2018 CBEES-BBS BARI, ITALY CONFERENCE ABSTRACT

2018 2nd International Conference on Computational Biology and Bioinformatics (ICCBB 2018)

October 11-13, 2018

Polytechnic University of Bari, Italy

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Introduction

Welcome to 2018 2nd International Conference on Computational Biology and Bioinformatics (ICCBB 2018) which is sponsored by Hong Kong Chemical, Biological & Environmental Engineering Society (CBEES), Biology and Bioinformatics (BBS) and co-sponsored by Polytechnic University of Bari, Italy. The aim of 2018 2nd International Conference on Computational Biology and Bioinformatics (ICCBB 2018) is to present the latest research and results of scientists related to Computational Biology and Bioinformatics topics. This conference provides opportunities for the different areas delegates to exchange new ideas and application experiences face to face, to establish business or research relations and to find global partners for future collaboration. We hope that the conference results constituted significant contribution to the knowledge in these up to date scientific field.

Papers will be published in one of the following conference proceeding:

ACM International Conference Proceedings (ISBN: 978-1-4503-6552-9), which will be archived in the ACM Digital Library, indexed by Ei Compendex and Scopus, and submitted to be reviewed by Thomson Reuters Conference Proceedings Citation Index (ISI Web of Science).

Conference website and email: **http://www.iccbb.org/; iccbb@cbees.net**

Presentation Instruction

Instruction for Oral Presentation

Devices Provided by the Conference Organizer:

Laptop Computer (MS Windows Operating System with MS PowerPoint and Adobe Acrobat Reader)
Digital Projectors and Screen
Laser Stick

Materials Provided by the Presenters:

PowerPoint or PDF Files (Files should be copied to the Conference laptop at the beginning of each Session.)

Duration of each Presentation (Tentatively):

Regular Oral Presentation: about **12** Minutes of Presentation and **3** Minutes of Question and Answer
Keynote Speech: about **40** Minutes of Presentation and **5** Minutes of Question and Answer

Instruction for Poster Presentation

Materials Provided by the Conference Organizer:

The place to put poster

Materials Provided by the Presenters:

Home-made Posters
Maximum poster size is A1
Load Capacity: Holds up to 0.5 kg

Best Presentation Award

One Best Oral Presentation will be selected from each presentation session, and the Certificate for Best Oral Presentation will be awarded at the end of each session on October 11 and 12, 2018.

Keynote Speaker Introduction

Keynote Speaker I

Prof. Roberto Brunelli
"La Sapienza" University, Italy

Prof. Roberto Brunelli, born in Roma (Italy) on 22 January 1962, holds a six years degree in Medicine (magna cum laude), a four years specialization in Obstetrics and Gynecology and a five years specialization in General Surgery from the University of Roma “La Sapienza” (Italy).

Prof. Brunelli is currently an associate professor at “La Sapienza” university. Besides this academic position, he directs the Division of Obstetrics and Gynecology at the Policlinico “Umberto I”, Roma.

Prof. Brunelli authored some 45 articles in ISI journals studying different aspects of obstetrical and gynecological sciences ranging from pathology to radiological diagnosis and nano-bioengineering. He participated to several national and international conferences. He serves as reviewer for a number of leading international journals in the fields of Obstetrics and Gynecology.

Topic: “*On the Role of Human Umbilical Chord Biomechanics*”

Abstract**—**The human umbilical cord Wharton Jelly (WJ) is a fetal organ composed of a collagen fibrillar network randomly spaced in a 3D spongy network. It binds and encases the three umbilical vessels (one straight vein and two coiled arteries) and maintains the efficiency of cordonal blood flow. The complexity of the dynamic structural and functional relations within the WJ, based on the mechano-sensory role of its constitutive cells that suit internal (hemodynamic) and external (fetal movements) loads, explains why detailed biomechanical data of this structure are still lacking.

This presentation will outline a multidisciplinary study including biomedical image processing, mechanical characterization and finite element simulations to demonstrate a complex level of structural and functional hierarchy of the WJ. It will offer a direct visual appreciation of its pivotal roles in cord hemodynamics and resistance to compression. A direct understanding of how some changes in WJ biomechanics may concur to fetal pathophysiology (e.g. intrauterine growth restriction or pregnancy induced hypertension) will be provided.

Keynote Speaker II

Prof. Domenico Ciavarella
University of Foggia, Italy

Prof. Domenico Ciavarella, born in Foggia (Italy) on 28 February 1979, holds a five years degree in Dentistry from the University of Ancona (Italy). He specialized in Orthodontics at the University of L'Aquila (Italy) and the C.H. Tweed International Foundation for Orthodontic Research of Tucson (USA). He was awarded of a post-degree grant for his studies on the oral carcinoma.

Prof. Ciavarella is currently an aggregate professor at University of Foggia, where he directs the Orthodontics division. Besides these scientific commitments, he is the coordinator of the post-degree specialization courses in Orthodontics.

Prof. Ciavarella authored about 60 indexed articles on dentistry, odontology, periodontology, craniofacial surgery and oral oncology, contributing as a speaker to several national and international conferences. He serves as reviewer for a number of indexed international journals in the fields of dentistry and oral oncology.

Topic: "*Digital 3D Revolution in Dentistry*"

***Abstract*—**In the last 10 years the use of digital 3d technology has changed dentistry and medicine in a multitude of ways, from electronic record-keeping and data analysis to new diagnostic tools, novel prevention methods and revolutionary treatment options.

The first digitalization in dentistry started with CAD/CAM systems and digital surgical guides solutions. Digital imaging can be used also in orthodontics for diagnosis improvement and treatment planning by using digital set up combined to CBCT. Digital dental models can be created through either indirect or direct techniques involving intraoral scanners. Using digital models alleviates many obstacles and challenges of plaster models made from conventional impressions (including the burden of storage, the risk of damage or breakage, and the difficulties in sharing the data with other clinicians involved in the patient's care), and may help the clinician in managing and simulating dental movements, and creating visible or invisible customized appliances.

Keynote Speaker III

Prof. Hesham H. Ali
University of Nebraska at Omaha, USA

Prof. Hesham H. Ali is a Professor of Computer Science and Lee and Wilma Seemann Distinguished Dean of the College of Information Science and Technology at the University of Nebraska at Omaha (UNO). He also serves as the director of the UNO Bioinformatics Core Facility that supports a large number of biomedical research projects in Nebraska. He has published numerous articles in various IT areas including scheduling, distributed systems, data analytics, wireless networks, and Bioinformatics. He has also published two books in scheduling and graph algorithms, and several book chapters in Bioinformatics. He has been serving as the PI or Co-PI of several projects funded by NSF, NIH and Nebraska Research Initiative in the areas of data analytics, wireless networks and Bioinformatics. He has also been leading a Research Group that focuses on developing innovative computational approaches to classify biological organisms and analyze big bioinformatics data. The research group is currently developing several next generation big data analytics tools for mining various types of large-scale biological and medical data. This includes the development of new graph theoretic models for assembling short reads obtained from high throughput instruments, as well as employing a novel correlation networks approach for analyzing large heterogeneous biological and health data associated with various biomedical research areas, particularly projects associated with aging and infectious diseases. He has also been leading two funded projects for developing secure and energy-aware wireless infrastructure to address tracking and monitoring problems in medical environments, particularly to study mobility profiling for healthcare research.

Topic: "*Big Data Analytics in Biomedical Informatics: Opportunities and Challenges*"

Abstract**—**With the increasing number and sophistication of biomedical instruments and data generation devices, there is even more increasing pressure on researchers to develop advanced data analytics tools to extract useful knowledge out of the massive collected data. This includes advanced sequencing technologies responsible for the generation of huge amounts of bioinformatics data as well as wearable devices and Internet of Things systems responsible for collecting different types of health and mobility related data. The currently available data is not only massive in size but it also exhibits all the features of big data systems with a high degree of variability, veracity and velocity. How to leverage this raw data to advance

biomedical research, particularly in dealing with outbreaks and infectious diseases, and improve health care, through personalized and targeted medicine, can be considered the most exciting scientific challenge of our generation. Developing innovative data integration and mining techniques along with clever parallel computational methods to implement them will be critical in efficiently meeting those challenges and take advantage of the potential opportunities. This talk present new big data analytics tools using graph modeling and network analysis along with how to effectively utilize High Performance Computing in implementing such tools. Case studies illustrating how proposed tools were used to analyze data associated with infectious diseases that led to new biological discoveries will also be presented.

Keynote Speaker IV

Prof. Andrey S. Krylov
Lomonosov Moscow State University, Russia

Prof. Andrey Krylov received the M.S., Ph.D., and Dr.Sc. degrees from the Faculty of Computational Mathematics & Cybernetics, Lomonosov Moscow State University (CMC MSU) in 1978, 1982 (supervisor – academician Andrey Tikhonov), and 2009, respectively. He was a member of scientific staff (1981-1988), senior researcher (1988-1998), head scientist (1988-2003), associated professor (2003-2009) CMC MSU and he is currently professor, head of the Laboratory of Mathematical Methods of Image Processing (http://imaging.cs.msu.ru). During his career he worked in applied mathematics in areas of nuclear physics, physical chemistry of liquid systems, multimedia and biomedical imaging.

In 1989 he received the Leninsky Komsomol Scientific Prize - the highest prize for scholars in the USSR. He has authored or coauthored over 150 published papers. He served as a reviewer for several international journals and conferences; he was in the board of international and national conferences. For a long period of time he is one of the organizers of the GraphiCon conference - the main international computer graphics, computer vision and image processing conference in Russia.

Topic: “*Fast Estimation of Downsampling Factor for Biomedical Image Registration*”

Abstract**—**An approach to fasten medical image registration algorithms is suggested. It is based on the preliminary estimation the possible downsampling factor before the registration. The estimation algorithm uses fast bidirectional empirical mode decomposition. An analysis and approvement of the method is performed by multiscale ridge analysis using retinal image database DRIVE, astrocyte images and images from Computed Tomography Emphysema Database. Proposed registration acceleration algorithm was tested for rigid registration methods with HeLa cells video data set.

Brief Schedule for Conference

Day 1	**October 11, 2018 (Thursday)** **Venue: Museo della Fotografia** Arrival Registration 10:00-17:00
	Afternoon Conference
	Venue: Aula Magna Orabona 13:30-13:45 **Opening Remarks** (Prof. Eugenio Di Sciascio) 13:45-14:30 **Keynote Speech I** (Prof. Roberto Brunelli) 14:30-15:15 **Keynote Speech II** (Prof. Domenico Ciavarella) 15:15-15:45 Coffee Break & Group Photo
	Session 1: 15:45-17:15 **Venue: Aula Magna Orabona** Topic: “Biomedical Engineering”--6 presentations
Day 2	**October 12, 2018 (Friday) 09:00-18:05**
	Morning Conference (Aula Magna Orabona)
	09:00-09:45 **Keynote Speech III** (Prof. Hesham H. Ali) 09:45-10:30 **Keynote Speech IV** (Prof. Andrey S. Krylov) 10:30-11:00 Coffee Break & Group Photo
	Session 2: 11:00-12:45 Topic: “Medical Image Processing”--7 presentations
	Lunch: 12:45-14:00 **(Restaurant)**
	Afternoon Conference (Aula Magna Orabona)
	Session 3: 14:00-15:45 Topic: “Bioinformatics and Computational Biology”--7 presentations
	Coffee Break: 15:45 -16:05
	Session 4: 16:05-18:05 Topic: “Biosignal Acquisition and Analysis”--8 presentations
	18:05-20:00 Dinner (Restaurant)
	Poster Session: 9:00-18:00 **(Venue: Museo della Fotografia)**
Day 3	**9:00-18:00 Academic Tour**

Tips: Please arrive at the Conference Room 10 minutes before the session begins to upload PPT into the laptop.

Detailed Schedule for Conference

October 11, 2018 (Thursday)

Venue: Museo della Fotografia

10:00-17:00	**Arrival and Registration**

Venue: Aula Magna Orabona

13:30-13:45	 **Opening Remarks** Prof. (President) Eugenio Di Sciascio Polytechnic University of Bari, Italy
13:45-14:30	 **Keynote Speech I** Prof. Roberto Brunelli "La Sapienza" University, Italy Topic: "*On the Role of Human Umbilical Chord Biomechanics*"
14:30-15:15	**Keynote Speech II** Prof. Domenico Ciavarella University of Foggia, Italy Topic: "*Digital 3D Revolution in Dentistry*"
15:15-15:45	**Coffee Break & Group Photo**
15:45-17:15	**Session 1, Aula Magna Orabona** Topic: "Biomedical Engineering"

October 12, 2018 (Friday)

Venue: Aula Magna Orabona

Morning Conference **Venue: Aula Magna Orabona**	
09:00-09:45	 **Keynote Speech III** Prof. Hesham H. Ali University of Nebraska at Omaha, USA Topic: "*Big Data Analytics in Biomedical Informatics: Opportunities and Challenges*"
09:45-10:30	 **Keynote Speech IV** Prof. Andrey S. Krylov Lomonosov Moscow State University, Russia Topic: "*Fast Estimation of Downsampling Factor for Biomedical Image Registration*"

10:30-11:00	**Coffee Break & Group Photo**
11:00-12:45	**Session 2** Topic: "Medical Image Processing"
12:45-14:00	**Lunch (Restaurant)**
Afternoon Conference **Venue: Aula Magna Orabona**	
14:00-15:45	**Session 3** Topic: "Bioinformatics and Computational Biology"
15:45-16:05	**Coffee Break**
16:05-18:05	**Session 4** Topic: "Biosignal Acquisition and Analysis"
18:05-20:00	**Dinner (Restaurant)**

Note: (1) The registration can also be done at any time during the conference.

(2) The organizer doesn't provide accommodation, and we suggest you make an early reservation.

(3) One Best Oral Presentation will be selected from each oral presentation session, and the Certificate for Presentation will be awarded at the end of each session on October 11 and 12, 2018.

Let's move to the session!

Session 1

Tips: The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

Afternoon, October 11, 2018 (Thursday)

Time: 15:45-17:15

Venue: Aula Magna Orabona

Session 1: Topic: "Biomedical Engineering"

Session Chair: Prof. Filippo Attivissimo and Dr. Attilio Di Nisio

B1004 Session 1 Presentation 1 (15:45-16:00)	Experimental Analysis of Pressures Exerted by an Orthodontic Aligner to Dental Arches C. Pappalettere, F. De Cillis, **C. Cianci**, G. Siciliani and F. Cervinara Politecnico di Bari, Italy *Abstract*—This study investigates the pressures exerted by an orthodontic aligner on dental arches. The aligners are devices able to produce the movement and alignment of one or more teeth through a number of steps defined by the orthodontist. In order to register pressures between aligner and tooth, two pressure films (PRESCALE film, Fujifilm) are interposed between them. One of these films becomes coloured when pressed, and the density of the colour obtained is proportional to the intensity of the pressure. The image of the sheet, digitized by a scanner, is analysed by the FPD-8010E software (Fujifilm), which converts the colour density on each film in pressure values. In this study, the pressures exerted by an active aligner that produces an orthodontic movement of a central upper incisor are registered. Measurements are made by positioning for 2 minutes the pressure films between the aligner and the cast of the patient's upper dental arch. The results show the average values of the pressures exerted and the contact areas through which the forces are transmitted from the aligner to the tooth.
B0010 Session 1 Presentation 2 (16:00-16:15)	Micro Disposable Biometric Authentication - An Application Using Fingernail Minute Textures for Nonsensitive Services - **Genki Sugimoto**, Masahiro Fujita, Yuto Mano, Tetsushi Ohki and Masakatsu Nishigaki Shizuoka University, Japan *Abstract*—Recently, biometric authentication has been applied to not only sensitive services such as in emigration/ immigration inspection systems and ATMs but also nonsensitive services such as entry/exit

	management systems of theme parks or coin lockers. However, biometric authentication requirements for sensitive and nonsensitive services differ; each service requires suitable biometric authentications. In this paper, disposable micro biometric authentication using minute fingernail texture for nonsensitive biometric authentication is proposed.
B2014 Session 1 Presentation 3 (16:15-16:30)	Estimating Invasion Time in Real Landscapes **Daniyah A. Aloqalaa**, Jenny A. Hodgson, Dariusz R. Kowalski and Prudence W.H. Wong University of Liverpool, UK *Abstract*—Species are threatened by climate changes, unless their populations have the ability to invade landscapes to search for new regions of suitable climate and conditions. It is therefore of utmost importance for ecologists to estimate the invasion time, as it is a crucial parameter used for environmental planning and may even determine survivability of the species. From a computational perspective, estimating the invasion time by running simulations is very time consuming, as the full model is based on a Markov Chain of exponential number of states with respect to the landscape size; therefore, in practice, this method is not suitable especially in case of frequent environmental changes or for environmental planning. In this paper, we propose a new way to estimate the time of invasion process using a powerful computational approach based on conductance and network flow theory. More specifically, wegive a new formula for estimating the invasion time using a combination of network flow methodologies, and prove asymptotic bounds on the quality of the obtained approximation. The proposed approach is analyzed mathematically and applied to real heterogeneous landscapes of the United Kingdom to estimate the duration of the process; the theoretical bounds obtained are compared with simulation results. The evaluations of the proposed approach demonstrate its accuracy and efficiency in approximating the invasion time.
B0025 Session 1 Presentation 4 (16:30-16:45)	Development of an Electromagnetic Tracking System for Surgical Instruments Positioning Filippo Attivissimo, Attilio Di Nisio Anna Maria Lucia Lanzolla, **Sergio Selicato** and Pietro Larizza Polytechnic University of Bari, Italy *Abstract*─Electromagnetic tracking systems are widely used in image-guided surgery to detect the position of surgical instrument in the patient's anatomical 3D model. The present study proposes the development and evaluation of a new EMTS able to provide a wide tracking volume. The innovation of this EMTS mainly consists in the design of a suitable Field Generator (FG), including five coils properly arranged in order to increase the magnetic field and, as a consequence,

	the sensor sensitivity in the working volume. Different methods to convert sensor voltage values in the Cartesian coordinates were investigated and compared in term of position accuracy. The results of experimental tests show good performances of the developed system that allows to increase the distance between sensor and FG with respect to currently EMTS on markets, ensuring a high accuracy of the measurement.
B1003 Session 1 Presentation 5 (16:45-17:00)	3D Deformation Analysis of Cardiac Walls from MRI Images **L. Lamberti**, C. Pappalettere and C.A. Sciammarella Politecnico di Bari, Italy *Abstract*—Three-dimensional deformation analysis of human organs is very important from both diagnostic and therapeutic point of view. For example, comparing the deformation field in healthy and pathologic cardiac walls during the systolic phase allows early and accurate information on the onset of heart diseases to be obtained. MRI tagging is utilized in medicine to visualize with a great deal of detail the structure and morphology of tissues. By exciting atomic nuclei in the tissue and by exploiting the phenomenon of nuclear magnetic resonance, MRI can image tissues with different consistency and mechanical properties. By modulating magnetization it is possible to inscribe lattice-patterns in the tissue volume. These lattices are fixed to underlying tissues for periods of time long enough to follow a cardiac cycle. This presentation will outline image processing techniques to extract 3D information on displacements and strains of heart walls from MRI tagging patterns. The nonlinear strain tensor is determined and diagonalized in order to determine the direction of principal strains.
B1002 Session 1 Presentation 6 (17:00-17:15)	Machine Learning and DSP Algorithms for Screening of Possible Osteoporosis Using Electronic Stethoscopes **Jamie Scanlan**, Francis F. Li, Olga Umnova, Gyorgy Rakoczy and Nóra Lövey University of Salford, United Kingdom *Abstract*—Osteoporosis is a prevalent but asymptomatic condition that affects a large population of the elderly, resulting in a high risk of fracture. Several methods have been developed and are available in general hospitals to indirectly assess the bone quality in terms of mineral material level and porosity. In this paper we describe a new method that uses a medical reflex hammer to exert testing stimuli, an electronic stethoscope to acquire impulse responses from tibia, and intelligent signal processing based on artificial neural network machine learning to determine the likelihood of osteoporosis. The proposed method makes decisions from the key components found in the time-frequency domain of impulse responses. Using two common pieces of clinical apparatus,

	this method might be suitable for the large population screening tests for the early diagnosis of osteoporosis, thus avoiding secondary complications. Following some discussions of the mechanism and procedure, this paper details the techniques of impulse response acquisition using a stethoscope and the subsequent signal processing and statistical machine learning algorithms for decision making. Pilot testing results achieved over 80% in detection sensitivity.

Session 2

Tips: The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

Morning, October 12, 2018 (Friday)

Time: 11:00-12:45

Venue: Aula Magna Orabona

Session 2: Topic: "Medical Image Processing"

Session Chair: Prof. Andrey S. Krylov and Dr. Giovanna Capurso

B0006 Session 2 Presentation 1 (11:00-11:15)	3D Detection of Spheric and Aspheric Femoral Heads in Coronal MR Images of Patients with Legg-Calve-Perthes Disease Using the Spherical Hough Transform **Abbas Memiş**, Songül Albayrak and Fuat Bilgili Yıldız Technical University, Turkey *Abstract*—This paper presents a study of 3D femoral head detection in coronal magnetic resonance (MR) imaging sequences to detect the spheric and aspheric femoral heads using the Spherical Hough Transform (SHT). Shape structure and functionality of the femoral head can be affected by a wide range of hip disorders. In most of the computerized analysis and assessment cases of the hip joint, segmentation of the proximal femur and femoral head is performed on the image sequences that are provided by the several medical imaging modalities. Determination of initial points, detection of the tissue boundaries and segmentation of the tissues are important challenges in automatic or semi-automatic proximal femur segmentation methods. In this paper, we aimed to perform a preliminary study based on 3D femoral head detection in bilateral MR hip images in coronal plane of patients with Legg-Calve-Perthes disease (LCPD). Firstly, MR sections are divided vertically into two equal halves automatically to separate the healthy and pathological hip joints and then Canny's edge detection method is performed to obtain edge images. Finally, 3D SHT is performed to detect the spherical structure of femoral heads. Automatic detection of the femoral head with SHT provides a starting point for the segmentation of the femoral head ball and proximal femur. Furthermore, it also allows for 3D segmentation of the femoral head sphere with the radius information that it provides with the 3D sphere center coordinates. Performance evaluations and experimental results observed on 8 bilateral MR imaging sequences belong to 6 subjects show that proposed method has

	promising results.
B0008 Session 2 Presentation 2 (11:15-11:30)	Non-Informative Frame Classification in Colonoscopy Videos Using CNNs ABM Rezbaul Islam, Ali Alammari1, **JungHwan Oh**, Wallapak Tavanapong, Johnny Wong and Piet C. de Groen University of North Texas, U.S.A. *Abstract*—In the US, colorectal cancer is the second leading cause of cancer-related deaths behind lung cancer, causing about 49,000 annual deaths. Colonoscopy is currently the gold standard procedure for colorectal cancer screening. However, recent data suggest that there is a significant (4-12%) miss-rate for the detection of even large polyps and cancers. To address this, we have been investigating an ‘automated feedback system’ which measures quality of colonoscopy automatically by analyzing colonoscopy video frames in order to assist the endoscopist to improve the quality of the actual procedure being performed. One of the fundamental steps analyzing colonoscopy video frames for the automated quality feedback system is to distinguish non-informative frames from informative ones. Most methods to detect and classify these non-informative frames are based on the hand-engineered features. However, it is very tedious to design optimal hand-engineered features. In this paper, we explore the effectiveness of Convolutional Neural Network (CNN) to detect and classify these non-informative frames. The experimental results show that the proposed approaches are promising.
B0009 Session 2 Presentation 3 (11:30-11:45)	Segmentation of Femoral Cartilage with a Hybrid Method Combining Voxel Classification and Active Appearance Models **Ceyda Nur Öztürk** and Songül Albayrak Uludağ University, Turkey *Abstract*—In this paper a hybrid segmentation method was proposed for delineation of the femoral cartilage compartment in knee MR images. A formerly developed voxel classification-based segmentation system was combined with an active appearance model (AAM) based segmentation system with an aim to solve the oversegmentation problems of purely classification-based approaches. The voxel classification-based segmentation was achieved through region-growing of sampled voxels depending on one-versus-all classifiers that used approximate nearest neighbour algorithm. Before the appearance model construction, dense set of correspondences were determined on the surfaces of cartilage atlases in 10 training MR images through an iterative shape-context-based non-rigid registration approach. Then, the appearance models for femoral cartilage compartment was constructed either using all of 10 training atlases or grouping these atlases as large and small depending on the physical examination information of the

	participants. The experimental analyses involved a comparative evaluation of the accuracies of these different AAM-based segmentations both individually and in combination with the voxel classification-based segmentations in 23 testing MR images as well as assessment of the misclassifications of the former segmentation system. As a result, the correspondence finding procedure worked successfully on the training atlases, and the hybrid segmentations with grouped appearance models achieved the closest accuracies to those of the voxel classification-based segmentation. The hybrid segmentations with appearance models that depended on the patient-specific information were evaluated as the most likely method to improve the segmentation accuracies with removal of oversegmented cartilage compartments in the case a more advanced information fusion procedure is adapted in the future.
B0018 Session 2 Presentation 4 (11:45-12:00)	Lung Segmentation Using a Fully Convolutional Neural Network with Weekly Supervision **Yuan Huang** and Fugen Zhou Beihang University, China *Abstract*—Most supervised methods for lung CT image segmentation require all training examples to be labeled with segmentation masks. This requirement makes it expensive to annotate varies categories of lung diseases. The goal of this paper is to propose a new weekly supervised training scheme, together with a lung patch feature extraction method, that enables training segmentation models on a large set of self-generated texture mosaics images, but only a small fraction of which have mask annotations. Such feature ex- traction is implemented by the empirical wavelet transform (EWT) followed by a fully convolutional neural network which consists of the final segmentation step. A generative adversarial networks (GAN) based partial supervised learning is also utilized to further refine the correction of the segmentation result. Our method deals with lung segmentation issue under normal or severe pathological conditions. The proposed method is tested on two public datasets and our experiment results without heavy work of mask annotations give similar results compared with the approach with fully labeled mask.
B0011 Session 2 Presentation 5 (12:00-12:15)	Three-Dimensional Reconstruction of Cardiac Structures Using CT Images Luis Lopez Diaz, Andersson Contreras Olmos, Alberto Cadena, Winston S. Percybrooks and **Juan Pablo Tello P.** Universidad del Norte, Colombia *Abstract*—This paper describes a software tool for building and displaying tri-dimensional cardiac structures from a sequence of Computer Tomography (CT) scan images. The development process

	followed for this work can be divided into 5 stages. During the first stage, suitable DICOM images are selected from a CT scan machine. In the second stage, the images are pre-processed in order to reduce noise levels and enhance relevant features. The third stage compares the performance of three image segmentation methods on the pre-processed images: Region growing, Otsu's algorithm and active contours. It was found that active contours achieves the best isolation of the Region of Interest (ROI), while the other two methods recognized morphological structures outside of the ROI. In the four stage, a 3D image of the ROI is renderized. Finally, the reconstructed 3D model is visualized in stage five using a custombuilt Graphical User Interface (GUI). The resulting 3D models are validated by visual inspection by three heart and imaging experts, which determine if the model is suitable for use in diagnosis or surgery planning.
B0021 Session 2 Presentation 6 (12:15-12:30)	Tissue Region Growing for Hispathology Image Segmentation **Zhaoyang Xu**, Carlos Fernádez Moro, Danyil Kuznyecov, Béla Bozóky, Le Dong and Qianni Zhang Queen Mary University of London, UK *Abstract*—The accurate identification of the tumour tissue border is of crucial importance for histopathology image analysis. However, due to the high morphology variance in histology images, especially in border regions where cancer tissue interfere into the normal region, it is challenging even for the pathologists to define the border, not to say for the machine. In this paper, we present an innovative framework to semantically segment the tumour border area in colorectal liver metastasis (CRLM) on pixel level by integrating the features from deep convolutional networks with spatial and statistical information of the cells. With annotations from the pathologists, a two-level deep neural network including a cell-level model and a tissue-level model, is trained to classify patches from the whole slide scan image. Based on the prediction of trained models, a growing-style algorithm is proposed to finalize the segmentation by leveraging the statistical and spatial properties of the cells. Evaluated against the ground truth created by the experts, the framework demonstrates a significant improvement over a conventional deep network model on the cell-level model or the tissue model alone.
B0017 Session 2 Presentation 7 (12:30-12:45)	ECG Biometrics Using Spectrograms and Deep Neural Networks Nuno Bento, **David Belo** and Hugo Gamboa Nova University of Lisbon, Portugal *Abstract*—The Electrocardiogram (ECG) is considered as a physiological signature and has previously been used for biometric purposes. The contamination of the signal due to noise adds undesired intra-variability

	in the ECG signals, creating the need for more robust biometric systems (BSs). With the increase of interest in the application of Deep Neural Networks (DNN) to the medical field, new solutions are also being explored in the identification and authentication of individuals. The proposed architecture exploits the potential of Convolutional Neural Networks (CNN) to identify healthy subjects using temporal frequency analysis, i.e. spectrograms.

Session 3

Tips: The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

Afternoon, October 12, 2018 (Friday)

Time: 14:00-15:45

Venue: Aula Magna Orabona

Session 3: Topic: "Bioinformatics and Computational Biology"

Session Chair: Prof. Carmine Pappalettere and Prof. Luciano Lamberti

B1005 Session 3 Presentation 1 (14:00-14:15)	Effect of Low Intensity Ultrasounds on MG-63 Osteosarcoma Cells **C. Pappalettere**, L. Lamberti, C. Cianci, L. Lo Muzio, G. Illuzzi, V. C. A. Caponio and D. Ciavarella Politecnico di Bari, Italy *Abstract*—Currently available therapies for the treatment of osteosarcoma are not really effective and moreover they result harmful for the whole organism. The present work investigates the interaction between low-intensity ultrasound and the MG-63 osteosarcoma cell line, in order to verify the possibility of defining an alternative therapy able to act selectively on tumor cells. In the first part of the study cells were cultured in 60 mm Petri dishes and then each of them was sonicated for 180 seconds at a different selected frequency (400, 510, 582, 800 and 1000 kHz), with the aim of identifying the frequencies able to cause the highest number of dead cells after sonication. After treatment, the count of live and dead cells was performed for each Petri dish using a TC20 Cell Counter. The frequencies of 800 and 1000 kHz determined the highest cell death rates. Subsequently, these two frequencies were used for further sonication experiments, and the related after sonication cell growth curves were obtained using an xCELLigence Real Time Cell Analysis Instrument. Finally, the behavior of cells during sonication and the subsequent hour was observed in time lapse using an EVOS FL Cell Imaging System microscopy.
B3003 Session 3 Presentation 2 (14:15-14:30)	Identification of a Gene-Expression Signature able to Predict Recurrence in Patients with Head and Neck Squamous Cell Carcinoma **Giuseppe Troiano**, Lorenzo Lo Muzio and Crescenzio Gallo University of Foggia, Italy *Abstract*—Head and neck cancer (HNC) is the sixth most common type of cancer worldwide and accounts for approximately 550,000 new cases

	annually. The 5-years survival rate of HNC patients is about 50% and has shown little improvement in the last decades. The present study attempts to find a gene expression signature able to predict the onset of a second tumor event after initial total remission in HNC patients. In particular, the present work is based on the elaboration of the expression profiles of 60483 genes available in the public dataset The Cancer Genome Atlas (TCGA) for the Head and Neck section. From such database, we downloaded data of gene expression of about 546 samples (the data of each sample are contained in two files of type “bed” and “meta”), obtaining a two-dimensional table of 546 rows (samples, identified by the relative barcode) and 60483 columns (genes, identified by the relative symbol). 91 samples were selected from the initial 546 with relapse data (total remission after the first surgery) constituting a new target binary variable (NO/YES) subject to prediction, added to the 60483 features constituted by genes. After a differential expression analysis and subsequent rank through FCBF (Fast Correlation-Based Filter, a 9-gene expression signature was selected. On the basis of such features, we proceeded to set some models of classification (prediction) of the values of relapse. In particular, we used the machine learning methods kNN (k-nearest neighbors), Neural Network, Random Forest, SVM (Support Vector Machine) and Naïve Bayes. These models were validated through the leave-one-out method, which showed as best classifiers the Naïve Bayes algorithms (with AUC [Area Under ROC Curve] equal to 0.856, CA [Computed Accuracy] = 0.802 and F1 [Precision+Recall index] = 0.790) and Neural Network (AUC=0.840, CA=0.846 and F1=0.841).
B2003 Session 3 Presentation 3 (14:30-14:45)	Looking at Alzheimer’s Disease Using Enhanced Algorithm for Feature Collection **Kefaya Qaddoum** Higher colleges of Technology, UAE *Abstract*—Machine learning technology has taken substantial leaps in the past few years. From the rise of voice recognition as an interface to interact with our computers to self-organizing photo albums and self-driving cars. Neural networks and deep learning contributed significantly to drive this revolution. Biomedicine is one of the research areas that have yet to fully embrace the possibilities of deep learning. The ability to learn hierarchical features makes deep learning models highly applicable to biomedicine and researchers have started to notice this. Deeper understanding can be enabled by the hierarchical features that marked in deep models. This paper explores the use of neural networks and deep learning models for the qualitative assessment of biomedical datasets using a non-iterative, data feature collection algorithm to preserve original features and provide qualitative analysis on their importance. This algorithm is employed in numerous areas including

	Pima Indian diabetes and children tumor detection. The learning coefficients found to contain clinically significant features. When combined, in a hierarchical way, these features reveal useful insights for the evaluation of treatment effectivity.
B2006 Session 3 Presentation 4 (14:45-15:00)	Deep Neural Network for Classification and Prediction of Oxygen Binding Proteins **Soumiya Hamena** and Souham Meshoul University Abdelhamid Mehri Constantine 2, Algeria *Abstract*—The accurate annotation of a protein function is important for understanding life at molecular level. Nowadays, powerful high throughput proteomics technologies provide an unprecedented understanding of the human biology and disease. These technologies are generating a deluge of protein sequences available in public databases. However, a critical challenge in making sense of these sequences is the assignment of functional roles to newly discovered proteins. The approaches proposed to address this problem use a variety of biological information, such as amino acid sequence, gene expression and protein-protein interaction. By another way, deep learning has emerged as the innovation of this last decade as it uses deep architectures to learn representations of high level entities and creates an improved functional space. In this paper, we propose an approach that proposes a deep neural network to achieve classification of oxygen binding proteins using amino acid composition for protein function prediction. Two alternatives are investigated. The first one casts the tackled problem as a multiclass classification problem and the second one as a binary classification problem. The validation of the approach is achieved using Keras platform and very promising and encouraging results that outperform other state of the art results have been obtained.
B2007 Session 3 Presentation 5 (15:00-15:15)	Computational Techniques for Analysis of Spatial Time Series on Fish Species Catch Quantity in Greece **Kolyo Onkov** and Georgios Tegos Agricultural University, Bulgaria *Abstract*—This paper is based on a Multidimensional Fishery Time Series Database of Greece that stores spatial, biological, temporal, technical and economic data extracted from National Statistical Service of the country. Time series on fish species catch quantity are aggregated in order to form the spatial data on three levels: total, fish region and fish area. It provides consistent view of the spatial distribution of fish species catch quantities and allows a multi-scale analysis performance. Computational procedure and software techniques based on intersection of datasets are developed to extract specific features of catch by fish regions, areas and species, as well. Four case studies present analytical

	capabilities of computational techniques in order to find out significant differences and similarities on fish species catch by regions and by areas. This paper illustrates the use of public information sources on exploitation of natural resources for scientific analysis.
B2009 Session 3 Presentation 6 (15:15-15:30)	Computational Study of Phosphatidylinositol-Dependent Membrane Localization of Toll/interleukin 1 Receptor Domain-Containing Adaptor Protein **Mahesh Chandra Patra** and Sangdun Choi Ajou University, South Korea *Abstract*—The Toll/interleukin 1 receptor (TIR) domain-containing adaptor protein (TIRAP) regulates Toll-like receptor (TLR)2, TLR4, TLR7, and TLR9 signaling pathways. TIRAP anchors to phosphatidylinositol (PI) 4,5-bisphosphate (PIP2) on plasma and PI (3,4,5)-trisphosphate (PIP3) on endosomal membranes. To date, the structure and mechanism of action of TIRAP are elusive. Here, we constructed a full-length TIRAP dimer using computational approaches. Molecular dynamics simulations revealed that PIP2 forms a stable microdomain for TIRAP in the dipalmitoylphosphatidylcholine bilayer. Calculated binding free energy suggest that the PI-binding domain (PBD) has greater affinity toward PIP2 and that the PI-binding motif (PBM) is crucial for PBD’s affinity for PIP2. Four PIP2 molecules can bind to distinct lysine-rich patches on the PBM. Along with the known PI-binding residues (K15, K16, K31, and K32), the residues K34, K35, and R36 interact strongly with PIP2. Alanine mutation of PI-binding residues reduced TIRAP's affinity for PIP2; however, K34, K35, and R36 interacted with PIP2 through hydrogen bond (H-bond) and electrostatic interactions. TIRAP had a PIP2-like interaction with PIP3 through H-bonds involving K34, K35, and R36. The present study enables us to understand the mechanism of TIRAP's membrane association that is useful for designing peptide-drugs for TLR2-, TLR4-, TLR7-, and TLR9-mediated autoimmune diseases.
B0014 Session 3 Presentation 7 (15:30-15:45)	Optical Device for Dental Elements 3D Shape Measurement **Giovanni Pappalettera**, Caterina Casavola, L. Lamberti and Carmine Pappalettere Politecnico di Bari, Italy *Abstract*─In this work considerations about designing an optical device for endoral contouring of teeth elements will be presented. The proposed approach has the potentiality to get high accuracy information about the shape of the analyzed dental elements. The process becomes, at the same time, less connected with the ability of the operator and it makes the patient more comfortable. The proposed system is mainly based on the fringe projection approach. In this specific case, the Young's interference

	from two adjacent fibers is adopted to generate the required fringe pattern. The phase of the pattern deformed by the surface under analysis contains information about the shape of the surface itself. However, to manage complex surfaces, hierarchical unwrapping is required. In this paper an innovative approach based on fringe contrast analysis is presented. Results obtained on calibrated specimens and 3D models of dental elements confirm the validity of the proposed approach

15:45-16:05	**Coffee Break**

Session 4

Tips: The schedule for each presentation is for reference only. In order not to miss your presentation, we strongly suggest that you attend the whole session.

Afternoon, October 12, 2018 (Friday)

Time: 16:05-18:05

Venue: Aula Magna Orabona

Session 3: Topic: “Biosignal Acquisition and Analysis”

Session Chair: Prof. Kolyo Onkov and Dr. Floriano Scioscia

B0007 Session 4 Presentation 1 (16:05-16:20)	ECG Monitoring and Anomaly Detection Based on Compressed Measurements **Alessandra Galli**, Claudio Narduzzi and Giada Giorgi University of Padova, Italy *Abstract*—Long-term monitoring systems based on wearable devices and local devices with computational capabilities -smartphone, smartwatch- could be used in the prevention of cardiovascular disease in risk subjects or during the follow-up for increasing the quality of life. In this paper we propose a lightweight solution that firstly exploits compressive sensing for locally reducing the amount of raw data, and successively employs a detection algorithm operating directly on the compressed domain for extracting only meaningful information to send at the medical staff. Performances of the proposed solution have been assessed under different conditions. Results show that the algorithm is able of identifying with a good precision and sensitivity the ECG features -QRS complexes and T, P waves- even with high compression ratios of about 20−50%.
B0013 Session 4 Presentation 2 (16:20-16:33)	Identification of Auditory Event-Related Potentials Using a Combination of Principal Component Analysis and Kalman Filtering Kevin Paulson and **Othman Alfahad** University of Hull, United Kingdom *Abstract*—The aim of this paper to develop a new method for separating auditory event-related potentials (ERP) signal from artefacts or noise. In experimental conditions, ERPs can be approximated by weighted sums of Principal Component Analysis (PCA) basis signals calculated from clean data. Projection of measured signals onto the PCA subspace significantly decreases noise. Furthermore, Kalman filtering has been used to optimize the combining of the PCA filtered signal with an a priori expected ERP. The main strength of the proposed algorithm arises

	from manipulating a priori cross-channel information in the form of a PCA weight covariance matrix. Here, the implementation of the method has been quantified using synthetic multi-channel ERP signals to which known amounts of synthetic noise is added to all the channels. The use of synthetic data means and signal and noise are known and so signal-to-noise enhancement may be quantified. For a wide range of initial SNRs, PCA filtering increases SNR by 10 dB and Kalman filtering yields an additional 10 dB improvement.
B0019 Session 4 Presentation 3 (16:35-16:50)	Decoding Imagined Hand Movement in Three-Dimensional Space Using Electrocorticographic Signals in Humans **Sang Jin Jang** and Jaeseung Jeong Korea Advanced Institute of Science and Technology (KAIST), South Korea *Abstract*—Decoding brain signals to predict hand movements allows a brain-computer interface (BCI) that can serve as assistive technology. While brain activity during real movements have been shown to be highly informative of movement, predictability of brain signals during imagined movements have been commonly underestimated. This study attempts decoding of electrocorticographic (ECoG) motor imagery brain signals recorded during reach-and-grasp movements of two epileptic patients and show that reconstruction of continuous hand trajectory is highly possible. Signals were preprocessed to extract spectral power and amplitude modulations. These features were used in multiple linear regression to predict hand trajectory. Peak decoding accuracies up to 0.4 (Pearson's correlation coefficient) were achieved for amplitude and power modulations in the beta band. Also, informative signals were not limited to the confines of the motor cortex and originated from other brain areas, suggesting that motor imagery may involve neural mechanisms beyond the motor and parietal regions.
B0020 Session 4 Presentation 4 (16:50-17:05)	Decoding Electrocorticography Signals of the Arm Movement Using Echo State Networks **Hoon-Hee Kim** and Jaeseung Jeong Korea Advanced Institute of Science and Technology (KAIST), South Korea *Abstract*—Electrocorticography(ECoG) is an invasive method for monitoring brain signals and is used in many clinical applications. The aim of this study is to suggest new methods for decoding ECoG signals. To design the decoder we made neural networks which followed echo state networks(ESN) paradigm. ESN have input, reservoir and readouts layers. Each weight of the inputs and reservoir are randomly initialized and fixed. The readouts linearly connected to the reservoir and the weights were trained by linear learning algorithms. We recorded ECoG

	signals when subjects carried out a arm reaching task. The decoder had three readouts which represented x, y, z arm positions. The correlation between readouts and arm position exceeded 0.6 and classification performance for target positions were over 70%. However, formal support vector machine showed a correlation less than 0.5 and classification performance less than 60%. These results show that ESN are a useful method for decoding ECoG.
B0024 Session 4 Presentation 5 (17:05-17:20)	Long-Term Sleep Assessment by Unobtrusive Pressure Sensor Arrays **S. Soleimani Gilakjani**, M. Bouchard, R. A. Goubran and F. Knoefel University of Ottawa, Canada *Abstract*─Due to a globally aging population, there is a growing demand for smart home technology which can serve to monitor the health and safety of older adults. Sleep monitoring has emerged as a crucial element of this monitoring. While polysomnography (PSG) is an effective and accurate tool for sleep monitoring, it is obtrusive as the user must wear the instruments during the experiment. Therefore, there has been a growing interest in deploying unobtrusive sleep monitoring devices, specifically for long-term patient monitoring. This paper performs a comprehensive investigation on long-term sleep pattern changes by investigating bed occupancy, number of bed exits during day and breathing rate variability. Measurements were made using unobtrusive pressure sensitive sensor arrays on data captured from several participants collected in a long-term basis, which provided a large volume of data. Multiple algorithms are proposed that can be described as movement detection, sensor data fusion and bed occupancy detection. The methods developed in the paper and the related findings can be of interest for future clinical remote patient monitoring systems.
B2002 Session 4 Presentation 6 (17:20-17:35)	Noninvasive Prediction of Atrial Fibrillation Recurrence Based on a Deep Learning Algorithm **Zhangjun Li**, Cuiwei Yang and Qingzhou Zhang Fudan University, Shanghai, China *Abstract*—Atrial fibrillation (AF) is an abnormal heart rhythm. The goal of radiofrequency ablation for AF is to regain a normal heart rhythm. Presently, the commonly used algorithms for prediction of AF recurrence face constraints such as no flexible feature selection and optimization. Deep learning algorithm, such as convolutional neural networks (CNN), can overcome these drawbacks by calculating features automatically. This study presents a noninvasive ECG-based approach with deep learning algorithm to predict AF recurrence according to preoperative AF signals of 14 patients. The features of cardiac activity can be extracted from the convolution neural network and then fed to multilayer perceptron (MLP) for classification. We have evaluated the result by

	measuring accuracy (ACC), sensitivity (SE) and specificity (SP). In the meantime, the optimal CNN combination of parameters are showed in a table. Our proposed method has shown good merits with ACC of 93.14%, SE of 83.5% and SP of 95.99%. It can be concluded that BSPM would contain more potential information because of its wide range of spatial coverage compared with traditional signal acquisition system, and the deep learning algorithm of CNN has more advantages in feature extraction for prediction of AF recurrence.
B2020 Session 4 Presentation 7 (17:35-17:50)	From Biosignals to Affective States: a Semantic Approach Floriano Scioscia, **Michele Ruta** and Eugenio Di Sciascio Polytechnic University of Bari, Italy *Abstract*—The final goal of Affective Computing is in allowing to recognize human emotional states by means of automatic procedures. Possible scenarios range from enhancing the human-machine interaction to biofeedback generation devoted to the improvement of a cognitive state and the wellbeing of a generic subject. In the same way, it is warmly welcome to adopt these techniques and tools to reduce potential risks the same subjects are exposed to. Despite scientific literature evidences the concrete usefulness of possible approaches based on biosignals analysis to detect and correclty classify emotions, existing systems and tools are generally too invasive for common subjects and in addition they are too intensive in terms of needed processing. Basically, they refer to common architectures supporting the processing of conventional biological data, extracted through complex sensing interfaces. This processing activity reveals distinguishing elements (also named *features*) of physiological signals by applying data mining and machine learning techniques for emotion classification. That procedures have a not negligible impact on computational resources. Hence, practical application and effectiveness of such kind of solutions is really limited to laboratory-controlled contexts and this seriously compromises their porting in real scenarios. Starting from such state of the art, this paper describes a novel wearable cyber-physical system based on a Wireless Body Area Network (WBAN) for emotion detection and classification. It is composed by: 1. A multi-sensing architecture able to measure most relevant bio-signals for emotion identification and dynamic tracking during given intervals. 2. A processing sub-system hosting a software multi-agent able to annotate physical signals in a high-level formalism for knowledge representation based on description logics and executing semantic-based inferences devoted to recognize emotions effectively.

	These peculiarities allow for making autonomous and independent such system from physical characteristics of the operating environment where it operates to reach a minimum invasiveness goal, so making the system itself suitable for a daily life adoption. The proposed system is also able to attempt an improvement of the emotional status of a user by identifying a feedback signal (physical stimulus), useful in orienting his/her physical and psychic wellbeing in an automatic fashion. Feasibility of the proposed approach has been evaluated by means of tests carried out on a reference synthetic dataset: effectiveness of emotion detection has been evaluated along with the needed computational complexity in sigh of a possible implementation on a fully mobile testbed.
B0022 Session 4 Presentation 8 (17:50-18:05)	Automatic Sleep Stage Classification with Multiclass Support Vector Machines Using Forehead and In-Ear EEG Electrodes **Dong-Hwa Jeong**, Pyeong Soo Kim, Jeungmin Lee and Jaeseung Jeong Korea Advanced Institute of Science and Technology (KAIST), South Korea *Abstract*—Sleep stage classification is essential to assessing the sleep quality. However, conventional sleep staging techniques using polysomnography (PSG) are difficult to use in daily life; inconvenience of wearing PSG electrodes and heavy work load of manual scoring. In this study, automatic sleep stage classification using simple and dry EEG electrodes is suggested. Forehead, in-ear EEG and PSG signals were obtained from 10 subjects. Well-trained experts manually scored sleep stages into five classes (wake, rapid-eye movement (REM), N1, N2, and N3&N4) using PSG data. Multi-class support vector machines (SVM) were trained with EEG features including filter-bank based amplitude modulation (AM), power spectral density (PSD), and approximate entropy (ApEn). In addition, the probability based post correction algorithm was developed for smoothing staging results. The classification accuracy of leave-one-out tests was successfully obtained when using forehead and in-ear EEG electrodes. These electrodes could be applied to eye mask- and ear plug-shaped wearable devices during sleep.

Poster Session

October 12, 2018 (Friday)

Time: 9:00-18:00

Venue: Museo della Fotografia

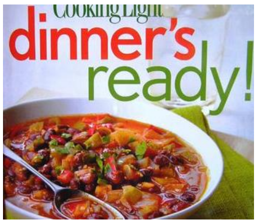
B0002 Poster 1	Comparing the Performances of PCA (Principle Component Analysis) and LDA (Linear Discriminant Analysis) Transformations on PAF (Paroxysmal Atrial Fibrillation) Patient Detection **Safa Sadaghiyanfam** and Mehmet Kuntalp Dokuz Eylül University, Turkey *Abstract*—Linear Discriminant Analysis (LDA) and Principle Component Analysis (PCA) are offered schemes for feature extraction and dimension reduction. They have been used extensively in many applications involving high-dimensional data. In this study, we compared the effectivity of features obtained from PCA and LDA for the diagnosis of Paroxysmal Atrial Fibrillation (PAF) from normal sinus rhythm (NSR) ECG records. Within this framework, a set of features obtained from PCA and LDA were used as an input to the same classification algorithm, which is chosen as the K-Nearest Neighbor (kNN) Algorithm. The obtained results elicit that LDA features have better discrimination capability than those obtained from PCA.
B0003 Poster 2	Effects of Different Nail Polish Colors on Arterial Blood Oxygen Saturation Values (SpO2) in Pakistani Population Ameena Haq, Kainat Zafar, **Mashal Fatima** and Muhammad Shafique Riphah International University, Pakistan *Abstract*—Pulse oximetry measures arterial oxygen saturation level (SpO2) in the blood. Low SpO2 value are associated with conditions such as hypothermia, hypoxemia, vascular dysfunction and other respiratory disorders. Although, it has been reported earlier that nail polish effects SpO2 values and gives inaccurate readings, most of these experiments were conducted in Europe and the U.S. Since accuracy of pulse oximeter is affected by the skin color, such results need to be verified in other regions of the world due to the variety in skin pigments amongst different population. The objective of this study was to determine the extent of effect which different colors of nail polish causes on SpO2 values in Pakistani population. Data was acquired from sixty four (64) healthy female volunteers (age=22+4 years). Six different nail polish colors black, blue, red, purple, yellow and green were used. The Masimo (SET) pulse oximeter was used to obtain SpO2 readings.

	Significant difference was found between nail polished fingers as compared to finger nails without nail polish. The variation in mean values is observed more on dark colors (<9%). Medium colors gave slight differences (<6%). Light colors gave no significant difference (<3%). Results from ANOVA test showed significant difference between the fingers SpO2 values of non-polished versus all polished nail fingers.
B0005 Poster 3	Automatic Segmentation of HEp-2 Cells Based on Active Contours Model **Donato Cascio**, Vincenzo Taormina and Giuseppe Raso University of Palermo, Italy *Abstract*—In the past years, a great deal of effort was put into research regarding Indirect Immunofluorescence techniques with the aim of development of CAD systems. In this work a method for segmenting HEp-2 cells in IIF images is presented. Such task is one of the most challenging of automated IIF analysis, because the segmentation algorithm has to cope with a large heterogeneity of shapes and textures. In order to address this problem, numerous techniques and their combinations were evaluated, in a process aimed at maximizing the figure of merit. The proposed method, for a greater definition of cellular contours, uses the active contours in the last phase of the process. The initial conditions, center position and initial curve of the active contour, were obtained using a randomized Hough transform for ellipse; the idea in identifying cells was to approximate them initially to ellipses. The purpose of the active contours, within the segmentation process, is to allow the separation of connected regions (such as two overlapping cells), in order to obtain a better definition of the objects to be analyzed (the cells). Our system has been developed and tested on public database. Segmentation performances were evaluated in terms of Dice index and the method was compared with other state-of-the-art workers. The results obtained demonstrate the goodness of the method in the characterization of HEp-2 cells. The developed method shows great strength and convergence speed. Furthermore, the flexibility of the proposed method allows it to be easily used in other biomedical contexts.
B2011 Poster 4	Using the SVM method for Lung Adenocarcinoma Prognosis Based on Expression Level **Tianqin Li**, Mingzhe Hu and Liao Zhang Sun Yat-Sen University, China *Abstract*—Lung cancer is the deadliest cancer in the word, leading to over a quarter of death in the United States in 2017. Gaining precise information on cancer prognosis for patients would greatly benefit their decision making for further treatment plans. While previous studies tend to use histology information and genomic signatures for cancer

	prognosis, this study explores the possibility of using expression level alone to predict prognosis. Using over 200 patients from publicly available datasets with overall survival length and transcriptomic information, we use support vector machines to predict prognosis. Our result proves the effectiveness of such methodology, encouraging transcriptomic data to be collected for patients routinely if possible given the decreasing cost of RNA-Seq.
B2012 Poster 5	Properties for Hesitant Information Sets **Manish Aggarwal** and Madasu Hanmandlu Indian Institute of Management, India *Abstract*—The concept of information sets is inspired by the way we perceive information source values. However, they lack a provision to represent the hesitancy inevitably associated with the perceived values. To this end, recently the concept of hesitant information set (HIS) is proposed in the literature. In contrast to an information set that maps an information source value to a single perceived information value, HIS gives a set of multiple perceived information values for a single information source value. This paper explores HIS further for its properties.
B2016 Poster 6	The Impact of Malaria Disease Transmission from Mother to the Newborn on the Spread of Malaria with the Efficacy of Malaria Vaccine **Ghoul Rafia**, Jing He, Djaidja Sana and As-Shareef Ebrahim Hunan University, China *Abstract*—The main objective of this paper is to analyze dynamics of malaria disease transmission for the human and mosquito populations, by including the impact of malaria transmission from mother to baby before or during birth (vertical transmission) and investigating the effects of malaria vaccine to the human population. The appropriate model divides the human population into three classes and the mosquito population into two classes. The obtained 5-dimensional nonlinear system incorporates and includes the infection newborn and the impact of the vaccine. The study shows that the disease-free equilibrium is globally asymptotically stable if $R_0 < 1$ and the endemic equilibrium is locally asymptotically stable if $R_0 > 1$ proved by Routh- Hurwitz criterion. Our numerical simulations and graphical results conform to the analysis predictions.
B3001 Poster 7	Genome-wide Analysis of the Cytochromes P450 Gene Family in *Aspergillus Oryzae* Zehao Zeng, Qinqin Wu, **Bin He** and Bin Zeng Jiangxi Science & Technology Normal University, China

	Abstract—Cytochromes P450 gene family has been shown to play significant roles in various physiological processes of *Aspergillus oryzae*, including the growth and development, abiotic and biotic stress responses and stress signaling. In this study, the members of CYP gene family in *Aspergillus oryzae* were identified and analyzed on the whole genome level by means of bioinformatics. The phylogenetic tree, gene structure and motifs were analyzed. The results showed that 58 CYP gene family members were identified in *A. oryzae*. The expression analysis of AoCYP under different salt environments and at different growth stages showed the distribution of the expression in different variables. The results of this study will lay a theoretical foundation for the cloning of the members of the CYP gene family and the identification of their functions. It will also provide reference information for studying the growth stages and osmotic pressure regulation mechanism of *A. oryzae*.
B3002 Poster 8	Knowledge, Attitudes and Practices Towards Seasonal Influenza and Vaccine Among Private High School Students in Connecticut **Zhiqi Zhang** Suffield Academy, USA *Abstract*—Background: The United States suffered from its worst influenza season since 2009 during the winter of 2017-2018. High school is prone to influenza outbreak due to the high density of students and close social spaces. In order to understand the weak points of knowledge, attitudes and practices towards seasonal influenza and its vaccine among high school students, a cross-sectional questionnaire study was conducted in Connecticut. Methods: From March to May, 2018, a close-ended self-administered questionnaire with 24 multiple choice questions about the knowledge, attitudes and practices towards seasonal influenza and vaccine was distributed to all the enrolled students in Suffield Academy, Connecticut. The knowledge score was calculated for each student, which was compared across demographic categories. Factors associated with uptake of seasonal influenza vaccine were explored using multivariate logistic regression. Results: 60% of the students responded to the questionnaire, of whom 228 were included in analysis. The number of respondents was balanced across grades, of whom 10.5% were international students. The average knowledge score was 11.6±1.4 out of 14 points. The score of international students was significantly lower than that of domestic students ($p<0.001$). Only 56.6% of students recognized that flu might cause serious complications, and nearly 60% mistakenly believed flu could be transmitted by food or blood. Most students get their flu knowledge from school (68.4%), while other information sources like public media and internet were underused. 84.2% and 57.9% students

	believed in the safety and effectiveness of seasonal flu vaccine, while few students felt a high risk to get a flu or to develop into severe illness (25.4% and 9.6% respectively). Respondents showed good compliance to preventive behaviors like wash hands and avoid contact with patients, and 60.1% of them got the flu shot annually in the past 3 years. High knowledge scores (OR=1.34, 95% CI 1.05-1.72), high perceived vaccine safety (OR=4.01, 95% CI 1.60-10.00) and effectiveness (OR=2.37, 95% CI 1.26-4.45) were significantly associated with vaccine uptake behavior after adjusting for gender, grade and nationality. The main reason for no vaccination was afraid of the pain of injection, while financial cost was the least consideration. The most persuasive messages focused on the direct and indirect benefits of the vaccine. Conclusion: More knowledge of influenza and positive attitudes towards the safety and effectiveness of seasonal influenza vaccine are positive predictors for vaccine uptake. Students tend to underestimate the risk of infection and the severity of the illness, and have misconception on the transmission mode of influenza. Future health promotion activities should improve the weak points of knowledge and emphasize the benefits of vaccination, with more attention paid to international student study in the US.



Dinner	
18:05-20:00	**Restaurant**

Conference Venue

Polytechnic University of Bari, Bari, Italy

Addr.: Polytechnic University of Bari, Campus E. Quagliariello, Via Edoardo Orabona, 4, 70126 Bari BA, Italy

Map

Academic Tour

October 13, 2018 (Saturday) 9:00-18:00

(Tips: 1.Please arrive at Campus Hotel before 8:50 a.m. 2. The following places are for references, and the final schedule should be adjusted to the actual notice. 3. Lunch is on own expense)

Time	Specific Arrangement
Morning	Matera
Afternoon	Alberobello
17:30	Go back to Campus Hotel

Matera is a city in the province of Matera in the region of Basilicata, in Southern Italy. It is the capital of the province of Matera and the capital of Basilicata from 1663 to 1806. The town lies in a small canyon carved out by the Gravina.

Known as la Città Sotterranea ("the Underground City"), Matera is one of the oldest continuously inhabited cities in the world, having been inhabited since the 10th millennium BC. Its historical center "Sassi", along with the Park of the Rupestrian Churches, is considered a World Heritage Site by UNESCO since 1993.

On 17 October 2014, Matera was declared Italian host of European Capital of Culture for 2019 with the Bulgarian town of Plovdiv.

Alberobello, in the region of Puglia in southern Italy, is a strange and picturesque destination which is becoming an important fixture on the travel itineraries of tour operators as well as independent travellers. The small town has been made a UNESCO World Heritage site for its unusual districts of trulli, the characteristic white-washed conical-roofed houses of the area. It makes an interesting day-trip destination or a pleasant base for a few days - especially if you stay in a trullo of your very own.

Note

Note

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Thank you for taking time to participate in this conference evaluation. Your comments will enable us to execute future conferences better and tailor them to your needs!