang *Urine as an Alternative to Blood for Cancer Liquid Biopsy and Precision Medicine*
P220	Jennifer Luyapan, Xuemei Ji, Dakai Zhu, Todd MacKenzie, Christopher Amos, and Jiang Gui *An Efficient Survival Multifactor Dimensionality Reduction Method for Detecting Gene-Gene Interactions of Lung Cancer Onset Age*
P223	Qingfeng Wang, Jie-Zhi Cheng, Zhiqin Liu, Jun Huang, Qiyu Liu, Ying Zhou, Weiyun Xu, Chao Wang, and Xuehai Zhou *Multi-order Transfer Learning for Pathologic Diagnosis of Pulmonary Nodule Malignancy*
P224	Ivan Arisi, Paola Bertolazzi, Eleonora Cappelli, Federica Conte, Fabio Cumbo, Giulia Fiscon, Michele Sonnessa, and Francesco Taglino *An ontology-based approach to improve data querying and organization of Alzheimer's Disease data*
P226	Jaehee Jung and Gangman Yi *A tool for analyzing evolutionary trees of reconciled genes and single gene*
P228	Yasuhiro Omiya, Takeshi Takano, Tomotaka Uraguchi, Mitsuteru Nakamura, Masakazu Higuchi, Shuji Shinohara, Shunji Mitsuyoshi, Mirai So, and Shinichi Tokuno *Estimating depressive status from voice*
P231	Soto Montalvo, Mario Almagro, Raquel Martínez, Víctor Fresno, Susana Lorenzo, María Carmen Morales, Beatriz González, Jacinto Álamo, and Alejandro García-Caro *Graphical User Interface for assistance with ICD-10 coding of Hospital Discharge Records*
P232	Ryo Matsuoka, Kohzoh Yoshino, Eiichi Watanabe, and Ken Kiyono *Analysis of multiscale entropy characteristics of heart rate variability in patients with permanent atrial fibrillation for predicting ischemic stroke risk*

WEDNESDAY 5th DECEMBER

Session 22: Genomics IV	
Short	B307 "LncRNA-disease association prediction based on neighborhood information aggregation in neural network" Hongjie Chen, Xuan Zhang, Tao Song, Xun Wang, Xiangxiang Zeng, and Alfonso Rodríguez-Patón
Short	B327 "The phylogenetic tree based Deep Forest for metagenomic data classification" Zhu Qiang, Jiang Xingpeng, He Tingting, and Hu Xiaohua
Short	B491 "DeepMVF-RBP: Deep Multi-view Fusion Representation Learning for RNA-binding Proteins Prediction" Xiuquan Du, Yanyu Diao, Yu Yao, Huaixu Zhu, Yuanting Yan, and Yanping Zhang
Short	B252 "Prediction of Long Non-coding RNA-protein Interaction through Kernel Soft-neighborhood Similarity" Yingjun Ma, Limin Yu, He Tingting, Hu Xiaohua, and Jiang Xingpeng
Short	B669 "Joint Prediction of Branchpoint and Splice Acceptor Sites in pre-mRNA Transcripts Using Sequence to Sequence Networks" Sanket Rajan Gupte and Rajgopal Srinivasan

Session 23: Genomics V	
Regular	B642 "Sample Size and Reproducibility of Gene Set Analysis" Farhad Maleki, Katie Ovens, Ian McQuillan, and Anthony J Kusalik
Regular	B539 "A Disease-related Gene Mining Method Based On Weakly Supervised Learning Model" Han Zhang, Xueting Huo, Xia Guo, Xin Su, Xiongwen Quan, and Chen Jin
Short	B625 "Efficient and Private Set Intersection of Human Genomes" Liyan Shen, Xiaojun Chen, Dakui Wang, Binxing Fang, and Ye Dong
Short	B392 “Kernel Soft-neighborhood network fusion for miRNA-Disease interaction prediction” Yingjun Ma, Leixin Ge, Yuanyuan Ma, Xiaohua Hu, Tingting He, and Xingpeng Jiang

Session 24: Biomedical text processing III	
Short	B639 "Early Prediction of Acute Kidney Injury in Critical Care Setting Using Clinical Notes" Yikuan Li, Liang Yao, Chengsheng Mao, Anand Srivastava, Xiaoqian Jiang, and Yuan Luo
Short	B654 "Hierarchical Recurrent Convolutional Neural Network for Chemical-protein Relation Extraction from Biomedical Literature" Cong Sun, Zhihao Yang, Lei Wang, yin Zhang, Hongfei Lin, Jian Wang, Yijia Zhang, Kan Xu, and Liang Yang
Short	B451 "A Knowledge Graph based Bidirectional Recurrent Neural Network Method for Literature-based Discovery" Shengtian Sang, Zhihao Yang, Xiaoxia Liu, Lei Wang, Yin Zhang, Hongfei

	Lin, Jian Wang, Kan Xu, Liang Yang, and Yijia Zhang
Short	B607 “Incorporating Syntactic Dependencies into Semantic Word Vector Model for Medical Text Processing” Maia Iyer, Chris Zou, and Xiao Luo
Short (Video)	B595 "SeDIE: A Semantic-Driven Engine for Integration of Healthcare Data" Houssein Dhayne, Rima Kilany, Rafiqul Haque, and Yehia Taher

Session 25: Analysis of medical images and graphs IV	
Short	B603 "Deep Homography Based Localization on Videos of Endoscopic Capsules" Gil Pinheiro, Paulo Coelho, Marta Salgado, Hélder Oliveira, and António Cunha
Short	B534 "Actor-Critic Reinforcement Learning for Automatic Left Atrial Appendage Segmentation" Walid Abdullah Al and Il Dong Yun
Short	B536 "Fiducial marker detection via deep learning approach for electron tomography" Yu Hao, Renmin Han, Xiaohua Wan, and Fa Zhang
Short	B561 "AAnchor: CNN guided detection of anchor amino acids in high resolution cryo-EM density maps" Mark Rozanov and Haim Wolfson

Session 26: Cheminformatics, drug representation and interaction III	
Regular (Video)	B288 "Drug Target Interaction Prediction with Non-random Missing Labels" Ni Sheng, Lin Chen, Xiangxiang Zeng, and Liang Yun
Regular	B380 "Full-attention Based Drug Drug Interaction Extraction Exploiting User-generated Content" Bo Xu, Xiufeng Shi, Zhehuan Zhao, Wei Zheng, Hongfei Lin, Zhihao Yang, Jian Wang, and Feng Xia
Short	B706 "CoDe-DTI: Collaborative Deep Learning-based Drug-Target Interaction Prediction" Nobuaki Yasuo, Yusuke Nakashima, and Masakazu Sekijima

Session 27: Proteins III	
Short	B597 "Learning Protein Structural Fingerprints under the Label-Free Supervision of Domain Knowledge" Yaosen Min, Shang Liu, and Xuefeng Cui
Short	B324 "PC-SENE: A node embedding based method for protein complex detection" Xiaoxia Liu, Zhihao Yang, Shengtian Sang, Lei Wang, Yin Zhang, Hongfei Lin, Bo Xu, Yijia Zhang, Liang Yang, Kan Xu, and Jian Wang
Short	B399 "Protein Complexes Detection Based on Global Network Representation Learning" Bo Xu, Kun Li, Xiaoxia Liu, Delong Liu, Yijia Zhang, Hongfei Lin, Zhihao Yang, Jian Wang, and Feng Xia

Short	B676 "TADeus - a tool for clinical interpretation of structural variants modifying chromatin organization" Barbara Poszewiecka, Paweł Stankiewicz, Tomasz Gambin, and Anna Gambin

Session 28: Genomics VI	
Regular	B746 "An embedded method for gene identification in heterogenous data involving unwanted heterogeneity" Meng Lu
Regular	B250 "A Unified Model for Robust Differential Expression Analysis of RNA-Seq data" Kefei Liu, Li Shen, and Hui Jiang
Regular	B666 "Multipath2vec: Predicting Pathogenic Genes via Heterogeneous Network Embedding" Bo Xu, Yu Liu, Shuo Yu, Lei Wang, Lei Liu, Hongfei Lin, Zhihao Yang, Jian Wang, and Feng Xia
Short	B424 "deSPI: efficient classification of metagenomics reads with lightweight de Bruijn graph-based reference indexing" Dengfeng Guan, Bo Liu, and Yadong Wang
Short	B502 "The Longest Common Exemplar Sequence Problem" Shu Zhang, Daming Zhu, and Haitao Jiang

Session 29: Descriptive languages, transcription and annotation	
Regular	B591 "OpenHI - An open source framework for annotating histopathological image" Pargorn Puttapirat, Haichuan Zhang, Yuchen Lian, Chunbao Wang, Xiangrong Zhang, Lixia Yao, and Chen Li
Regular	B415 "AiProAnnotator: Low-rank Approximation with network side information for high-performance, large-scale human Protein abnormality Annotator" Gao Junning, Yao Shuwei, Hiroshi Mamitsuka, and Shanfeng Zhu
Short	B449 "Modeling biological complexity using Biology System Description Language (BiSDL)" Alfredo Benso, Roberta Bardini, Stefano Di Carlo, Gianfranco Politano, Flavia Muggiano, and Eileen Hu

Session 30: Biomedical text processing IV	
Regular	B241 "Detecting Serendipitous Drug Usage in Social Media with Deep Neural Network Models" Boshu Ru, Dingcheng Li, and Lixia Yao
Regular	B455 "RADAR: Representation Learning across Disease Information Networks for Similar Disease Detection" Ruiqi Qin, Lei Duan, Huiru Zheng, Jesse Li-Ling, Kaiwen Song, and Xuan Lan
Regular	B521 "Predicting Disease-related Associations by Heterogeneous Network Embedding" Yun Xiong, Lu Ruan, Mengjie Guo, Xiangnan Kong, Yangyong Zhu, and Wei Wang

Short	B335 "Semantic Characteristic Prediction of Pulmonary Nodules Using the Causal Discovery Based on Streaming Features Algorithm" Na Li, Jing Yang, and Shuai Fang
Short	B434 "Biomedical Event Trigger Detection Based on BLSTM Integrating Attention Mechanism and Sentence Vector" Xinyu He, Lishuang Li, Jia Wan, Dingxin Song, and Zhanjie Wang

Session 31: Biomedical text processing V	
Regular	B367 “PENNER: Pattern-enhanced Nested Named Entity Recognition in Biomedical Literature” Xuan Wang, Yu Zhang, Qi Li, Cathy Wu, and Jiawei Han
Regular	B397 "A Hybrid Deep Learning Framework for Bacterial Named Entity Recognition" Xusheng Li, Xiaoyan Wang, Ran Zhong, Duo Zhong, Tingting He, Xingpeng Jiang, and Xiaohua Hu
Regular	B358 "Fast and Accurate Recognition of Chinese Clinical Named Entities with Residual Dilated Convolutions" Jiahui Qiu, Qi Wang, Yangming Zhou, Tong Ruan, and Ju Gao
Short	B488 "A multi-task learning based approach to biomedical entity relation extraction" Qingqing Li, Zhihao Yang, Ling Luo, Lei Wang, yin Zhang, Hongfei Lin, Jian Wang, Kan Xu, Yijia Zhang, and Liang Yang
Short	B627 "Recognising Named Entity of Medical Imaging Procedures in Clinical Notes" Wei Ruan and Wonsook Lee

Session 32: Analysis of medical images and graphs V	
Regular	B403 "Improved V-Net Based Image Segmentation for 3D Neuron Reconstruction" Min Liu, Huiqiong Luo, Yinghui Tan, Xueping Wang, and WeiXun Chen
Regular	B364 "Automated framework to reconstruct 3D model of cardiac Z-disk: an image processing approach" Afshin Khadangi, Eric Hanssen, and Vijay Rajagopal
Regular	B473 "3D Neurite Branch Points Detection in Microscopy Images" Min Liu, Chao Wang, and WeiXun Chen
Short	B222 "Automatic 3D Neuron Tracing Based on Terminations Detection" Chao Wang, WeiXun Chen, and Min Liu
Short	B330 "3D Convolutional Neural Networks Fusion Model for Lung Nodule Detection on Clinical CT Scans" Guitao Cao, Tiantian Huang, Wenming Cao, Kai Hou, Peng Liu, and Jiawei Zhang

Poster session II	
P233	Shogo Yata, Akinori Iyama, Saburo Sakoda, and Kohzoh Yoshino *Analysis of heart rate response to sleep apnea events in patients with Parkinson's disease*
P237	Junjie Zhang, Liping Wang, Wenjie Zhang, and Junjie Yao *A Signal Quality Assessment Method for Electrocardiography Acquired by Mobile Device*
P239	Mitsuteru Nakamura, Shuji Shinohara, Yasuhiro Omiya, Masakazu Higuchi, Takeshi Takano, Shunji Mitsuyoshi, Hiroyuki Toda, Taku Saito, Masaaki Tanichi, Aihide Yoshino, and Shinichi Tokuno *Feasibility Study for Estimation of Depression Severity Using Voice Analysis*
P240	Wenhao Zhang, Liangcai Gao, Zhi Tang, Menglong Ran, and Zhimiao Lin *A Benchmark for Automatic Acral Melanoma Preliminary Screening*
P242	Mingyu Kim, Ahra Lee, Hwijun Kwon, Jiwoong Kim, and IL KON KIM *Sharing Medical Questionnaries based on Blockchain*
P244	Maxim Ryzhii and Elena Ryzhii *Development of Simplified Model of Atrioventricular Node with Dual Pathway*
P245	Guang Zheng and Fei Hou *Cantharidin Triggers Apoptosis via ALB and PPP2R4 against Lung Cancer*
P247	Tatsuki Hirozawa, Takeshi Yamada, and Hayato Ohwada *New Survival Prediction System for Terminal Patients based on Machine Learning*
P248	Belen Marin, Carlos Alquezar-Baeta, Monica Hernandez, and Elvira Mayordomo *Evolution of GWAS results through ADNI cohorts*
P249	Zahra Mungloo-Dilmohamud, Gary Marigliano, Yasmina Jaufeerally-Fakim, and Carlos Peña-Reyes *A Comparative Study of Feature Selection Methods for Biomarker Discovery*
P251	Ivan Arisi, Mara D'Onofrio, Rossella Brandi, Michele Sonnessa, Alessandra Campanelli, Francesca Malerba, Rita Florio, Valentina Sposato, Antonino Cattaneo, Patrizia Mecocci, Giuseppe Bruno, Marco Canevelli, Magda Tsolaki, Natalia Pelteki, Fabrizio Stocchi, Laura Vacca, Giulia Fiscon, and Paola Bertolazzi *Mining clinical and laboratory data of neurodegenerative diseases by Machine Learning: transcriptomic biomarkers*
P252	Elizaveta Saifutdinova, Daniela Urbaczka Dudysova, Lenka Lhotska, Vaclav Gerla, and Martin Macas *Artifact Detection in Multichannel Sleep EEG using Random Forest Classifier*
P253	Usama Bakry, Mohamed Fares, Ali Kishk, and Mohamed El-Hadidi *MetaFlow: an interactive user-friendly workflow for automated analysis of whole genome shotgun sequencing metagenomic data*
P254	DeAndre Tomlinson, David Molik, Michael Pfrender, and Scott Emrich *The Effects of Normalization, Transformation, and Rarefaction on Clustering of*

	OTU Abundance
P255	Dankyu Yoon, Su-Jin Baek, Kipoong Kim, Hye-Ryun Kang, and Jeom Kyu Lee *East Asian specific asthma associated variants were discovered via exome-sequencing*
P256	Jan Jelínek, Petr Škoda, and David Hoksza *Software framework for similarity-based prediction of protein interfaces*
P257	Robert Aduviri, Daniel Matos, and Edwin Villanueva *Feature selection algorithm recommendation for gene expression data through gradient boosting and neural network metamodels*

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Session 33: Genomics VII	
Regular	B447 "Measuring the three-dimensional structural properties of topologically associating domains" Tong Liu and Zheng Wang
Regular	B631 "BLRM: A Basic Linear Ranking Model for ProteinInterface Prediction" Basir Shariat, Don Neumann, and Asa Ben-Hur
Regular	B401 "BioRank: A Similarity Assessment Method for Single Cell Clustering" Yunpei Xu, Hongdong Li, Yi Pan, Feng Luo, and Jianxin Wang

Session 34: Acceleration, optimization, scalability and computability II	
Short	B693 "Automatic hyperparameter selection in Autodock" Hojjat Rakhshani, Lhassane Idoumghar, Julien Lepagnot, and Mathieu Brevilliers
Short	B703 "SORA: Scalable Overlap-graph Reduction Algorithms for Genome Assembly using Apache Spark in the Cloud" Alexander Paul, Dylan Lawrence, Myoungkyu Song, Seung-Hwan Lim, Chongle Pan, and Tae-Hyuk Ahn
Short	B463 "Paean: Parallel transcriptome quantification combing gene expression and alternative splicing event using GPU" Jiefu Li, Jiawen Guan, Jiaqiang Qian, Yanghan Feng, Ruijie Yao, Zefeng Wang, and Rui Fan
Short	B244 "Phylogenetic Reconstructions Using an Indicator-Based Bat Algorithm for Multicore Processors" Sergio Santander-Jiménez, Miguel A. Vega-Rodríguez, and Leonel Sousa

Session 35: Diagnosis, clinical procedures, progression and recovery II	
Short	B257 "Application of machine learning on colonoscopy screening records for predicting colorectal polyp recurrence" Lia Harrington, Arief Suriawinata, Todd MacKenzie, and Saeed Hassanpour
Short	B701 "Using Whole Knee Cartilage Damage Index to Predict Knee Osteoarthritis: A Two-year Longitudinal Study" Yaodong Du, Juan Shan, Rania Almajalid, and Ming Zhang
Regular *(Video)*	B587 "Multivariate Sleep Stage Classification using Hybrid Self-Attentive Deep Learning Networks" Ye Yuan, Kebin Jia, Fenglong Ma, Guangxu Xun, Yaqing Wang, Lu Su, and Aidong Zhang

Session 36: Cancer III	
Regular	B247 "Fusing heterogeneous genomic data to discover cancer progression related dynamic modules" Xiaoke Ma and Penggang Sun
Short	B700 "Centrality of cancer-related genes in human biological pathways: A graph analysis perspective" Pourya Naderi Yeganeh, Erik Saule, and M. Taghi Mostafavi
Short	B659 "Scrutinizing functional interaction networks from RNA-binding proteins to their targets in cancer" Sajal Kumar, Hua Zhong, Ruby Sharma, Yiyi Li, and Mingzhou Song

Session 37: Industry track II	
Regular	N209 "Learning Latent Patterns in Molecular Data for Explainable Drug Side Effects Prediction" Pengwei Hu, Zhu-Hong You, Tiantian He, Shaochun Li, Shuhang Gu, and Keith C.C. Chan
Regular	N205 "Domain-Aware Abstractive Text Summarization for Medical Documents" Paul Gigioli, Nikhita Sagar, Joseph Voyles, and Anand Rao,
Short	N203 "Content-bootstrapped Collaborative Filtering for Medical Article Recommendations" Wenbin Zhang and Jianwu Wang,

Session 38: Biomedical text processing VI	
Regular	B374 "Neural Precision Medicine by Mining Implicit Treatment Concepts" Canjia Li and Ben He
Regular	B249 "Layered Multistep Bidirectional Long Short-Term Memory Networks for Biomedical Word Sense Disambiguation." Daniel Bis, Canlin Zhang, Xiuwen Liu, and Zhe He
Regular	B368 "Pattern Discovery for Wide-Window Open Information Extraction in Biomedical Literature" Qi Li, Xuan Wang, Yu Zhang, Fei Ling, Cathy Wu, and Jiawei Han
Short	B630 "Boundary Detection by Determining the Difference of Classification Probabilities of Sequences: Topic Segmentation of Clinical Notes" Wei Ruan and Wonsook Lee
Short	B370 "An Attention-based Bi-GRU-CapsNet Model for Hypernymy Detection between Compound Entities" Qi Wang, Chenming Xu, Yangming Zhou, Tong Ruan, Daqi Gao, and Ping He

Session 39: Analysis of medical images and graphs VII (95 minutes)	
Regular	B753 "Curvilinear Structure Enhancement by Multiscale Top-Hat Tensor in 2D/3D Images" Shuaa S Alharbi, Cigdem Sazak, Carl J Nelson, and Boguslaw Obara

Regular	B292 "Deep Learning based fetal Middle Cerebral Artery Segmentation in Large-scale Ultrasound Images" Shuo Wang, Yang Hua, Yunyun Cao, Tao Song, Zhengui Xue, Xiaoping Gong, Guanjie Wang, Ruhui Ma, and Haibing Guan
Regular	B224 "Automatic Liver Segmentation Using Multi-plane Integrated Fully Convolutional Neural Networks" Chi Wang, Lei Chen, Song Hong, Qiang Li, Jian Yang, and Xiaohua Hu
Regular	B513 "Automated Pancreas Segmentation Using Recurrent Adversarial Learning" Yang Ning, Zhongyi Han, Li Zhong, and Caiming Zhang
Short	B702 "Whole Knee Cartilage Quantification Based on Informative Locations" Ming Zhang, Juan Shan, Yaodong Du, and Rania Almajalid

Session 40: Patient adaptation and representation	
Regular	B577 "A Deep Predictive Model in Healthcare for Inpatients" Xiao Xu, Ying Wang, Tao Jin, and Jianmin Wang
Regular	B388 "An Effective Patient Representation Learning for Time-series Prediction Tasks Based on EHRs" Liqi Lei, Yangming Zhou, Jie Zhai, Le Zhang, Zhijia Fang, Ping He, and Ju Gao
Regular	B481 "Temporal sequence alignment in electronic health records for computable patient representation" Ming Huang, Maryam Zolnoori, Nilay Shah, and Lixia Yao
Short	B573 "Patient-Specific Heartbeat Classification Based on I-Vector Adapted Deep Neural Networks" Sean Shensheng Xu, Man-Wai Mak, and Chi-Chung Cheung
Short	B698 "Opening the Black Box: Discovering and Explaining Hidden Variables in Type 2 Diabetic Patient Modelling" Leila Yousefi, Stephen Swift, Mahir Arzoky, Lucia Sacchi, Luca Chiovato, and Allan Tucker

Session 41: Heterogeneous and large data analysis	
Regular	B232 "Exploring Disease Similarity by Integrating Multiple Data Sources" Lei Deng, Danyi Ye, Junmin zhao, and Jingpu Zhang
Regular	B398 "Heterogeneous Information Network Based Clustering for Categorizations of Traditional Chinese Medicine Formula" Xintian Chen, Chunyang Ruan, Yanchun Zhang, and Huijuan Chen
Short	B667 "A method for improving the reliability of causal inference from large-scale data in biomedicine" Yitao Liu, Xiaoqing Lyu, Haihua Xie, Xiaotong Yan, Bei Wang, and Zhi Tang
Short *(Video)*	B282 “SURI: Feature Selection Based on Unique Relevant Information for Health Data” Shiyu Liu, Chongyu Zhou, Jia Yao, and Mehul Motani
Short	B754 "Multi-view Factorization AutoEncoder with Network Constraints for Multi-omic Integrative Analysis" Tianle Ma and Aidong Zhang

Session 42: Genomics VIII	
Regular	B614 "Detecting Novel Structural Variants in Genomes By Leveraging Parent-Child Relatedness" Melissa Spence, Mario Banuelos, Roummel Marcia, and Suzanne Sindi
Regular	B467 "Predicting Local Inversions Using Rectangle Clustering and Representative Rectangle Prediction" Shenglong Zhu, Scott Emrich, and Danny Chen
Short	B606 "Inferring time-consistent and well-supported horizontal gene transfers" Agnieszka Mykowiecka, Anna Muszewska, and Paweł Górecki
Short	B638 "Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms" Yizhen Zhong, Luke Rasmussen, Jennifer Pacheco, Maureen Smith, Justin Starren, and Yuan Luo

Session 43: Brain and EEG	
Regular	B581 “Task-Independent EEG Identification via Low-Rank Matrix Decomposition” Xianghao Kong, Wanzeng Kong, Qiaonan Fan, Qibin Zhao, and Andrzej Cichocki
Regular	B444 "Fast Multi-Task SCCA Learning with Feature Selection for Multi-Modal Brain Imaging Genetics" Lei Du, Kefei Liu, Xiaohui Yao, Shannon Risacher, Junwei Han, Lei Guo, Andrew Saykin, and Li Shen
Regular *(Video)*	B221 "Region level Bi-directional Deep Learning Framework for EEG-based Image Classification" Ahmed Fares, Sheng-hua Zhong, and Jianmin Jiang
Short	B242 "Deep reinforcement learning from error-related potentials via an EEG-based brain-computer interface" Tian-jian Luo, Ya-chao Fan, Ji-tu Lv, and Chang-le Zhou

Session 44: Microbiome	
Regular	B466 "PAAM-ML : A novel Phylogeny and Abundance aware Machine Learning Modelling for Microbiome Classification" Jyotsna Talreja Wassan, Haiying Wang, Fiona Browne, and Huiru Zheng
Regular	B325 "An Ensemble Feature Selection Method Based on Deep Forest for Microbiome-Wide Association Studies" Zhu Qiang, Jiang Xingpeng, He Tingting, and Hu Xiaohua
Regular *(Video)*	B469 "Read cloud sequencing elucidates microbiome dynamics in a hematopoietic cell transplant patient" Joyce Kang, Benjamin Siranosian, Eli Moss, Tessa Andermann, and Ami Bhatt
Regular	B687 "A Graph-Theoretic Approach for Identifying Bacterial Inter-correlations and Functional Pathways in Microbiome Data" Suyeon Kim, Ishwor Thapa, and Hesham Ali

Session 45: Obstetrics and fetal studies	
Short	B208 "Automatic Segmentation of Neonates Thermal Imaging for Evaluation of Trunk Thermal Asymmetry" Thyago Maia Tavares de Farias, Manoel Eusebio de Lima, Sandra da Silva Mattos, Juliana Souza Soares de Araujo, Lucia Roberta D. N. Mozer, and Felipe Alves Mourato
Short	B302 "A tree-search method for single-channel fetal QRS complexes detection in fetal heart rate monitoring" Wei Zhong, Zhongping Cao, Wen Ding, Xuemei Guo, and Guoli Wang
Short	B671 "A Data Mining Approach for Biomarker Discovery Using Transcriptomics in Endometriosis" Sadia Akter, Dong Xu, Susan Nagel, and Trupti Joshi

Session 46: Diagnosis, clinical procedures, progression and recovery III	
Regular	B361 "Disease Inference with Symptom Extraction and Based on Bidirectional Recurrent Neural Network" Donglin Guo, Min Li, Ying Yu, Yaohang Li, Guihua Duan, Fang-Xiang Wu, and Jianxin Wang
Short	B220 "Deepwound: Automated Postoperative Wound Assessment and Surgical Site Surveillance through Convolutional Neural Networks" Varun Shenoy, Elizabeth Foster, Lauren Aalami, Bakar Majeed, and Oliver Aalami
Short	B350 "Convolutional Gated Recurrent Units for Medical Relation Classification" Bin He, Yi Guan, and Rui Dai
Short	B699 "On accurate, automated and insightful deviation analysis of clinical protocols" Hui Yan, Xudong Lu, Pieter Van Gorp, Serge Jan Hubert Heines, Shan Nan, Uzay Kaymak, and Huilong Duan