

IWBBIO 2020

**INTERNATIONAL WORK-CONFERENCE ON
BIOINFORMATICS AND
BIOMEDICAL ENGINEERING**

PROGRAM

**30 September- 2 October 2020
Granada (SPAIN)**

IWBBIO 2020 Short Program

Wednesday, September 30th, 2020	
9:15-10:30	Session A.1: Biomarker identification
10:30-10:45	Break
10:45-12:00	Session A.2: Biomedical Engineering
12:00-12:15	Break
12:15-13:00	Session A.3: Biomedical signal analysis
13:00-14:00	Session A.4: Computational proteomics and protein-protein interactions
14:00-15:00	Break
15:00-16:15	Session A.5: Data Mining from UV/VIS/NIR Imaging and Spectrophotometry
16:15-16:30	Break
16:30-17:30	Session A.6: E-Health technology, services and applications

Thursday, October 1st, 2020

9:30-11:00	Session A.7: High performance in Bioinformatics
11:00-11:15	Break
11:15-12:00	Session A.8: Bio-nanotechnology
12:00-12:15	Break
12:15-14:00	Session A.9: High-throughput genomics: bioinformatic tools and medical applications
14:00-14:30	Break
14:30-17:00	Session A.10: New advances in bioinformatics and biomedicine

Friday, October 2nd, 2020

9:30-11:00	Session A.11: Machine learning in Bioinformatics
11:00-11:15	Break
11:15-13:00	Session A.12: Medical Image Processing
13:00-13:15	Break
13:15-14:15	Session A.13: Simulation and visualization of biological systems
14:15-15:00	Session A.14: Computational Approaches for Drug Design and Personalized Medicine

During all the conference:

Session A.15: VIRTUAL SESSION

<http://iwbbio.ugr.es/virtual.php>

IWBBIO 2020 FULL PROGRAM

Wednesday, September 30th 2020

Session A.1: Biomarker identification

Identification of common gene signatures in microarray and RNA-sequencing data using network-based regularization

Inês Diegues, Susana Vinga and Marta Lopes

Network-based variable selection for survival outcomes in oncological data

Eunice Carrasquinha, André Veríssimo, Marta Lopes and Susana Vinga

Blood Plasma Trophic Growth Factors Predict the Outcome in Patients with Acute Ischemic Stroke

Valeriia Roslavtceva, Evgeniy Bushmelev, Pavel Astanin, Tatyana Zabrodskaya, Alla Salmina, Semen Prokopenko, Vera Laptchenkova and Michael Sadovsky

Analyzing the immune response of neoepitopes for personalized vaccine design

Iker Malaina, Leire Legarreta, María Dolores Boyano, Santos Alonso, Ildefonso M. de la Fuente and Luis Martínez

A Data Integration Approach for Detecting Biomarkers of Breast Cancer Survivability

Huy Quang Pham, Luis Rueda and Alioune Ngom

Functional variant prioritization in rare diseases using a mechanistic approach

Ana M Pérez-Gutiérrez, Rosario Carmona, Virginia Aquino-Quintans, Javier Pérez-Florido, Kinza Rian, María Peña-Chilet and Joaquín Dopazo

Enhancing Breast Cancer classification via information and multi-model integration

J.C. Morales, Francisco Carrillo-Perez, Daniel Castillo-Secilla, Ignacio Rojas and Luis Javier Herrera

Identification of Coding Regions in Prokaryotic DNA Sequences Using Bayesian Classification

Mohammad Al Bataineh

Session A.2: Biomedical Engineering

Effects of the distribution in space of the velocity-inlet condition in hemodynamic simulations of the thoracic aorta

Maria Nicole Antonuccio, Alessandro Mariotti, Simona Celi and Maria Vittoria Salvetti

Graph databases for contact analysis in infections using spatial temporal models

Lorena Pujante, Manuel Campos, Jose M. Juarez, Bernardo Cánovas Segura and Antonio Morales

Window functions in Rhythm based Biometric Authentication

Ondrej Krejcar and Orcan Alpar

Coupled Electro-mechanical Behavior of Microtubules

Sundeep Singh and Roderick Melnik

Relationships between muscular power and bone health parameters in a group of young Lebanese adults

Patchina Sabbagh, Pierre Kamle, Antonio Pinti, Hayman Saddick, Eddy Zakhem, Boutros Finianos, Gautier Zunquin, Georges Baquet and Rawad El Hage

Comparison of Corneal Morphologic Parameters and High Order Aberrations in Keratoconus and Normal eyes

Jose Sebastián Velázquez Blázquez, Francisco Cavas Martínez, Jose Miguel Bolarín Guillén and Jorge Luciano Alió

Assisted generation of bone fracture patterns

Gema Parra-Cabrera, Francisco Daniel Pérez-Cano, Adrián Luque-Luque and Juan José Jiménez-Delgado

Session A.3: Biomedical signal analysis

Thermal behavior of children during American football sports training

Irving A. Cruz-Albarran, Pierre Burciaga-Zuñiga, Ma. Guadalupe Perea-Ortiz and Luis A. Morales-Hernandez

An approach to detecting and eliminating artifacts from the sleep EEG signals

Rym Nihel Sekkal, Fethi Bereksi Reguig, Nabil Dib and Daniel Ruiz Fernandez

Positioning Algorithm for Arterial Blood Pressure Pneumatic Sensor

Viacheslav Antsiperov and Gennady Mansurov

A machine learning computer aided diagnostic system to detect focal fold nodules by using features extracted from voice recordings

Fernando Calle-Alonso, Carlos Javier Pérez, Yolanda Campos-Roca and Sandra Paniagua

Session A.4: Computational proteomics and protein-protein interactions

Comorbidity network analyses of global rheumatoid arthritis and type 2 diabetes reveal IL2 and IL6 as common role players

Tuck Onn Liew, Rohit Mishra and Chandrajit Lahiri

Topological Analysis of Cancer Protein Subnetwork in Deubiquitinase (DUB) Interactome

Nurulisa Zulkifli

Prediction of Structure and Molecular Interaction with DNA of BvrR, a Virulence-Associated Regulatory Protein of Brucella

Edgar Adrián Ramírez González, Martha Cecilia Moreno Lafont, Alfonso Méndez Tenorio, Mario Eugenio Cancino Díaz, Iris Estrada García and Rubén López Santiago

Graph Based Automatic Protein Function Annotation Improved By Semantic Similarity

Bishnu Sarker, Navya Khare, Marie-Dominique Devignes and Sabeur Aridhi

Proteomes and Genomes Analysis of Lactobacillus spp. and Bifidobacterium spp. to Evaluate the Presence and Frequency of Bacteriocin

Najaf Allahyari Fard and Nasrin Darvishi

Session A.5: Data Mining from UV/VIS/NIR Imaging and Spectrophotometry

Cancer detection based on Image classification by using Convolution Neural Network (CNN)

Mohammad Anas Shah, Abdala Nour and Dr. Alioune Ngom

Steps to Visible Aquaphotomics

Vladyslav Bozhynov, Zoltan Kovacs and Jan Urban

Automatic calibration, acquisition, and analysis for color experiments

Jan Urban

Classification of fish species using silhouettes

Pavla Urbanova, Vladyslav Bozhynov, Petr Císar and Milos Zelezny

Session A.6: E-Health technology, services and applications

Spa-neg: an approach for negation detection in clinical text written in Spanish.

Oswaldo Solarte-Pabón, Ernestina Menasalvas and Alejandro Rodriguez

In-bed Posture Classification from Pressure Mat Sensors for the Prevention of Pressure Ulcers using Convolutional Neural Networks

Aurora Polo, David Gil, Chris Nugent and Javier Medina-Quero

Pin-code authentication by local proximity based touchstroke classifier

Ondrej Krejcar and Orcan Alpar

Behavioral Risk Factors Based Cancer Prediction Model utilizing Public and Personal Health Records

Emil Saweros and Yeong-Tae Song

IoMT-driven eHealth: A technological innovation proposal based on smart speakers

David DomÍnguez, Leticia Morales Trujillo, Nicolas SÁnchez and Jose Manuel Navarro

Fast and reliable uTAD for creatinine monitoring by patients

Miguel M Erenas, Manuel J Arroyo, Ignacio De Orbe-Payá, Kevin Cantrell, José A Dobado, Alfonso Salinas-Castillo and Luis Fermín Capitán-Vallvey

Thursday, October 1st, 2020

Session A.7: High performance in Bioinformatics

Search and Match

Pedro Martins, Maryam Abbasi and Filipe Sá

Highly Parallel Convolution Method to Compare DNA Sequences with Enforced In/Del and Mutation Tolerance

Michael Sadovsky, Anna Moliavko, Eugenia Karepova and Vladimir Shaidurov

Maximizing the electrostatic similarity in drug discovery through evolutionary algorithms.

S. Puertas-Martín, J. L. Redondo, H. Pérez-Sánchez and P. M. Ortigosa

Role of Homeobox Genes in the Development of *Pinus sylvestris*

Tatiana Guseva, Vladislav Biryukov and Michael Sadovsky

Function vs. taxonomy: further reading from fungal mitochondrial ATP synthases

Victory Fedotovskaya, Michael Sadovsky, Anna Kolesnikova, Tatiana Shpagina and Julia Putinzeva

A Mini Review on Parallel Processing of Brain Magnetic Resonance Imaging

Ondrej Krejcar, Ayca Kirimtat, Rafael Dolezal and Ali Selamat

Watershed Segmentation for Peak Picking in Mass Spectrometry Data

Vojtech Barton, Markéta Nykrýnová and Helena Skutkova

Discovering the most characteristic motif from a set of peak sequences

Gines Almagro-Hernandez and Jesualdo Tomás Fernández-Breis

Session A.8: Bio-nanotechnology

Production of 3D-Printed Tympanic Membrane Scaffolds as a Tissue Engineering Application

Elif Ilhan, Songül Ulag, Nazmi Ekren, Osman Kiliç, Oguzhan Gündüz and Faik Nüzhet Oktar

Controlled Release of Metformin Loaded Polyvinyl Alcohol (PVA) Microbubble / Nanoparticles Using Microfluidic Device for the Treatment of Type 2 Diabetes Mellitus

Sumeyye Cesur, Muhammet Emin Cam, Fatih Serdar Sayin, Sena Su and Oguzhan Gunduz

Patch-Based Technology for Corneal Microbial Keratitis

Songul Ulag, Elif Ilhan, Timur Hakan Barak, Nazmi Ekren, Osman Kilic and Oguzhan Gunduz

Session A.9: High-throughput genomics: bioinformatic tools and medical applications

Evaluation of basic next generation sequencing parameters in relation to true/false positivity's findings of rare variants in an isolated population from the Czech Republic South-Eastern Moravia region with high incidence of Parkinsonism.

Radek Vodicka, Kristyna Kolarikova, Radek Vrtel, Katerina Mensikova, Petr Kanovsky and Martin Prochazka

LuxHS: DNA methylation analysis with spatially varying correlation structure

Viivi Halla-Aho and Harri Lähdesmäki

Unravelling Disease Presentation Patterns in ALS using Biclustering for Discriminative Meta-features Discovery

Joana Matos, Sofia Pires, Helena Aidos, Marta Gomicho, Susana Pinto, Mamede de Cavalho and Sara Madeira

Patient Stratification in Amyotrophic Lateral Sclerosis using Clinical and Patient Profiles

Sofia Pires, Marta Gromicho, Susana Pinto, Mamede de Carvalho and Sara Madeira

Microvariations from RNA-seq experiments

Elena Espinosa, Macarena Arroyo, Rafael Larrosa, M. Gonzalo Claros and Rocío Bautista

Detection of highly variable genome fragments in unmapped reads of Escherichia coli genomes

Marketa Nykrynova, Vojtech Barton, Matej Bezdicek, Martina Lengerova and Helena Skutkova

CSVS: the spanish population variability database and the first Spanish genome reference imputation panel

Maria Peña-Chilet, Gema Roldán, Javier Perez-Florido, Francisco M. Ortuno, Rosario Carmona, Virginia Aquino, Daniel Lopez, Jose Luis Fernandez-Rueda and Joaquin Dopazo

Session A.10: New advances in bioinformatics and biomedicine

An integrated web application to analyse transcriptomic and proteomic data - OMnalysis

Punit Tyagi and Mangesh Bhide

Targeted Next Generation Sequencing of a custom capture panel to target sequence 112 cancer related genes in breast cancer tumours ERBB2 positive from Lleida (Spain)

Ana Velasco, Serafin Morales, Ariadna Gasol, Anna Serrate and Xavier Matias-Guiu

Variant Analysis from bacterial isolates affirms DnaK crucial for multidrug resistance

Shama Mujawar and Chandrajit Lahiri

Ecmo in sepsis using cytoadsorption and novel biomarkers with advanced haemodynamic monitoring: a retrospective observational study including with review of literature

Dr. Mayadhar Barik

Evolving Towards Digital Twins in Healthcare

Cecilio Angulo, Luis Gonzalez-Abril, Cristóbal Raya and Juan Antonio Ortega

Anonymizing Personal Images using Generative Adversarial Networks

Esteban Piacentino and Cecilio Angulo

Generating Fake Data using GANs for Anonymizing Healthcare Data

Esteban Piacentino and Cecilio Angulo

Genetic variability and phylogeny of Indian isolate of the Soybean mosaic virus

Nisha Choudhary, Isha Singal and Dr. Rakesh Kumar Verma Verma

Molecular genetic analysis of Chilli veinal mottle virus infecting chilli in Rajasthan, India suggests distinctive evolutionary pattern

Isha Singal Singal, Nisha Choudhary Choudhary and Dr. Rakesh Kumar Verma Verma

Effect of Temperature Control Liner Materials on Long Term Outcomes of Prosthesis Use

Robert Johnston, Danielle Sell, Goeran Fiedler, Anita Singh and James Peters

Identification of multiple synovial fibroblast subsets in hip OA patients by single cell sequencing

Susanne Wijesinghe, Amel Badoume, Dominika Nanus, Edward Davis, Mark Lindsay and Simon Jones

Prediction of Antimicrobial Peptides from *Chondrus crispus* using an Ensemble of Machine Classifiers

Michela Caprani, Orla Slattery, Joan O'Keeffe and John Healy

Enrichment Analysis of Protein-protein interaction and drug discovery for associated diseases: A bioinformatics approach

Md Rakibul Hasan, Bikash Kumar Paul, Kawsar Ahmed and Dr. Touhid Bhuiyan

Automated nerve fibres identification and morphometry analysis with neural network based tool in MATLAB

Michal Kopka and Wiktor Paskal

Acute toxicity effect of sea mud

Arba Pramundita Ramadani, Farida Hayati, Munawwarah and Rosmayati Evi

HeritaGen: Genetic and Genealogical Heritage Unification for Clinical Decision Making Support in Inherited Diseases

José Luis González-Sánchez, Bernabe Dieguez-Roda, Jose Antonio García-Trujillo, Jonathan Gómez-Raja, Felipe Lemus-Prieto, Ana María Núñez-Cansado, María Peguero-Ramos, Álvaro Rodríguez-San Pedro, and Silvia Romero-Chala

New bioinformatic tools for circular RNA detection and functional predictions: application in acute lymphoblastic leukemia with MLL rearrangements.

Anna Dal Molin, Enrico Gaffo, Caterina Tretti, Alessia Buratin, Silvia Bresolin, Geertruij Te Kronnie and Stefania Bortoluzzi

Friday October 2nd, 2020

Session A.11: Machine learning in Bioinformatics

Clustering reveals common check-point and growth factor receptor genes expressed in six different cancer types

Shrikant Pawar and Chandrajit Lahiri

Predicting infectious diseases by using machine learning classifiers

Juan A. Gómez-Pulido, José M. Romero-Muelas, José M. Gómez-Pulido, José L. Castillo Sequera, José Sanz Moreno, María-Luz Polo-Luque and Alberto Garcés-Jiménez

Bayesian optimization improves tissue-specific prediction of active regulatory regions with deep neural networks

Luca Cappelletti, Alessandro Petrini, Jessica Gliozzo, Elena Casiraghi, Max Schubach, Martin Kircher and Giorgio Valentini

DiS-TSS: An annotation agnostic algorithm for TSS identification

Dimitris Grigoriadis, Nikos Perdikopanis, Georgios K. Georgakilas and Artemis Hatzigeorgiou

LM-based Word Embeddings Improve Biomedical Named Entity Recognition: a Detailed Analysis

Liliya Akhtyamova and John Cardiff

Evaluating mutual information and Chi-square metrics in text features selection process: A study case applied to the text classification in PubMed

José Párraga-Valle, Rodolfo García-Bermúdez, Fernando Rojas, Christian Torres-Morán and Alfredo Simón-Cuevas

Profiling Environmental Conditions from DNA

Sambriddhi Mainali, Max Garzon and Fredy A Colorado

Stability of Feature Selection Methods: A Study of Metrics across Different Gene Expression Datasets

Zahra Mungloo-Dilmohamud, Yasmina Jauferally Fakim and Carlos Peña-Reyes

Session A.12: Medical Image Processing

Influence of sarcopenia on bone health parameters in a group of elderly men

Antoun Amal, Saddick Hayman, Antonio Pinti, Eric Watelain, Eric Lespessailles, Hechmi Toumi and Rawad El Hage

Novel Thermal Image Classification based on Techniques Derived from Mathematical Morphology: Case Study on Breast Cancer

Ondrej Krejcar, Petra Maresova, Ali Selamat, Kamil Kuca and Jean Sebastien Mambou

Data preprocessing via multi-sequences MRI mixture to improve brain tumor segmentation

Vladimir Groza, Bair Tuchinov, Evgeniy Pavlovskiy, Evgeniya Amelina and Mihail Amelin

Brain MRI Modality Understanding: A Guide for Image Processing and Segmentation

Ondrej Krejcar, Ayca Kiritat and Ali Selamat

Computer-Aided Breast Cancer Diagnosis from Thermal Images using Transfer Learning

Hasan Ogul and Cagri Cabioglu

Blood Cell Types Classification using CNN

Ishpreet Singh, Narinder Pal Singh, Saharsh Bawankar and Harnoor Singh

Medical image data upscaling with generative adversarial networks

Ondrej Krejcar, Ali Selamat, Michal Dobrovolny, Karel Mls and Jean Sebastien Mambou

Session A.13: Simulation and visualization of biological systems

Kernel based approaches to identify hidden connections in gene networks using NetAnalyzer

Fernando Moreno Jabato, Elena Rojano, James R. Perkins, Juan Antonio García Ranea and Pedro Seoane-Zonjic

Comprehensive analysis of patients with undiagnosed genetic diseases using the Patient Exploration Tools Suite (PETS)

Elena Rojano, Pedro Seoane, Fernando Moreno Jabato, James Perkins and Juan Ranea

Automated tracking of red blood cells in images

František Kajánek, Ivan Cimrák and Peter Tarábek

A Novel Prediction Model for Discovering Beneficial Effects of Natural Compounds in Drug Repurposing

Suganya Chandrababu and Dhundy Bastola

Session A.14: Computational Approaches for Drug Design and Personalized Medicine

MARCO gene variations and their association in cardiovascular diseases:
In-silico analysis

Kholoud Sanak, Maryame Azzouzi, Mounia Abik and Fouzia Radouani

Computational Approaches for Drug Design: A Focus on Drug
Repurposing

Suyeon Kim, Ishwor Thapa, Fariat Samadi and Hesham Ali

IWBBIO 2020. Virtual presentations

Session A.15: VIRTUAL SESSION

Attitudes of patients towards online communication activities with healthcare professionals

Maria Bujnowska-Fedak, Edward Puchala and Paulina Wegierek

Epileptic Seizure Detection Using a Neuromorphic-compatible Deep Spiking Neural Network

Pouya Soltani Zarrin, Romain Zimmer, Christian Wenger and Timothée Masquelier

Using deep learning to predict piRNA

Ziting Zhang, Fuze Wei and Xiaoyong Sun

Predicting miRNA target with deep learning

Dan Jiang, Yu Cai and Xiaoyong Sun

Using deep learning to predict circRNA splicing site

Kai Sun, Xiaoyong Sun, Qinggong Wei and Yujun Xu

Effects of *Curculigo pilosa* Supplementation on Antidiabetic and Antioxidant Activities of Yam Flour

Kayode Karigidi and Charles Olaiya

Global Dynamics of a Fractional order SIR Epidemic Model with Memory

Parvaiz Ahmad Naik and Jian Zu

Analysis of invasive risk factors and establishment of a predictive nomogram for early lung adenocarcinoma shown as pure ground glass nodules

Yi Ma

Rapid detection of bacterial contamination in the platelet using recombinase polymerase amplification

Hyeong Woo Lee, Sang Rak Lee, Yoon Hee Bae, Jae Hyun Lee, Dal Sik Kim, Jihyang Lim, Nam Yong Lee, Duck Cho, Hee Jae Huh, Yoo Na Chung and Yong Cho

Comparative analysis of false discovery rate control methodologies

Sin June Kim, Gyeongmi Yu and Jaesik Jeong

Method of detecting 3D rotation of red blood cells based on video data

Kristína Kovalčíková and Michal Duracik

New Genomic Information Systems (GenIS): Species Delimitation and Identification

Max Garzon and Fredy Alexander Colorado-Garzon

Gene regulation in H9c2 cells by 72h electrical microcurrent exposure - Serca2a as an example

Johannes Mueller

An improvement of ComiR algorithm for microRNA target prediction by exploiting coding region sequences of mRNAs

Giorgio Bertolazzi, Panayiotis Benos, Michele Tumminello and Claudia Coronello

Exploring associations between Depression, Schizophrenia and smoking addiction based on explainable AI algorithms

Dingzhou Fei

Inferring Ligand-Receptor Intercellular Networks from Single-Cell Transcriptomics Data

Simon Cabello-Aguilar and Jacques Colinge

The evaluation of the study of bioequivalence of generic drugs relating to the group of analogues of endogenous compounds (on the example of colecalciferol)

Dmitry Romodanovsky and Alexandr Khohlov

Regulation of mammalian thiamine (vitamin B1)-dependent metabolism by p53

Victoria Bunik, Vasily Aleshin, Xiaoshan Zhou, Shuba Krishnan and Anna Karsson

Investigation of particle interactions within ELEKTA 6 MV photon beam using Monte Carlo GATE simulation

Deae-Eddine Krim, Abdeslem Rrhiaou, Mustapha Zerfaoui, Dikra Bakari and Nacira Hanouf

Right Atrium Spatio-temporal Organisation to Predict Atrial Fibrillation Ablation Recurrence

Raquel Cervigón, Julián Pérez-Villacastín and Javier Moreno

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