

# CONFERENCE ABSTRACT

**2019 11th International Conference on Bioinformatics and  
Biomedical Technology (ICBBT 2019)**

**Stockholm, Sweden**

**May 29-31, 2019**



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# Introduction

Welcome to 2019 11th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2019) which is supported by Hong Kong Chemical, Biological & Environmental Engineering Society (CBEES), Biology and Bioinformatics (BBS), and Linkoping University, Sweden. The objective of 2019 11th International Conference on Bioinformatics and Biomedical Technology (ICBBT 2019) is to provide a platform for researchers, engineers, academicians as well as industrial professionals from all over the world to present their research results and development activities in Bioinformatics and Biomedical Technology.

Papers will be published in the following proceedings or journal:



**ACM Conference Proceedings (ISBN: 978-1-4503-6231-3)**, 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).



**International Journal of Pharma Medicine and Biological Sciences (IJPMBBS, ISSN: 2278-5221)**, included in the Engineering & Technology Digital Library, and indexed by Embase (Under elsevier), ProQuest, Google Scholar, Chemical Abstracts Services (CAS), Indian Science, ICMJE(International Committee Medical Journal Editors), HINARI(World Health Organization), and NYU(Health Sciences Library)

Conference website and email: <http://www.icbbt.org>; [icbbt@cbees.org](mailto:icbbt@cbees.org)

# 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):**

Keynote Speech: about **30** Minutes of Presentation and **5** Minutes of Question and Answer

Invited Speech: about **15** Minutes of Presentation and **5** Minutes of Question and Answer

Oral Presentation: about **12** Minutes of Presentation and **3** 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: Submit the poster to the staff when signing in

Poster Size: A1 (841\*594mm)

Load Capacity: Holds up to 0.5 kg

## Best Presentation Award

One Best Presentation will be selected from each session, and the Certificate for Best Presentation will be awarded at the end of each session on May 30, 2019.

## Dress Code

Please wear formal clothes or national representative of clothing.

# Honored Speaker Introduction

## Keynote Speaker I



Prof. Ralf Hofestädt  
Bielefeld University, Germany

**Prof. Ralf Hofestädt** studied Computer Science and Bioinformatics at the University of Bonn. He finished his PhD 1990 (University Bonn) and his Habilitation (Applied Computer Science and Bioinformatics) 1995 at the University of Koblenz. From 1996 to 2001, he was Professor for Applied Computer Science at the University of Magdeburg. Since 2001, he is Professor for Bioinformatics and Medical Informatics at the University Bielefeld. The research topics of the department concentrate on biomedical data management, modeling and simulation of metabolic processes, parallel computing and multimedia implementation of virtual scenarios.

*Topic: "New Drug Targets for the Treatment of Co-Morbid Multifunctional Diseases"*

**Abstract**—A set of genes has been prioritized to find genes potentially involved in asthma and hypertension comorbidity. The prioritization was carried out using well-known methods of textmining. Furthermore, a new database was developed and implemented, which presents the positive and negative drug list for asthma and hypertension. A web based implementation of this data base allows the access to this information via internet (<https://genconet.kalis-amts.de>).

## Keynote Speaker II



Prof. Patrick Bours

Norwegian University of Science and Technology, Norway

**Patrick Bours** received his MSc and PhD degree in the area of Discrete Mathematics from the Eindhoven University of Technology in the Netherlands, in 1990 and 1994. From 1995 until June 2005 he worked as a senior policy member in the area of cryptology for the Netherlands National Communication Security Agency (NLNCSA). From July 2005 he worked at the Gjøvik University College in Gjøvik, Norway. First as a Postdoc (2005-2008), then as an associate professor (2008-2012) and since 2012 he holds a professor position. Gjøvik University College merged with NTNU in 2016. Since 2005 he is working in the area of biometrics, and in particular behavioural biometrics. He has over 100 publications in the area of gait recognition, keystroke and mouse dynamics, as well as ear, fingerprint, face and retina recognition. His current research interest is in the area of keystroke dynamics, in particular continuous authentication and application of keystroke dynamics. Patrick Bours is reviewer for various conferences and journals in the area of biometrics and he is an associate editor for Wiley's journal on Security and Privacy (SPY).

*Topic: "Using Behavioural Biometrics Beyond Gaining Access"*

**Abstract**—Biometrics is traditionally used to gain access to a system. Fingerprint and face are used to gain access to our phones, iris scans are used at boarder control to gain access to a restricted area and finger vein biometrics is applied to withdraw money from ATM machines. Behavioural biometrics in particular can be used far beyond such applications, mainly because we can measure the behaviour of a person unobtrusively over longer periods of time. In particular will I show how behavioural biometrics can be used to add an additional layer of security to your computer or mobile device and how we can use it to provide safety online for vulnerable members of society.

## Keynote Speaker III



Prof. Andre Ribeiro

Tampere University of Technology, Finland

**Andre Ribeiro** ([andre.ribeiro@axt.tut.fi](mailto:andre.ribeiro@axt.tut.fi)) is a Professor at University of Tampere, Finland. He was born in 1976, graduated in Physics in the University of Lisbon (1999), and has a PhD in Physics Engineering from IST, Technical University of Lisbon, Portugal (2004). From 2004-07, he was a Postdoc at the University of Calgary, Canada. Since 2008, he is the PI of the Laboratory of Biosystem Dynamics (LBD) at Tampere University of Technology, Finland. Since June 2017, he is a Professor at the BiomedTech Institute, TUT. His studies focus on the *in vivo* dynamics and regulatory mechanisms of bacterial gene expression and genetic circuits at the single-cell, single-molecule level using time-lapse microscopy, stochastic models, molecular biosensors, single-cell signal processing, and synthetic gene engineering. The aims are to understand how genes and genetic circuits are regulated and unravel their range of functionalities, thereby assisting in the comprehensive engineering of synthetic circuits for regulating cellular processes. He also studies the biophysics inside cells, to better understand their spatial-dynamics organization.

*Topic: "Quantitative Characterization and Modelling of the in vivo Kinetics of Transcription Halting in Escherichia coli"*

**Abstract**—The genetic circuits of *Escherichia coli* are poised with regulatory mechanisms that have evolved with the purpose of handling the mechanical challenges of the process of transcription. One of these challenges is the accumulation of positive supercoiling during transcription elongation, which can cause transcription halts. As these events are common, particularly in highly expressed operons, they need to be accounted for when studying the dynamics of gene expression in this organism. Applying a methodology based on quantitative fluorescence-based steady-state assays, we analyze in detail the dynamics of transcription halting. In particular, we make use of fluorescently tagged RNA molecules along with measurements of Gyrase and RNA polymerase concentrations in live cells, to characterize how often does transcription halts and how long does it remain locked as a function of the dynamics of the gene of interest. After characterizing this dynamical component in one gene, we propose and exemplify how to make use of an integrative approach that combines data from more genes in order to develop a model capable of predicting the kinetics of halting of any given gene based on a set of parameters of its dynamics of transcription. These models are expected to provide a better insight on the dynamical limitations of the gene regulatory network of *E. coli*.

## Keynote Speaker IV



Prof. Guoying Zhao  
University of Oulu, Finland

**Guoying Zhao** received the Ph.D. degree in computer science from the Chinese Academy of Sciences, Beijing, China, in 2005. She is currently a Professor with the Center for Machine Vision and Signal Analysis, University of Oulu, Finland, where she worked as a senior researcher since 2005 and an Associate Professor since 2014. She has authored or co-authored more than 190 papers in journals and conferences. Her papers have currently over 9300 citations in Google Scholar (h-index 43). She was co-publicity chair for FG2018, has served as area chairs for several conferences and is associate editor for Pattern Recognition, IEEE Transactions on Circuits and Systems for Video Technology, and Image and Vision Computing Journals. She has lectured tutorials at ICPR 2006, ICCV 2009, SCIA 2013 and FG 2018, authored/edited three books and eight special issues in journals. Dr. Zhao was a Co-Chair of many International Workshops at ECCV, ICCV, CVPR, ACCV and BMVC. Her current research interests include image and video descriptors, facial-expression and micro-expression recognition, gait analysis, dynamic-texture recognition, human motion analysis, and person identification. Her research has been reported by Finnish TV programs, newspapers and MIT Technology Review.

*Topic: "Face Anti-Spoofing with Remote Heart Rate Estimation from Videos"*

**Abstract**—Face biometric systems should be robust to spoofing attacks, including a falsified image, video or 3D mask of a valid user. Some widely used approaches for differentiating genuine faces from fake ones has been to capture their inherent differences in (2D or 3D) texture using local descriptors or depth information. This talk touches the topic in a very different viewangle, from detecting pulse from face videos. Based on the fact that a pulse signal exists in a real living face but not in any mask or print material, the remote heart rate estimation method could be a generalized solution for face liveness detection. This talk starts from remote heart rate measure method which works in realistic situations, to adapting the method to face mask anti-spoofing. Experiments and comparison show interesting and promising results for potential real world applications.

## Keynote Speaker V



Dr. Gert E Nilsson  
Wheelsbridge AB, Sweden

**Gert E Nilsson** is the founder and president of Wheelsbridge AB that developed and brought the Tissue Viability Imaging technology to market. He is former professor of Biomedical Instrumentation at the Department of Biomedical Engineering, Linköping University, Linköping, Sweden and inventor of the Evaporimeter (EP1) for measurement of transepidermal water loss, the Laser Doppler Flowmeter (Periflux) for monitoring of skin blood flow, the Laser Doppler Perfusion Imager (PIM) for mapping of tissue microcirculation and the Tissue Viability Imager (TiVi) for assessment of erythema and blanching and other skin parameters. Dr. Nilsson has served as head of the Department of Biomedical Engineering, Linköping University, 1990 – 1993, coordinator for the EU-project High Resolution Laser Doppler perfusion imaging dermatology (HIRELADO), 1995 – 2000 and director for the Competence Centre NIMED at Linköping University 2002-2005.

*Topic: "Using the Digital Camera as a Transducer for Assessment of Skin Parameters"*

**Abstract**—Although skin care product candidates should be carefully tested for both safety and efficacy prior to being released on the market, far-reaching claims associated with the performance of these new products are frequently difficult to substantiate. This is primarily due to a lack of suitable technologies capable of accurately assessing alterations in skin properties effectively at the point of sales as well as in the laboratory. *Polarisation Spectroscopy Imaging* (SPI) – utilizing high-end digital cameras - is an emerging technology that maps the microcirculation of the skin and other dermal properties by looking beneath the surface layer and capturing sub-epidermal images. This technology, also known as *Tissue Viability Imaging* (TiVi), employs a methodology uniquely capable of profiling the selective light-absorption behaviour of haemoglobin molecules present in red blood cells. These molecules absorb a significantly greater proportion of light in the green wavelength band compared to that of the surrounding tissue. In this respect, haemoglobin molecules are reliable biological markers for mapping and quantifying skin erythema and blanching. SPI is particularly useful for assessing cosmetic and personal care safety, efficacy and consistency with regulatory guidelines.

## Keynote Speaker VI



Assoc. Prof. Julian Fierrez  
Universidad Autonoma De Madrid, Spain

**Julian Fierrez** received the MSc and the PhD degrees in telecommunications engineering from Universidad Politecnica de Madrid, Spain, in 2001 and 2006, respectively. Since 2002 he was affiliated as a PhD candidate with the Universidad Politecnica de Madrid, and since 2004 he is at Universidad Autonoma de Madrid, where he is currently an Associate Professor since 2010. From 2007 to 2009 he was a visiting researcher at Michigan State University in USA under a Marie Curie fellowship. His research interests include general signal and image processing, pattern recognition, and biometrics. Since 2016 he is Associate Editor for Elsevier's Information Fusion, IEEE Trans. on Information Forensics and Security, and IEEE Trans. on Image Processing. Prof. Fierrez has been actively involved in multiple EU projects focused on biometrics (e.g. TABULA RASA and BEAT), has attracted notable impact for his research, and is the recipient of a number of distinctions, including: EBF European Biometric Industry Award 2006, EURASIP Best PhD Award 2012, Medal in the Young Researcher Awards 2015 by the Spanish Royal Academy of Engineering, and the Miguel Catalan Award to the Best Researcher under 40 in the Community of Madrid in the general area of Science and Technology. In 2017 he has been also awarded the IAPR Young Biometrics Investigator Award, given to a single researcher worldwide every two years under the age of 40, whose research work has had a major impact in biometrics.

*Topic: "Blockchain and Biometrics: Opportunities and Challenges"*

**Abstract**—We will first discuss opportunities and challenges in the integration of blockchain and biometrics, with emphasis in biometric template storage and protection, a key problem in biometrics still largely unsolved. Blockchain technologies provide excellent architectures and practical tools for securing and managing the sensitive and private data stored in biometric templates, but at a cost. We will then report preliminary experiments studying the key tradeoffs involved in that integration, namely: latency, processing time, economic cost, and biometric performance. The experiments reported are based on a smart contract implemented on Ethereum for biometric template storage, whose cost-performance is evaluated by varying the complexity of state-of-the-art schemes for face and handwritten signature biometrics, including deep learning approaches and databases captured in the wild. Finally, we will discuss that straightforward schemes for data storage in blockchain (i.e., direct and hash-based) may be prohibitive for biometric template storage using state-of-the-art biometric methods, and we will then outline new architectures for overcoming that challenge.

## Invited Speaker I



Prof. Xiaoyi Feng  
Northwestern Polytechnical University, China

**Feng Xiaoyi** is currently a professor and doctoral supervisor at the School of Electronic Information, Northwest Polytechnic University. She is deputy director of the Key Laboratory of Aerospace Electronic Information Perception and Optical Control, Ministry of Education. She is also member of the council of the Chinese Society of Image Graphics, and Vice President of Shaanxi Society of Image Graphics. Her research interests include computer vision, image processing and pattern recognition. Her recent research focuses on human-centered computing, including face expression recognition, false face attack recognition, face-based parent-child relationship estimation and so on.

*Topic: "Face Spoofing Detection Based on Deep Learning"*

**Abstract**—As one of the most natural clues for identifying individuals, face images have been used as the preferred biometric trait in many identity recognition systems. However, face spoofing becomes a clear threat for these recognition systems. In this talk, I will explore the ideas on how to use deep learning based models to detect face spoofing in 2D fake face images, videos and 3D face masks by our research group. Several specific-designed deep models will be introduced and compared to existing handcrafted features in the experimental evaluation.

## Invited Speaker II



Prof. Kolyo Onkov  
Agricultural University, Bulgaria

**Prof. Kolyo Onkov** has graduated from Technical University in Prague, Czech Republic and received doctoral degree from Czech Academy of Sciences, Institute of Information Theory and Automation. Since 2012 he is Professor of Computer Science. The research interests of Prof. Kolyo Onkov are focused on concepts for hierarchical structuring and analysis of multidimensional time series databases in agriculture and demography. He has developed and applied data mining algorithms and statistical software techniques to study fish species at risk and biodiversity. Prof. Kolyo Onkov also works on integrating and modelling expert chemical and biological information used in Plant medicine (Phytopharmacy). He always strives to find practical solutions to transform heterogeneous, semi-structured chemical and biological data into intelligent computer based system. Prof. Kolyo Onkov has published 3 books and more than 65 scientific papers. He has supervised 4 PhD students in Computer science and assisted to PhD students in natural and agricultural sciences on data processing and analysis.

*Topic: "Computational Procedure for Analysis of Fish Diversity in Greece"*

*Authors: Kolyo Onkov and Georgios Tegos*

**Abstract**—Fishery Time Series Database of Greece stores time series by means of spatial, biological, technical and economic aspects. Through the aggregation, the time series on fish catch quantity by species, areas and regions and total are presented in the form of data cubes. Computational procedure estimates Shannon diversity index on data cubes respecting fish groups. The computation of descriptive statistics on time series containing the obtained values of Shannon index gives the opportunity for a comparative and multi-scale analysis on three levels: total, fish region and fish area. The computational procedure provides also the extraction of some specific features of the fish diversity dynamics. In addition, the differences and similarities between fish diversity of Greek regions and areas are discussed. The developed procedure and software can be also applied on other countries and regions on sea fish species and freshwater fish species. Finally, spatial and temporal estimation of fish diversity has ecological and economic aspects. The obtained information can be useful for an effective management of fish resources.

## Brief Schedule of Conference

<b>Day One</b> <b>May 29, 2019</b> <b>(Wednesday)</b>	10:00-16:00	<b>Venue: Hotel Lobby</b> <b>Arrival Registration</b>
<b>Day Two</b> <b>May 30, 2019</b> <b>(Thursday)</b>	<b>Venue: Gästrikesalen</b>	
	09:00-09:05	<b>Opening Remarks</b> Prof. Tuan D. Pham Linköping University, Sweden
	09:05-09:40	<b>Keynote Speech I</b> Prof. Ralf Hofest ädt Bielefeld University, Germany Topic: " New Drug Targets for the Treatment of Co-Morbid Multifunctional Diseases"
	09:40-10:15	<b>Keynote Speech II</b> Prof. Patrick Bours Norwegian University of Science and Technology, Norway Topic: "Using Behavioural Biometrics Beyond Gaining Access"
	10:15-10:40	<b>Coffee Break &amp; Group Photo</b>
	10:40-11:15	<b>Keynote Speech III</b> Prof. Andre Ribeiro Tampere University of Technology, Finland Topic: "Quantitative Characterization and Modelling of the <i>in vivo</i> Kinetics of Transcription Halting in <i>Escherichia coli</i> "
	11:15-11:50	<b>Keynote Speech IV</b> Prof. Guoying Zhao University of Oulu, Finland Topic: "Face Anti-Spoofing with Remote Heart Rate Estimation from Videos"
	11:50-12:25	<b>Keynote Speech V</b> Dr. Gert E Nilsson Wheelsbridge AB, Sweden Topic: "Using the Digital Camera as a Transducer for Assessment of Skin Parameters"
	<b>12:25-13:25 Lunch (Taabla)</b>	

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<b>Day Two May 30, 2019 (Thursday)</b>	13:25-14:00	<b>Keynote Speech VI</b> Assoc. Prof. Julian Fierrez Universidad Autonoma De Madrid, Spain Topic: " Blockchain and Biometrics: Opportunities and Challenges "
	<b>Venue: H älsingesalen</b> 14:00-14:20	<b>Venue: G ästrikesalen</b> 14:00-14:20
	<b>Invited Speech I</b> Prof. Xiaoyi Feng Northwestern Polytechnical University, China Topic: " Face Spoofing Detection Based on Deep Learning"	<b>Invited Speech II</b> Prof. Kolyo Onkov Agricultural University, Bulgaria Topic: "Computational Procedure for Analysis of Fish Diversity in Greece"
	<b>Session 1:</b> 14:20-16:05 Topic: "Biometric Image Recognition" 7 presentations	<b>Session 2:</b> 14:20-16:05 Topic: "Biomedical Information and Systems" 7 presentations
	<b>16:05-16:20 Coffee Break</b>	
	<b>Session 3:</b> 16:20-18:05 <b>Venue: H älsingesalen</b> Topic: "Biometric Recognition and Classification" 7 presentations	<b>Session 4:</b> 16:20-18:05 <b>Venue: G ästrikesalen</b> Topic: "Biomedical Images and Signals" 7 presentations
	<b>Poster Session</b> <b>13:25-18:00 (Lounge of G ästrikesalen)</b>	
	<b>18:30-20:00 Dinner (Taabla)</b>	
<b>Day Three May 31, 2019 (Friday)</b>	9:00-17:30	<b>Academic Visit &amp; Tour</b>

**Tips:** Please arrive at the Conference Room 10 minutes before the session begins to upload PPT into the laptop; submit the poster to the staff when signing in.

# 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, May 30, 2019 (Thursday)**

**Time: 14:20-16:05**

**Venue: Gästrikesalen**

**Topic: “Biometric Image Recognition”**

**Session Chair: Prof. Xiaoyi Feng**

<p>M2005 Session 1 Presentation 1 (14:20-14:35)</p>	<p>Learning of Brain Connectivity Features for EEG-based Person Identification <b>Ndifreke Okon Nyah</b> and Nikolas Christou University of Bedfordshire, United Kingdom</p> <p><i>Abstract</i>—The brain activity observed on multiple EEG electrodes is influenced by volume conductance and functional connectivity of a person performing a task. When the task is a biometric test, EEG signals represent the unique ‘brain print’ which is genetically defined by the functional connectivity that is represented by interactions between the electrodes, whilst the conductance component causes trivial correlations in EEG signals. Orthogonalisation using autoregressive modelling minimises the conductance component, and the connectivity features can be then extracted from the residuals. However, the results cannot be reliable for high-dimensional EEG data recorded via a multi-electrode system. The proposed method shows that the dimensionality can be significantly reduced if baselines that are required for estimating the residuals can be modelled by using EEG electrodes that make important contribution to the functional connectivity. The results show that the required models can be learnt by Machine Learning techniques which are capable of providing the maximal performance in the case of multidimensional EEG data. The study which has been conducted on a EEG benchmark including 109 participants shows a significant improvement of the identification accuracy.</p>
<p>M2006 Session 1 Presentation 2 (14:35-14:50)</p>	<p>Empirical Evaluation of Texture-Based Print and Contact Lens Iris Presentation Attack Detection Methods <b>Hareesh Mandalapu</b>, Raghavendra Ramachandra and Christoph Busch Norwegian University of Science and Technology, Norway</p> <p><i>Abstract</i>—Iris-based identification methods have been popularly used in realworld applications due to the unique characteristics of iris when compared to other biometric characteristics like face and fingerprint. As</p>

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	<p>technological advances and low-cost artefacts are becoming more available, vulnerabilities to iris biometrics due to presentation attacks (PAs) are becoming a challenging problem. Presentation attack detection (PAD) algorithms have been employed in biometric capture devices and it has been an active research topic in the past years. In this study, a detailed survey and evaluation of state-of-the-art texture-based iris PAD methods are performed. Five different PAD methods are tested on four different datasets consisting of print and contact lens presentation attacks. Extensive experiments are performed on four different scenarios of presentation attack and results are presented. The properties of PAD algorithms like the quality of the database, the generalization abilities are mainly discussed in this work. It has been observed that fusion-based PAD methods perform better than other methods.</p>
<p>M2010 Session 1 Presentation 3 (14:50-15:05)</p>	<p>Face Liveness Detection by rPPG Features and Contextual Patch-Based CNN <b>Bofan Lin</b>, Zitong Yu, Xiaobai Li and Guoying Zhao University of Oulu, Finland</p> <p><i>Abstract</i>—Face anti-spoofing plays a vital role in security systems including face payment systems and face recognition systems. Previous studies showed that live faces and presentation attacks have significant differences in both remote photoplethysmography (rPPG) and texture information, we propose a generalized method exploiting both rPPG and texture features for face anti-spoofing task. First, multi-scale long-term statistical spectral (MS-LTSS) features with variant granularities are designed for representation of rPPG information. Second, a contextual patch-based convolutional neural network (CP-CNN) is used for extracting global-local and multi-level deep texture features simultaneously. Finally, weight summation strategy is employed for decision level fusion, which helps to generalize the method for not only print attack and replay attack but also mask attack. Comprehensive experiments were conducted on five databases, namely 3DMAD, HKBU-Mars V1, MSU-MFSD, CASIA-FASD, and OULU-NPU, to show the superior results of the proposed method compared with state-of-the-art methods.</p>
<p>M2012 Session 1 Presentation 4 (15:05-15:20)</p>	<p>Graph Embedding for Offline Handwritten Signature Verification <b>Michael Stauffer</b>, Paul Maergner, Andreas Fischer and Kaspar Riesen University of Applied Sciences and Arts Northwestern Switzerland, Switzerland</p> <p><i>Abstract</i>—Due to the high availability and applicability, handwritten signatures are an eminent biometric authentication measure in our life. To mitigate the risk of a potential misuse, automatic signature verification tries to distinguish between genuine and forged signatures. Most of the available signature verification approaches make use of vectorial rather</p>

	<p>than graph-based representations of the handwriting. This is rather surprising as graphs offer some inherent advantages. Graphs are, for instance, able to directly adapt their size and structure to the size and complexity of the respective handwritten entities. Moreover, several fast graph matching algorithms have been proposed recently that allow to employ graphs also in domains with large amounts of data. The present paper proposes to use different graph embedding approaches in conjunction with a recent graph-based signature verification framework. That is, signature graphs are not directly matched with each other, but first compared with a set of predefined prototype graphs, in order to obtain a dissimilarity representation. In an experimental evaluation, we employ the proposed method on two widely used benchmark datasets. On both datasets, we empirically confirm that the learning-free graph embedding outperforms state-of-the-art methods with respect to both accuracy and runtime.</p>
<p>M2013 Session 1 Presentation 5 (15:20-15:35)</p>	<p>Finger Vein Image Compression with Uniform Background <b>Babak Maser</b>, Tamara Lipowski, Jutta H änmerle-Uhl and Andreas Uhl University of Salzburg, Austria</p> <p><i>Abstract</i>—We propose to replace the background data in finger vein imagery by uniform gray data and implications on (i) achieved lossless compression performance and (ii) obtained recognition accuracy in case of lossy compression are determined to employ 2 public datasets. Results indicate that replacement of original background by uniform one is definitely profitable for lossless compression, while the lossy case with impact on recognition accuracy has to be handled with caution as introduced sharp edges between finger area and background lead to artifacts which in turn degrade recognition performance. After having smoothed those areas, recognition performance is improved when replacing background for all settings.</p>
<p>M2003 Session 1 Presentation 6 (15:35-15:50)</p>	<p>Subjective Versus Objective Face Image Quality Evaluation for Face Recognition <b>Ali Khodabakhsh</b>, Marius Pedersen and Christoph Busch Norwegian University of Science and Technology, Norway</p> <p><i>Abstract</i>—The performance of any face recognition system gets affected by the quality of the probe and the reference images. Rejecting or recapturing images with low-quality can improve the overall performance of the biometric system. There are many statistical as well as learning-based methods that provide quality scores given an image for the task of face recognition. In this study, we take a different approach by asking 26 participants to provide subjective quality scores that represent the ease of recognizing the face on the images from a smartphone based face image dataset. These scores are then compared to measures implemented from ISO/IEC TR 29794-5. We observe that the subjective</p>

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	<p>scores outperform the implemented objective scores while having a low correlation with them. Furthermore, we analyze the effect of pose, illumination, and distance on face recognition similarity scores as well as the generated mean opinion scores.</p>
<p>M0007 Session 1 Presentation 7 (15:50-16:05)</p>	<p>Visualizing the Correspondence of Feature Point Mapping Between DICOM Images Before and After Surgery <b>Hiroshi Noborio</b>, Shota Uchibori, Masanao Koeda and Kaoru Watanabe Osaka Electro-Communication University, Japan</p> <p><i>Abstract</i>—We extract feature point mapping between preoperative and postoperative Digital Imaging and Communications in Medicine (DICOM) images from magnetic resonance imaging (MRI) or from computer tomography (CT). The aim is to quantitatively investigate brain shift during intraoperative surgery. First, using 124 two-dimensional images constituting DICOM, a large number of 2D feature points are extracted as uniformly as possible inside the brain. Next, we extract one pair from the 124 preoperative images and the 124 postoperative images and construct map correspondences of similar feature points with a range of DICOM gray values. If the Euclidean distance between the two feature points in the 2D images is too large, the pair of feature points is deleted to prevent mis-mapping; brain shifts are usually less than 2–3 cm. Finally, we find image pairs with the highest number of mappings from DICOM images before and after surgery (two-dimensional stacked three-dimensional images), and generate graph representing correspondences between image pairs with the highest number. Finally, we visualize 3D correspondences between DICOM images before and after surgery.</p>

# 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.

**Afternoon, May 30, 2019 (Thursday)**

**Time: 14:20-16:05**

**Venue: Häisingesalen**

**Topic: “Biomedical Information and Systems”**

**Session Chair: Prof. Kolyo Onkov**

<p>M1002 Session 2 Presentation 1 (14:20-14:35)</p>	<p>Healthcare Data Transmission by Using NB-IoT <b>Thitapa Prompinit,</b> Amonwan Jenjirataworn and SarinpornVisitsattapongse King Mongkut’s Institute of Technology Ladkrabang Bangkok, Thailand</p> <p><i>Abstract</i>—This project is to create a medical healthcare data transmission by using NB-IoT. The objective is to reduce step of working and redundant of collecting healthcare data from patients. And to collect data as a system for tracking the treatment of chronic patients who live in outskirts. Narrow Band Internet of Thing (NB-IoT) is used as an intermediary to send data to the database, for making healthcare information that can be used easily in the process of patient treatment and for development of service quality of staff. Processing of healthcare data transmission begin with set up and connect Bluetooth into healthcare instrument and into data transmission device or NB-IoT board for allowing data communicate between them. Then connect NB-IoT to database on server by using functional of Node-Red programming. In this project, the database is designed and tested with one person for bringing data to show in potable graph and to follow data trending on application. The result of the experiment, see that, NB-IoT can sent the data immediately to database, including with display the lasted data and trending on dashboard in real- time. So, the advantage of this project is to reduce step of work in data storage system, easy to access the database and easy to use the data for analyzing.</p>
<p>M0004 Session 2 Presentation 2 (14:35-14:50)</p>	<p>Reconstructing Double Minute Chromosome Amplicons Using a Hidden-Markov Model-Based Approach Ruslan Mardugalliamov, Kamal Al Nasr and <b>Matthew Hayes</b> Xavier University of Louisiana, USA</p> <p><i>Abstract</i>—Double minute chromosomes (DM) are circular fragments of extrachromosomal DNA. They are a mechanism for extreme gene amplification in the cells of some malignant tumors. Their existence</p>

	<p>strongly correlates with malignant tumor cell behavior and drug resistance. Locating DMs is important for informing precision therapy to cancer treatment. Furthermore, accurate detection of double minutes requires precise reconstruction of their amplicons which are the highly-amplified gene-carrying contiguous segments that adjoin to form DMs. This work presents AmpliconFinder -- a Hidden-Markov Model-based approach to detect DM amplicons. To assess its efficacy, AmpliconFinder was used to augment an earlier framework for DM detection (DMFinder), thus improving its robustness to noisy sequence data, and thus improving its sensitivity to detect DMs. Experiments on simulated genomic data have shown that augmenting DmFinder with AmpliconFinder significantly increased the sensitivity of DmFinder on these data. Moreover, DmFinder with AmpliconFinder found all previously reported DMs in three pediatric medulloblastoma datasets, whereas the original DmFinder framework found none.</p>
<p>M1005 Session 2 Presentation 3 (14:50-15:05)</p>	<p>The Pharmacy Automatically Machine <b>Boonyarat Phimmasorn</b> and Sarinporn Visitsattapongse King Mongkut's Institute of Technology Ladkrabang Bangkok, Thailand</p> <p><i>Abstract</i>—This paper introduces the design and fabrication of a scalable prototype of machine medicine dispenser for the use of pharmacists. It has an automated capability to count the medicines and dispense into basket. The ability of this machine in terms of scalability is achieved by the utilizations of High-quality materials and components that can be scaled with respect to the user end preferences.</p>
<p>M0027 Session 2 Presentation 4 (15:05-15:20)</p>	<p>Diffusion Kernel Based Fast Adaptive Clustering of Single Cell RNA-seq Data Samina Kausar, Xu Huahu, <b>Rashid Mehmood</b> and Muhammad Shahid Iqbal Karolinska Institutet, Sweden</p> <p><i>Abstract</i>—Recently, with the advent of high throughput single-cell technologies, it has become possible to quantify the whole transcriptome of individual cells; however, it remains challenging to discover intrinsic rare cell-types from high throughput genes expression data. To overcome this challenge, various unsupervised clustering based approaches have been proposed such as GiniClust, SC3 and SIMLR clustering. These approaches identified appropriate rare cell types based on the ambiguous parametric settings and employed clustering algorithms are inefficient to discover meaningful clusters adaptively. However, the appropriate signal of interest can be observed along with the robust filtration, normalization, and transformation of raw count samples of single-cell data. Filtration, normalization, and transformation have become the essential primary procedure for down-stream analysis of single-cell data and to eliminate</p>

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	<p>the risk of biological variation and technical noise. In this paper, we will evaluate the various methods to detect the rare cell-types from a large population and develop fast novel diffusion kernel based unsupervised framework (DKBUF) to identify rare cell types from single-cell RNA-seq data, more in an adaptive and attractive fashion. The DKBUF filters the non-stable genes, normalizes the genes, attractively detects subpopulations within single-cell datasets, and visualizes the discovered distinct subpopulations. Extensive experiments on single-cell datasets and comparisons with state-of-the-art methods validate the robustness of the DKBUF.</p>
<p>M1016 Session 2 Presentation 5 (15:20-15:35)</p>	<p>The Role of Color in Palliative Care for Children <b>Andrew Chixiao Yang</b> Holderness School, USA</p> <p><i>Abstract</i>—This paper is dedicated to investigating and analyzing the role of color in palliative care for children with life-threatening conditions. Although the color-emotion association for children has been addressed by various studies, the differences between healthy and seriously sick children on how to perceive and preference colors are rarely touched upon from a psychological and clinical perspective. Eighty children (39 boys, 41 girls), aged from 6 to 8, consisted of healthy and ill participants. A combination of questionnaire and color assessment was used to determine whether or not the participants' health condition is independent of the selection and preference of the colors and emotions they have chosen. A bunch of interesting findings are examined and discussed, which might be of certain significance to the future psychological assessment, intervention and treatment for children in a palliative setting.</p>
<p>M1006 Session 2 Presentation 6 (15:35-15:50)</p>	<p>Designing, Development and Testing of Indigenous Paired Neck Chamber Device for Evaluation of Baroreflex Sensitivity <b>Prathamesh H Kamble</b>, Pratik Paliwal, Kaushal Desai, Rajesh K Sharma and Anish Singhal All India Institute of Medical Sciences Nagpur, India</p> <p><i>Abstract</i>—Carotid baroreceptors are the sensors of blood pressure buffer system, a type of stretch receptors, which can be stimulated non-invasively by creating external pressure around the neck. With this hypothesis, we conceptualized and designed of neck chamber device using CAD then it went through many cycles of design modification, 3D-printing and testing after obtaining Institutional Ethics clearance. The final neck chamber prototype consisted of circumferential suction mechanism to hold device to neck and the inner chamber connected to pump to create controlled positive and negative pressure using designed auxiliary system with special attention to safety measures and valves. Then, 30 young healthy volunteers within age 20-25 years were recruited for testing. Neck chamber stimulation was given in steps of -20, -40, -60,</p>

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	<p>0, +20, +40 and +60 mm of Hg with the gap of 60 seconds between each stimulation. The changes in RR interval, HR and BP were recorded. Then saturation point, threshold point and optimal gain was calculated using logistic equation derivative and gain curve plot. The mean optimal gain or baroreceptor sensitivity was <math>-0.579 \pm 0.045</math>, while the saturation point and threshold point were <math>0.028 \pm 0.0018</math> and <math>-0.028 \pm 0.0018</math> respectively. The results were consistent with the gain estimated using other invasive methods. Thus, we have developed a non-invasive, indigenous System for stimulation of Carotid Baroreceptors both unilaterally and/or bilaterally.</p>
<p>M0009 Session 2 Presentation 7 (15:50-16:05)</p>	<p>Testing Methods to Minimise Range-shifting Time with Conservation Actions Daniyah A. Aloqalaa, Jenny A. Hodgson, <b>Dariusz R. Kowalski</b> and Prudence W. H. Wong University of Liverpool, UK</p> <p><i>Abstract</i>—Climate change is a global threat to species, and their capability to invade and colonise new landscapes could be limited by the habitat fragmentation. Improving landscapes by adding additional resources to landscapes is an important initiative to restore habitats. Such improvements will be particularly important to promote species recovery in fragmented landscapes and to understand as well as facilitate range-shifting for species (also called an invasion). We use a recent method to approximate the time taken by species to invade landscapes and reach the new areas of suitable environment, which based on network flow theory. Based on this, we propose and test a new method that can help to compute the best locations in landscapes in order to restore habitat which leads to minimising the expected time taken by species to invade and reach targets. The new optimisation method has been compared with other two baseline methods. The evaluation conducted using real heterogeneous landscapes shows that the proposed method outperforms the competitive baseline methods in terms of proposing landscape modifications that minimise the expected time of the invasion process.</p>

<p><b>16:05-16:20</b></p>	<p><b>Coffee Break</b></p>
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# 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, May 30, 2019 (Thursday)**

**Time: 16:20-18:05**

**Venue: Gästrikesalen**

**Topic: “Biometric Recognition and Classification”**

**Session Chair: Prof. Guoying Zhao**

<p>M1008 Session 3 Presentation 1 (16:20-16:35)</p>	<p>Footprint Pressure-Based Personal Recognition <b>Tanapon Keatsamarn</b>, Chuchart Pintavirooj and Sarinporn Visitsattapongse King Mongkut’s Institute of Technology Ladkrabang Bangkok, Thailand</p> <p><i>Abstract</i>—In human, footprint pressure is the biometric system. Everyone has specific pressure patterns. It can help doctors diagnose foot-related diseases. Especially in diabetic patients, who have a problem caused by lack of sensation in the foot, they don’t feel any pain when they have ulcers at the high-pressure point. In addition, The specific pressure patterns can be used instead of user authentication because the biometric system is more secure than the password-based system. The password-based system cannot verify that the person who entered the password is valid or not. Therefore the specific pressure patterns are the alternative to user authentication or patient classification. For these reasons, it’s interesting to use footprint pressure patterns in personal recognition for diagnosing and classification. In this paper, we used the footprint pressure patterns to identify <math>n = 65</math> subjects with classification rates of 90.56% using convolutional neural network training for deep learning classification</p>
<p>M2009 Session 3 Presentation 2 (16:35-16:50)</p>	<p>Cross-Database Micro-Expression Recognition with Deep Convolutional Networks <b>Zhaoqiang Xia</b>, Huan Liang, Xiaopeng Hong and Xiaoyi Feng Northwestern Polytechnical University, China</p> <p><i>Abstract</i>—Micro-expression recognition (MER) is attracting more and more interests as it has important applications for analyzing human behaviors. Since the recognition ability for individual datasets has been improved greatly, few works have been devoted to the cross-database task of MER, which is more challenging for capturing the subtle changes of samples from different environments. In this paper, we employ an end-to-end deep model for learning the representation and classifier</p>

	<p>automatically. In the deep model, the recurrent convolutional layers are utilized to exploit the learning ability with the optical flow fields of micro-expression sequences. To ease the influence of samples from different datasets (environments), we present three normalization methods (sample-wise, subject-wise and dataset-wise methods) to restrain the variations of samples. The experiments are performed on the cross-database of MERC2019 challenge, and achieve comparative performance than the baseline method.</p>
<p>M0028 Session 3 Presentation 3 (16:50-17:05)</p>	<p>Automated Spore Counting Using Morphology and Shape <b>Punnarai Siricharoen</b> and Usa Humphries King Mongkut's University of Technology Thonburi, Thailand</p> <p><i>Abstract</i>—Pyricularia Oryzae is a type of fungal spores which can lead to the most damaging rice blast disease. We have developed a quick and robust tool for counting the number of spores for measuring spore concentration using image processing techniques. The image is first thresholded using auto-Otsu's thresholding and adaptive Gaussian threshold. Morphological operations are employed to reduce some noise. With elongated shape of the spore, region properties are considered in the counting process. Our proposed technique is evaluated on 10x and 40x image sets using statistical measures; it outperforms the previous techniques and can be used for early disease diagnosis and further studying spore-related factors.</p>
<p>M3003 Session 3 Presentation 4 (17:05-17:20)</p>	<p>SmartHandle: A Novel Behavioral Biometric-Based Authentication Scheme for Smart Lock Systems <b>Sandeep Gupta</b>, Attaullah Buriro and Bruno Crispo University of Trento, Italy</p> <p><i>Abstract</i>—Over recent years, smart locks have evolved as cyber-physical devices that can be operated by digital keypads, physiological biometrics sensors, smart-card readers, or mobile devices pairing, to secure door access. However, the underlying authentication schemes, i.e., knowledge-based (e.g., PIN/passwords), possession-based (e.g., smartphones, smart cards), or physiological biometric-based (e.g., fingerprint, face), utilized in smart locks, have shown several drawbacks. Studies have determined that these authentication schemes are vulnerable to various attacks as well as lack usability. This paper presents SmartHandle - a novel behavioral biometric-based transparent user authentication scheme for smart locks that exploits users' hand-movement while they rotate the door handle to unlock the door. More specifically, our solution models the user's hand-movement in 3-dimensional space by fetching the X, Y, and Z coordinates from 3 sensors, namely, accelerometer, magnetometer, and gyroscope corresponding to the hand-movement trajectory, to generate a user-identification-signature. We validated our solution for a multi-class classification scenario and achieve</p>

	<p>a True Acceptance Rate (TAR) of 87.27% at the False Acceptance Rate (FAR) of 1.39% with the Linear Discriminant Classifier (LDC) on our collected dataset from 11 users. The solution can be easily deployed at the main entrance of homes and offices offering a secure and usable authentication scheme to their legitimate users.</p>
<p>M2002 Session 3 Presentation 5 (17:20-17:35)</p>	<p>Detecting Liars in Chats Using Keystroke Dynamics <b>Parisa Rezaee Borj</b> and Patrick Bours Norwegian University of Science and Technology, Norway</p> <p><i>Abstract</i>—In this paper we will investigate the possibilities for detecting liars in chat rooms who have taken on a different identity. While using a different identity people might require more time to reply to questions of the chat partner, or might use corrections to change their text to avoid inconsistencies in their answers. These issues will cause differences in the typing behavior, which can be measured in the typing rhythm. We have shown in this paper that, with a high accuracy, we can distinguish between a chat of a person who uses his/her own identity and is honest in his/her answers, and a chat of a person who is lying because his/her answers need to be consistent to an assumed identity. We obtained a correct classification of a single message in a chat with an accuracy of more than 70% and a correct classification of a full chat with well over 90% accuracy.</p>
<p>M0011 Session 3 Presentation 6 (17:35-17:50)</p>	<p>Automatic Breast Cancer Grading of Histological Images Using Dilated Residual Network <b>Yanyuet Man</b> and Hailong Yao Tsinghua University, China</p> <p><i>Abstract</i>—Breast cancer is one of the leading causes of female death worldwide. Histological evaluation of the breast biopsies is essential in the early detection. Recently, deep learning methods are developed to automatically grade breast cancer of histological images. For the critical local and global features of histological images, few existing deep learning methods effectively extract both of them. Most methods extract one at the loss of the other, with degraded multi-class classification accuracy. In this paper, we propose an effective breast cancer classification method of histology images based on a modified dilated residual network (DRN). The proposed method effectively captures the global feature while maintaining the local information, and thus achieves notably high multi-class classification accuracy. Experimental results show that for the four-class breast cancer classification problem, an accuracy of 89.5% can be obtained, which outperforms all the prevalent methods. In comparison to the manual diagnosis accuracy of 89% from pathologists, the proposed automatic diagnosis method is practical and promising.</p>

<p>M2004 Session 3 Presentation 7 (17:50-18:05)</p>	<p>Surface Normals Based Landmarking for 3D Face Recognition Using Photometric Stereo Captures <b>Jiangning Gao</b>, Mark Hansen, Melvyn L. Smith and Adrian N. Evans Uppsala University, Sweden</p> <p><i>Abstract</i>—In recent decades, many 3D data acquisition methods have been developed to provide accurate and cost-effective 3D captures of the human face. An example system, which can accommodate both research and commercial applications, is the Photoface device. Photoface is based on the photometric stereo imaging technique. To improve the recognition performance using Photoface captures, a novel landmarking algorithm is first proposed by thresholding surface normals maps. The development of landmarking algorithms specifically for photometric stereo captures enables region-based feature extraction and fills a gap in the 3D face landmarking literature. Nasal curves and spherical patches are then used respectively for recognition and are evaluated on the 3DE-VISIR database, which contains Photoface captures including expressions. The neutral vs. non-neutral matching results demonstrate high face recognition performance using spherical patches and a KFA classifier, achieving a R1RR of 97.26% when only 24 patches are selected for matching.</p>
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# 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, May 30, 2019 (Thursday)**

**Time: 16:20-18:05**

**Venue: Hälsingesalen**

**Topic: “Biomedical Images and Signals”**

**Session Chair: Prof. Hiroshi Noborio**

<p>M0033 Session 4 Presentation 1 (16:20-16:35)</p>	<p>A Deep Learning Approach for Slice to Volume Biomedical Image Integration <b>Bassam Almogadwy</b>, Kenneth McLeod and Albert Burger Heriot-Watt University, UK</p> <p><i>Abstract</i>—Biomedical atlas images obtained from multiple sources need to be aligned and transformed into a single coordinate system so as to be able to integrate and relate these different sets of data. Formally known as image registration, this process of image pre-processing has proven to be integral in a wide array of computer vision applications, most notably in the area of medical imaging. During the last decade slice-to-volume registration, a particular case of image registration problem, has received further attention in the medical imaging community due to the emergence of several medical applications of slice-to-volume mapping. This paper proposes a Convolutional Neural Network (CNN) based deep learning approach for registering a 2D image slice to the 3D volume of images in a Biomedical atlas. The proposed CNN model is trained to determine the distance and pitch values that are used to describe the position of the 2D slice in the atlas coordinate system. High-level features are automatically extracted from the training dataset of images, which addresses the limitation of shallow machine learning techniques for handcrafted features followed by the classification task. Then on the basis of predicted values of distance and pitch, the target image is registered to the 3D volume of images. Experimental results showing the effect on the similarity of images with variation in distance and the impact of varying the distances among the classes on the regression are presented. It was observed that using the successive images at a distance of 10 lead to the maximum accuracy. These results demonstrate the applicability of the proposed approach to slice-to-volume image registration.</p>
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<p>M0023</p> <p>Session 4</p> <p>Presentation 2</p> <p>(16:35-16:50)</p>	<p>Selective Detection and Segmentation of Cervical Cells</p> <p><b>Jing Ke</b>, Zhaoming Jiang, Changchang Liu, Tomasz Bednarz, Arcot Sowmya and Xiaoyao Liang</p> <p>University of New South Wales, Australia</p> <p><i>Abstract</i>—Accurate detection and segmentation of cervical cells is often considered as a critical prerequisite of the prediction of dysplasia or cancer either by a pap smear or the lately developed liquid-based cytology (LBC). The computer-aided detection in microscope images can relieve the pathologists from strenuous manual labors with higher accuracy and efficiency. In the segmentation tasks of real-life clinical data, one challenging issue is the mis-identification of other cells, such as inflammatory cells, with similar appearance of nuclei in shape, size and texture. With a large distribution in the whole slide, even overlap up to 50% to 75% percentage of normal or abnormal cells, these cells are usually detected and segmented as nuclei. In this paper, compared with the typical three-catalogue segmentation methods of nuclei, cytoplasm and background proposed in the literature, we provide a discrimination between inflammatory cells and nuclei by adding a new catalogue. We present two novel convolutional neural networks (CNN), a deeply fine-tuned model and a trained from scratch model. The models enable us to sensitively detect and remove background noises such as mucus or red blood cells. We also profile a detailed performance comparison between these two methods, with the advantages of either network presented. The experiments are based on the sufficient clinical dataset we collected, and the results show the effectiveness of proposed approaches in selective cell detection and segmentation.</p>
<p>M0026</p> <p>Session 4</p> <p>Presentation 3</p> <p>(16:50-17:05)</p>	<p>Comparing Deep Learners with Variability Grading for Cancer Detection on Limited Histopathology Dataset</p> <p><b>Pedro Furtado</b></p> <p>U. Coimbra / CISUC, Portugal</p> <p><i>Abstract</i>—State-of-the-art deep convolution neural networks (CNN) can be applied to various domains, including the grading of cancers in histopathology images, and are most promising approaches. However, it is well-known that CNNs require huge amounts of tagged images and resources to train and work well, and some prior works on cancer grading also achieved top accuracy by analyzing how cancer affects structures, such as cells, in terms of variability of characteristics. The aim of this work is to compare CNN-based classification of medical images with automated analysis of multiple structures. This is done experimentally, by implementing the alternatives and comparing classification accuracy on a public cancer grading dataset. The results show that a well-designed automated analysis of structures improved accuracy by 4% when compared with the best CNN result, showing that it is worth to study</p>

	further and establish procedures based on that analysis.
M1011 Session 4 Presentation 4 (17:05-17:20)	<p><b>Sketch-Based Registration of 3D Cine MRI to 4D Flow MRI</b>  <b>Samin Sabokrohiyeh</b>, Kathleen Ang, Mohammed Elbaz and Faramarz Samavati  University of Calgary, Canada</p> <p><i>Abstract</i>—Cardiac 4D Flow magnetic resonance imaging (4D Flow MRI) is a recent powerful technology that uniquely enables in-vivo acquisition of time-varying volumetric blood flow velocity field information in the three spatial dimensions over the cardiac cycle. Hence, 4D Flow MRI has emerged as an important medical diagnostic tool for evaluation of blood flow alteration in the heart chambers and great vessels. A critical requirement for accurate quantification and visualization of blood flow within the different heart chambers (e.g. the left ventricle (LV)) is the accurate anatomical context of cardiac chambers, which is missing in the 4D Flow MRI data. To tackle this problem, recent studies have proposed fusing the 4D Flow data with a complementary anatomical MRI scan (short axis 3D (multiple 2D slices) cine SSFP) through registration. However, since image registration is a non-linear optimization problem, the registration is slow and may not be accurate (e.g. the left ventricle can be incorrectly aligned to the right ventricle). To improve the registration performance and accuracy, localization techniques can be used. In this paper, we propose two sketch-based methods for effective localization of 4D Flow MRI to 3D cine MRI registration. We evaluate these methods and compare them with other localization methods.</p>
M1014 Session 4 Presentation 5 (17:20-17:35)	<p><b>Tensor Decomposition of Non-EEG Physiological Signals for Visualization and Recognition of Human Stress</b>  Thi T.T. Pham, Héctor Rodríguez Déniz and <b>Tuan D. Pham</b>  Linköping University, Sweden</p> <p><i>Abstract</i>—Recognition of physical and mental responses to stress is important for the purpose of stress management to reduce its negative effects in health. Wearable technology, mainly using electroencephalogram (EEG), provides information such as tracking fitness activity, disease detection, and neurological states of individuals. However, the recording of EEG signals from a wearable device is inconvenient. This study introduces the application of tensor decomposition of nonEEG data for visualizing and tracking neurological status with implication to human stress recognition. Results obtained from testing the proposed method using a PhyioNet database show visualizations that can well separate four groups of neurological statuses obtained from twenty healthy subjects, and very high up to 100% classification of the neurological statuses. The investigation suggests the potential application of tensor decomposition for the analysis of physiological measurements collected from multiple sensors. The proposed study can significantly contribute to the advancement of wearable technology for human stress monitoring.</p>

ICBBT 2019 CONFERENCE ABSTRACT

<p>M0032</p> <p>Session 4</p> <p>Presentation 6</p> <p>(17:35-17:50)</p>	<p>ECG Denoising by Using FIR and IIR Filtering Techniques: An Experimental Study</p> <p><b>Nancy Betancourt</b>, Marco Flores-Calero and Carlos Almeida</p> <p>Universidad de las Fuerzas Armadas ESPE, Ecuador</p> <p><i>Abstract</i>—In this work an experimental study is presented by verifying the performance of the FIR and IIR filters. These techniques have been used to eliminate the different types of intrinsic noise of the ECG signal. In order to measure the quality of the filters the MIT-BIH database and the metrics, percentage root mean square difference (PRD), signal to noise ratio (SNR) and mean square error (MSE) have been used. The results indicate that the filter IIR 7 has better quality to eliminate power line interference and base line wander.</p>
<p>M0020</p> <p>Session 4</p> <p>Presentation 7</p> <p>(17:50-18:05)</p>	<p>New Insights to Hydrogen Bonds to Provide Stability in the EGFR Related to Non-Small Cell Lung Cancer</p> <p><b>Avirup Ghosh</b> and Hong Yan</p> <p>City University of Hong Kong, Hong Kong</p> <p><i>Abstract</i>—Lung cancer is the most common cancer in the world, but it is one of the most preventable. Non-small cell lung cancer accounts for approximately 85% of all lung cancers. Epidermal growth factor receptor or EGFR is the class of high-affinity cell surface receptors which are essential in regulating biological processes including cell differentiation, cell survival or death, and cellular metabolism. An amino acid substitution at the 858th position of EGFR, from a Leucine(L) to an Arginine(R) causes L858R mutation within exon 21, which encodes part of the kinase domain and drives to NSCLC. For over 60% of EGFR-mutated NSCLC, another mutation T790M can cause drug resistance to erlotinib or gefitinib. In our research work, we considered three structures of EGFR, wild-type, with L858R mutation and with L858R/T790M drug-resistance mutation. The number of hydrogen bond decreases when the EGFR becomes mutated and it reduces even more in its drug-resistance structure. We perform 200 frames of molecular dynamics (MD) simulation to analyze the behavioral changes in hydrogen bonds for all three structures. Since the hydrogen bonds contribute to the conformational stability of the protein and molecular recognition, the knowledge, and results achieved from this study lead to useful insight into the mechanism of NSCLC drug resistance.</p>

<b>Dinner</b>	
<b>18:30-20:00</b>	<b>Taaba</b>

# Poster Session

May 30, 2019 (Thursday)

Time: 13:25-18:00

Venue: Lounge of Gästrikesalen

<p>M0012 Poster 1</p>	<p>Serum miR-193b-5p Serves as a Biomarker for Breast Cancer and Modulates Invasion and Migration of Tumor Cells by Targeting CD44v6 <b>Yan Du</b>, Song Hu, Yiwen Liu and <b>Feng Gao</b> Shanghai Jiao Tong University Affiliated Sixth People's Hospital, China</p> <p><i>Abstract</i>—Breast cancer is the highest mortality of cancer due to the result of metastasis. CD44 containing variant exon v6 (CD44v6) is related with tumor invasion and metastasis. However, the detailed regulating mechanism of CD44v6 is still unclear. Here, we found that CD44v6 is significantly up-regulated in invasive breast cancer cell lines (Hs-578t and BT-549) compared with low invasive ones (MCF-7 and T-47D). CD44v6 down-regulation could suppress the migration and invasion. According to the analysis of miRWalk and RNAhybrid software, CD44v6 was identified as the target of miR-193b-5p which binds to the exon v6 region. MiR-193b-5p up-regulation inhibited the Hs-578t and BT-549 migration and invasion, and restoration of CD44v6 rescued the effects of miR-193b-5p. Moreover, we used serum samples to explore whether miR-193b-5p was a potential biomarker for breast cancer. MiR-193b-5p displayed significantly low expression in breast cancer samples. Taken together, our results suggest that miR-193b-5p could be a candidate for therapy of breast cancer and serum miR-193b-5p may serve as a biomarker for breast cancer diagnosis.</p>
<p>M2007 Poster 2</p>	<p>Analysis of Factors on BVP Signal Extraction Based on Imaging Principle Xiaobiao Zhang, Xiaoyi Feng and <b>Zhaoqiang Xia</b> Northwestern Polytechnical University, China</p> <p><i>Abstract</i>—DNA glycosylase, as one member of DNA repair machineries, plays an essential role in correcting mismatched/damaged DNA base pair by cleaving the N-glycosidic bond between the sugar and target base through base excision repair (BER) pathways. Efficient corrections of these DNA lesions are critical for maintaining genome integrity and preventing premature aging and cancer. The target-site searching and recognition mechanism by DNA glycosylase, however, remains unknown and experimental characterization of the above process is still challenging due to the limited spatiotemporal resolutions. In this work, by employing</p>

	<p>high performance computing, combined with markov state model construction based on extensive all-atom molecular dynamics (MD) simulations, we identify the key intermediates of thymine DNA glycosylase (TDG) involved in the target-searching process. In particular, our studies reveal the atomistic-level details of how TDG participates in sculpturing DNA backbone and penetrates into DNA minor groove. Moreover, we also evaluate the substituent effects of various chemical modifications of the pyrimidine rings on the target searching dynamics. More importantly, our model provides the kinetic properties associated with each conformational transition.</p>
<p>M0016 Poster 3</p>	<p>Cervical Cancer Risk Prediction Model and Analysis of Risk Factors Based on Machine Learning Wenyang Yang, Xin Gou, Tongqing Xu, Xiping Yi and <b>Maohong Jiang</b> University of Twente, Netherlands</p> <p><i>Abstract</i>—Cervical cancer, as one of the most common malignant tumor among women, is difficult to be diagnosed and studied due to its complexity of disease factors and challenged prediction. In this paper, a real data-driven powerful machine learning model is employed. With this technique, we model the detection methods of cervical cancer and determine the diagnostic accuracy of current mainstream methods for cervical cancer by multi-layer perceptron. Finally, the importance index of cervical cancer risk factors can be analyzed by random forest. The experiment results have shown that there is a close relationship between the risk factors and cervical cancer. And compared with other risk factors, age, number of sexual partners, hormonal contraceptives have a greater influence on the diagnosis of cervical cancer. Therefore, our research not only improves the predictability of cervical cancer risk, but also inspires the development of pathological model based on MLP and random forest.</p>
<p>M0022 Poster 4</p>	<p>Predicting Essential Genes of <i>Escherichia coli</i> Based on Clustering Method Xiao Liu, <b>Ting He</b>, Zhirui Guo and Meixiang Ren Chongqing University, China</p> <p><i>Abstract</i>—Essential genes are important to the survival or reproduction of organisms. Computational methods for predicting essential genes are mainly supervised classification methods. These methods need label information of genes which the newly sequenced genes are absence. This encourage us to use unsupervised methods to predict essential genes. Here, the K-means clustering algorithm was used to predict the essential genes of <i>Escherichia coli</i> after the Relief algorithm was used to weight</p>

	<p>the features. A membership calculation method based on Euclidean distance between genes was designed to get AUC (area under curve) score. The average AUC score was 0.989. This research enables a satisfied prediction of essential genes.</p>
<p>M0024 Poster 5</p>	<p>DNA Digital Data Storage Based on Distributed Method <b>Yu Wang</b>, Yang Zhang and Yi Zhao Harbin Institute of Technology (Shenzhen), China</p> <p><i>Abstract</i>—DNA digital data storage refers to the technique of storing digital information on synthetic DNA. This paper introduces the method of converting digital information into genetic code based on ternary data conversion method. The “end-to-end” gene storage model was proposed without the use of address bits, which enabling unlimited information storage. With the distributed model, the information is evenly distributed among a plurality of storage tubes. Each storage tube eliminates a certain amount of data according to the congruence misplacement, and each of the chains adds 8-bit error correction bits. As a result, even if the order is disrupted, the regular order of genes can be still recovered by comparing the points. The error rate can be controlled at the average of <math>10^{-5}</math>, and the highest is <math>5.9968 \times 10^{-5}</math>, which is robust and secure.</p>
<p>M0029 Poster 6</p>	<p>Computer Aided Detection of Normal and Abnormal Heart Sound Using PCG <b>Muhammad Fahad Khan</b>, Maliha Atteeq and Adnan N. Qureshi University of Central Punjab, Pakistan</p> <p><i>Abstract</i>—A PCG (phonocardiogram) is a method of plotting of heart sounds and murmurs during a cardiac cycle, with the help of machine called phonocardiograph. A PCG can be visually represented. PCG recordings comprise of bio-acoustic statistics indicating the functional condition of the heart. Intelligent and automated analysis of the PCG is therefore very important not only in detection of cardiac diseases but also in monitoring the effect of certain cardiac drugs on the condition of the heart. PCG analysis includes segmentation of the PCG signal, feature extraction from the segmented signal and then classification. We used Kaggle data sets [10] and have extracted feature sets of different domains i.e. Time domain, frequency domain and statistical domain. We used 8 features of 118 recordings and train our different classifiers (Bagged Tree, subspace Discriminant, Subspace KNN, LDA, Quadratic SVM and Fine Tree) to obtain and compare accuracy and results. We use only two classes for classification i.e. normal and abnormal. Out of these 6 classifiers Bagged tree gave highest accuracy of 80.5%.</p>

<p>M0034 Poster 7</p>	<p>Motion Capture Based Dynamic Assessment of Hip Joint Cartilage Contact Pressure During Daily Activities <b>Xianqiang Liu</b>, Xiaoyan Zhang and Sheng-hua Zhong Shenzhen University, China</p> <p><i>Abstract</i>—Hip joint cartilage contact stresses are clinically relevant and necessary to improve our understanding of hip osteoarthritis. Therefore, the objective of this paper is to assess the contact pressure changes during series of dynamic postures such as slow walking, normal walking, fast walking, descending stairs and ascending stairs. A standard anatomical model is built from CT images and twenty kinematical models are constructed using a motion capture system. A two-step adjusted-iterative closest point method is proposed to register the anatomical model with the motion capture recorded kinematical model. After the registration, acetabular cartilage contact pressure is analyzed by a <i>_nite</i> element method. According to simulation results among twenty subjects, the contact pressure distribution of walking and stairs movements are mostly uniform during a cycle of movement. The peak of contact pressure appears at the transition location from superior to posterior. The peak of contact pressure happens almost at the time of heel-strike. The contact area is changing from anterior to superior-posterior and ending at anterior for all the activities. These results demonstrate the trends for normal hip contact pressure in cartilage during daily activities. These results also provide guidance for the diagnosis of osteoarthritis. The location at transition from superior to posterior should be paid more attention in the diagnosis of osteoarthritis. And the osteoarthritis patient should try to avoid the movement of ascending and descending stairs.</p>
<p>M0030 Poster 8</p>	<p>Fetus Heart Beat Extraction from Mother's Pcg Using Blind Source Separation <b>Maliha Atteeq</b>, Muhammad Fahad Khan and Adnan N. Qureshi University of Central Punjab, Pakistan</p> <p><i>Abstract</i>—Fetal monitoring through phonocardiography is non-invasive and very challenging technique. It is very crucial to know about the fetus heart status. Extraction of fetus heart beat from mother heart sound is very challenging and difficult task due to the presence of additional sounds like mother organ sound, mother respiration and external noises. Benchmarked datasets and literature are also not available. In this research we extract fetus heart beat from mother beat using Blind source separation technique like STFT. Shiraz University Fetal Heart Sounds Database of Physionet has been used. 92 maternal heart sounds are used. It can be seen that the algorithm well separates the mixed source into maternal and fetal heart sounds.</p>

<p>M1012 Poster 9</p>	<p>Analysis of the Target Genes of Transcription Factor ZNF536 in Lung Adenocarcinoma <b>Xintong Xu</b> Rutgers Preparatory School, USA</p> <p><i>Abstract</i>—Lung cancer is becoming one of the most common and deadly cancers. We calculated the mutation frequency of all the transcription factors from the downloaded lung adenocarcinoma (LUAD) data from TCGA and found ZNF536 had a relatively high mutation frequency. To further reveal the potential functional roles of ZNF536 on lung adenocarcinoma, RNA-Seq data of LUAD were downloaded, and classified into the mutant and wild groups based on ZNF536 mutant states, then the differentially expressed genes between these two groups were calculated. A p-value lower than 0.05 suggests a significant difference. As a result, among a total of 20,531 genes, 1,174 genes were upregulated and 863 genes were downregulated in the ZNF536 mutant group compared with the wild group. Functional enrichment analysis revealed that these dysregulated genes were mainly related to cell cycle, mismatch repair, and DNA replication, and so on. By reviewing studies on lung ADC by other scientists, upregulated genes, HDAC2, EP300, MAPK1, KRAS, NRAS, which regulate the initiation, growth, invasion and metastasis of lung ADC cells. Taken together, these findings suggest that ZNF536 plays a critical part in the development of lung ADC and may serve as a potential target for new medications in treating lung ADC.</p>
<p>M1015 Poster 10</p>	<p>S1 and S2 Heart Sound Recognition Using Optimized BP Neural Network Xu Chundong, <b>Long Qinghua</b> and Zhou Jing Jiangxi University of Science and Technology, China</p> <p><i>Abstract</i>—For the problems of Back Propagation(BP) neural network relying on initial weights, slowing convergence and easily falling into local extremum, the development ability of standard Artificial Bees Colony algorithm is weak, local search ability is poor, etc, propose an improved artificial bees colony algorithm to optimize BP neural network for fundamental heart sound(FHS) recognition. A novel improving following bees global search and probability selection algorithm, applying the optimized BP neural network to the FHS recognition is proposed. For the problems of heart sound contain noisy and Mel Frequency Cepstrum Coefficient(MFCC) feature parameters of heart sound signal are not effective under the condition of low signal-to-noise ratio(SNR). Propose an improved method to extract MFCC parameters, experimental results show that heart sound improved Mel Frequency Cepstrum Coefficient(IMFCC) feature is superior to MFCC and homomorphic envelope(Homo-Env) feature in the same case of classifier. In the same feature parameters, the improved Artificial Bees Colony algorithm optimization of BP neural network recognition accuracy has a greater degree of improvement, comparing with the classical BP, Random forest, support vector machine, k-Nearest Neighbor algorithm.</p>

<p>M1009 Poster 11</p>	<p>Magnetically Targeted Drug Delivery System Through Imaging Technology PID Feedback Control, and MATLAB  <b>Faizan Saifullah</b>, Hafsa Inam, Murtaza Najabat Ali and Umar Ansari  National University of Sciences and Technology, Islamabad Pakistan</p> <p><i>Abstract</i>—Conventional dose such as capsules which are used traditionally have severe side effects including raising of blood sugar level by dissolution of drug in blood, can be overcome by replacing traditional drug delivery with specifically targeted drug delivery system. The main concept of using magnetic levitation for drug delivery is to deliver the drug to a specific point via magnetic actuation and imaging technique, magnetic material coated by drug can rupture the artery by getting strongly attracted towards externally applied magnetic field. By taking magnetically levitated drug to the targeted area, it will minimize the risk of rupturing of the artery. Dispersion of drug will be minimized as drug-coated core will be under influence of applied electromagnetic field, drug can be released by altering electromagnetic fields. In this study, one-dimensional (1D) force system is used. Two forces counter each other i.e. electromagnetic force and gravitational force. Addition of <math>K_i</math> to <math>K_p</math> and <math>K_d</math> speeds up the motion when reaching to the targeted set point, blob stays in levitated condition around the set point thus stability is increased by the addition of <math>K_i</math> but oscillations are still present that hinder the stability of the system. Exponential function is introduced to decrease the power of <math>K_p</math>, in result, it supplies the power when the error is large, power gets zero when error is reduced to zero. In this stable system, <math>K_p</math> and <math>K_d</math> gain are applied to minimize the oscillations and keep the blob levitated at targeted set point.</p>
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## Listener

Name	Affiliation
Ki-Yeol Kim	Yonsei University College of Dentistry, Republic of Korea
Georgios Tegos	Alexander Technological Educational Institution of Thessaloniki, Greece
Weiwei Chen	Guangxi Medical University, China
Qian Liu	Guangxi Medical University, China
Jiamin Liang	Guangxi Medical University, China
Xinxi Mo	Guangxi Medical University, China
Ogunyemi Daniel Oluwafemi	N/A
Maeen Swileh	Roseneft for Oil and Gas Services, Yemen
Sadeq Al-Ashwal	Roseneft for Oil and Gas Services, Yemen
Kadiatou Traore	Niger Sahel Energie Co., Mali
Mohamed Traore	Niger Sahel Energie Co., Mali
Sinali Kouyate	Niger Sahel Energie Co., Mali

# Conference Venue

## Elite Palace Hotel, Stockholm

<https://www.elite.se/en/hotels/stockholm/palace-hotel/>  
S:t Eriksgatan 115 113 43 Stockholm



Elite Palace Hotel is a modern hotel located in downtown Stockholm. The hotel guests can enjoy the nearness to all city attractions while still in a peaceful environment near walking paths by the water. Nearby the hotel you will find many pubs, restaurants and cafes from all over the world. At the hotel you enjoy delicious meals in The British style pub Bishops Arms, who invite you to exciting taste experiences, as it offers exclusive beer and whisky tastings.

For relaxation and recreation we are pleased to offer Palace Spa Relax and gym. As our guest you will receive a discount at the gym. The hotel supports wireless Internet and has got great transportation opportunities. The airport bus stops just outside the hotel and the subway station is only a 5 minute walk away. From the 10th of July, there will be a 3 minute walking distance to the commuter train connected to subway station Stockholm Odenplan. If you are travelling by car the hotel offers indoor parking.

**Note:** The registration fee does not cover the accommodation. It is suggest that an early reservation be done because of peak season.

# Academic Visit & Tour

9:00-17:30, May 31, 2019 (Friday)

(Tips: Please arrive at the Lobby of Elite Palace Hotel, Stockholm on 8:50 a.m. The following schedule is only for participants who registered the Academic Visit & Tour. The following places are for references, and the final schedule should be adjusted to the actual notice. The bus ticket and the entrance ticket of ABBA The Museum were included. Other paying items should be paid by participants.)

## 1. Departure from Elite Palace Hotel, Stockholm (9:00)



## 2. Visit The City Hall (9:30-10:30)

The Stockholm City Hall is one of Sweden's most famous buildings, and one of the capital's most visited tourist attractions. It is famous for its grand ceremonial halls and unique pieces of art and is the venue of the Nobel Prize banquet held on 10th of December each year. It also houses offices for 200 people including the Municipal Council.

## 3. Visit Stockholm Gamla Stan (11:00-12:00)

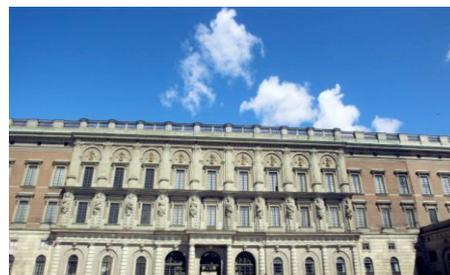
Gamla Stan (Old Town) is the historic heart of Stockholm. It is a favorite with tourists thanks to the appealing medieval streets and the many sights. Gamla Stan is packed with interesting historical sights and museums. The most famous attraction is the Royal Palace, built in the early eighteenth century at the site of the former castle. Nearby is one of the oldest buildings in Gamla Stan, the Storkyrkan (Great Church), Stockholm's cathedral, originally built Stortorget, Gamla Stan, Stockholm Stortorget in the early fourteenth century.



## 4. Lunch at Gamla Stan (12:00-13:00)

## 5. Visit The Royal Palace (13:00-14:00)

The palace is built in baroque style by the architect Nicodemus Tessin and is formed as a Roman palace. The palace has more than 600 rooms divided between eleven floors with a state apartment facing the city and smaller living rooms facing the inner courtyard. The palace contains many interesting things to see. In addition to the Royal Apartments there are three museums steeped in regal history: the Treasury with the regalia, the Tre Kronor Museum that portrays the palaces medieval history and Gustav III's Museum of Antiquities.



**6. Visit Vasa Museum (14:30-16:00)**

The Vasa Museum (Swedish: Vasamuseet) is a maritime museum in Stockholm, Sweden. Located on the island of Djurgården, the museum displays the only almost fully intact 17th century ship that has ever been salvaged, the 64-gun warship Vasa that sank on her maiden voyage in 1628. The Vasa Museum opened in 1990 and, according to the official web site, is the most visited museum in Scandinavia. Together with other museums such as the Stockholm Maritime Museum, it belongs to the Swedish National Maritime Museums (SNMM).



**7. Visit ABBA The Museum (16:30-17:30)**

ABBA The Museum is not a conventional museum. While you can see exhibits with the band's original outfits, instruments and other memorabilia, the museum is focused on interaction and invites you to sing and dance as the fifth member of Sweden's most famous band. The museum is housed in a rather unassuming building on the Djurgarden island in central Stockholm, which is also home to the Swedish Music Hall of Fame and the Pop House Hotel.









## Feedback Information

(Please fill this form and return it to conference specialist during the conference days.)

<b>Personal Information</b>					
Conference Name and Paper ID					
Full Name					
E-mail Address					
Area of Research					
Affiliation					
<b>Please indicate your overall satisfaction with this conference with “√”</b>					
	Very Satisfied	Somewhat Satisfied	Neutral	Somewhat Dissatisfied	Very Dissatisfied
Conference Content					
Presentation and Paper Value					
Registration Process					
Venue					
Food and Beverage					
Are You A Member of CBEES	Yes <input type="checkbox"/> No <input type="checkbox"/> (If “No”, you may apply membership from <a href="http://www.cbees.org/member.htm">http://www.cbees.org/member.htm</a> )				
Do You Willing to Receive CBEES Future Conferences Information Via E-mail	Yes <input type="checkbox"/> No <input type="checkbox"/>				
Where did you get the conference information?					
Would you please specify the main reason for attending this conference?					
Did the conference fulfill your reason for attending?	Yes- Absolutely <input type="checkbox"/> Yes- But not to my full extent <input type="checkbox"/> No <input type="checkbox"/> (If “No”, please tell us the main reason)				

ICBBT 2019 CONFERENCE ABSTRACT

<p>Would you please list the top 3 to 5 universities in your city?</p>	
<p>Other Field of Interest</p>	
<p>Any Other Suggestions/Comments</p>	

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!