IEEE BIBE 2013

13th IEEE International Conference on BioInformatics and BioEngineering

November 10-13, Chania, Greece

Technical Program and Book of Abstracts

Sponsors

National Technical University of Athens

Institute of Electrical and Electronic Engineers

Biological and Artificial Intelligence Foundation

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University of Patras

Unit of Medical Technology & Intelligent Information Systems

Foundation for Research and Technology-Hellas - Institute of Molecular Biology and Biotechnology

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Contents

Welcome Message

Dear colleagues and students,

On behalf of the Organizing Committee, we would like to cordially invite you to the 13th International Conference on BioInformatics and BioEngineering (IEEE BIBE 2013).

The aim of IEEE BIBE 2013 is to cover a broad spectrum of up-to-date topics of Bioinformatics and Bioengineering by giving the opportunity to scientists from diverse fields and disciplines to participate in the presentation, discussion and evaluation of the latest advances, research challenges, and opportunities that these two important and complementary disciplines bring to modern science.

The event is organized and sponsored by the Institute of Electrical and Electronic Engineers (IEEE) and by the Artificial Intelligence Foundation (BAIF). The IEEE Greece Section, the IEEE EMBS Greece Chapter, the National Technical University of Athens (NTUA), the University of Ioannina (UOI), the University of Patras (UOP), the Technical University of Crete (TUC), the Wright State University (WSU), the Institute of Communication and Computer Systems (ICCS), the Unit of Medical Technology &

Intelligent Information Systems and the Foundation for Research and Technology-Hellas - Institute of Molecular Biology and Biotechnology are co-organizing the event.

IEEE BIBE 2013 marks the continuation of the previous 12 successful conferences held in Washington DC,USA, in 2000, in Bethesda, USA, in 2001, in Bethesda, USA, 2003, in Taichung, Taiwan, in 2004, in Minneapolis, USA, in 2005, in Washington DC,USA, in 2006, in Boston, USA, in 2007, in Athens, Greece, in 2008, in Taichung, Taiwan, in 2009, in Philadelphia, USA, in 2010, in Taichung, Taiwan, in 2011 and in Larnaca, Cyprus, in 2012.

Around 200 papers authored by 658 scientists, engineers, and physicians will be presented under the *Bioiinformatics Track*, the *Bioengineering Track*, the 6th IEEE International Symposium on Monitoring and Surveillance Research: Healthcare and BioInformatics and the *Special Sessions on Risk Analysis and Prediction in Cardiovascular Applications, on Porting Bio and Health Informatics to the Cloud, on Computational BioEngineering, on The Digital Patient concept: Vision and Early Demonstrations and on Advanced Concepts in Endoscopic Imaging and Engineering*.

Extended versions of the best papers of the conference will be invited for publication in journal special issues of the IEEE Journal of Biomedical and Health Informatics, the International Journal on Artificial Intelligence Tools, and the International Journal on Monitoring & Surveillance Technologies Research.

We would like to thank all the track chairs and reviewers who put a lot of time and effort, under very tight deadlines during summer time, in order to help us review all the papers and put the program together.

The program features nine keynote presentations from distinguished colleagues. The first keynote will be given by ***Prof. Robert W. Williams***, UT-Oak Ridge National Laboratory Chair in Computational Genomics, Center for Integrative and Translational Genomics, Department of Anatomy and Neurobiology, University of Tennessee Health Science Center, Memphis USA. The second keynote will be given by ***Mr. Anastasius Gavras***, Steering board member of the FI-PPP, Member of the editorial board of the Eurescom. The third keynote will be given by ***Prof. Constantinos S. Pattichis***, Department of Computer Science, University of Cyprus. The forth keynote will be given by ***Prof. Bruce Wheeler***, Department of Biomedical Engineering, University of Florida, Gainesville, IEEE EMBS President. The fifth keynote will be given by ***Prof. Anthony Guiseppi–Eli****e*, Sc.D., FAIMBE Professor, Clemson University. The sixth keynote will be given by ***Prof. Metin Akay***, Founding Chair, John S Dunn Endowed Chair Professor, Department of Biomedical Engineering, Cullen College of Engineering, University of Houston, Houston, TX, USA. The seventh keynote will be given by ***Prof. Yuan-Ting Zhang***, Director of Joint Research Center for Biomedical Engineering at EE, the Chinese University of Hong Kong, Hong Kong, China, Director of the Key Lab for Health Informatics of Chinese Academy of Sciences (HICAS) at SIAT, Shenzhen, China. The eighth keynote will be given by ***Prof. Jose C. Principe***, Computational NeuroEngineering Laboratory, University of Florida, Gainesville. The last keynote will be given by ***Prof. Luis Kun***, IEEE Fellow - Distinguished Visitor CS / SSIT William Perry, Center for Hemispheric Defense Studies at the National Defense University, USA.

This year’s BIBE is held in the sunny island of Crete - Chania, an island with a huge recorded history and cultural heritage. We hope that you will find time to explore the island.

On behalf of the Organizing Committee, we would like to wish you all a very stimulating and exciting Conference.

Dimitrios I. Fotiadis
Konstantina S. Nikita
Conference Chairs

Organization and Committees

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Dimitrios I. Fotiadis, UOI, Greece

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H. Papadopoulos, Cyprus
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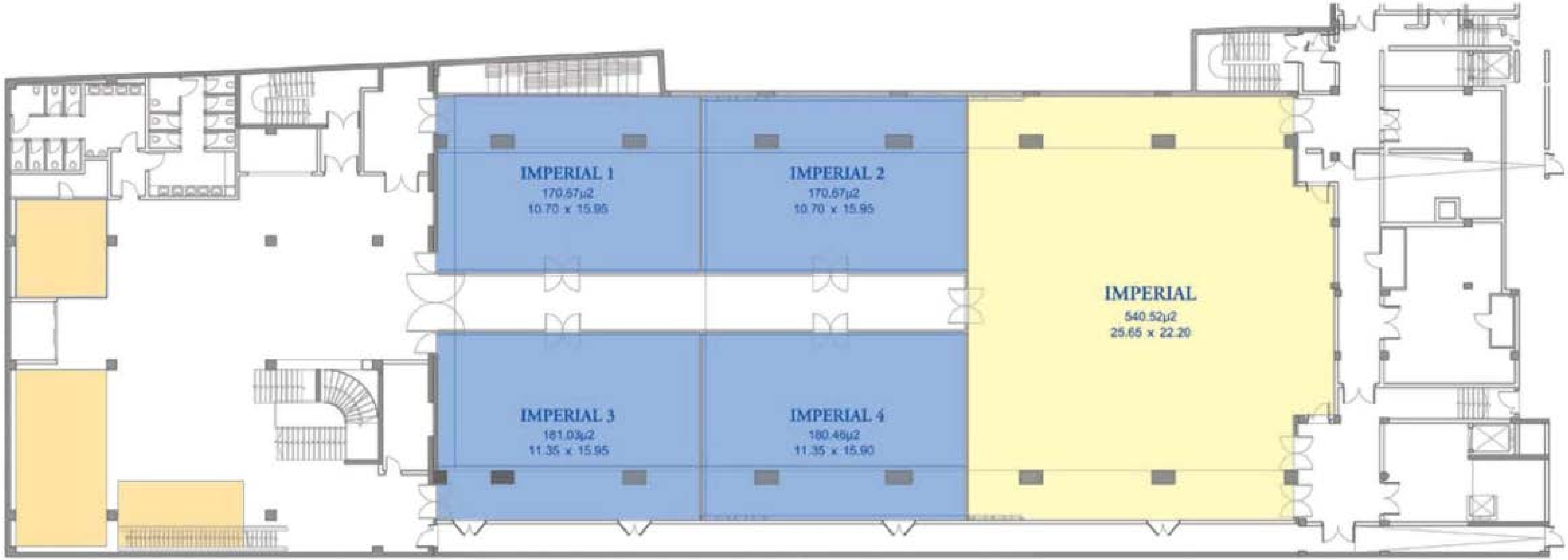
Imperial Congress Hall Plan



Registration

Registration desk of the conference will be open from November 9th at 14:00 until the end of the conference. On-site registration is also available.

Registration includes: Access to all sessions, exhibits, welcome reception, conference program, conference proceedings on USB flash, plus additional conference handouts.

Social Program

Opening Ceremony

Sunday, 10 November 2013 at 18:30

18:30 Welcome by the Conference Chairs
Prof. Konstantina S. Nikita
National Technical University of Athens

Prof. Dimitrios I. Fotiadis
University of Ioannina

18:45 Welcome by the rector of Technical University of Crete
Prof. Vassilios Digalakis
Technical University of Crete

19:00 Plenary Lecture
Prof. Robert W. Williams,
University of Tennessee Health Science Center, Memphis, USA
"Systems Genetics: Experimental and Computational Challenges"

19:30 Plenary Lecture
Mr. AnastasiusGavras,
Member of the editorial board of the Eurescom
"Emerging trends for decentralized e-health services in smart cities"

20:00 Presentation of achievement award to
Prof. Nikolaos Bourbakis
Wright State University, Biological and Artificial Intelligence Foundation, USA

Prof. Yuan-Ting Zhang
Director of Joint Research Center for Biomedical Engineering at EE,the Chinese University of Hong Kong, Hong Kong, China.
Director of the Key Lab for Health Informatics of Chinese Academy of Sciences (HICAS) at SIAT, Shenzhen, China.

The Opening Ceremony will be held in Imperial room of Imperial Congress hall of Minoa Palace Resort & Spa hotel.

Welcome Reception

Sunday, 10 November 2013 at 20:30

After the opening ceremony and the award of Prof. N. Bourbakis and Prof. Y.T. Zhang, the day will close with a welcome cocktail for all registered delegates and registered accompanying persons at the “Galini” bar of Minoa Palace Resort & Spa.

Barbeque

Monday, 11 November 2013 at 21:00

On Monday evening after the end of the sessions, barbeque will be organized at “Elia” restaurant of Minoa Palace Resort and Spa hotel. This will be free for all the student participants of the conference. The students participants that are interested in participating are kindly asked to bring five songs from their countries.

Excursion

Tuesday, 12 November 2013 at 15:30

Please note that on Tuesday, we have organized a beautiful excursion to the old city of Chania. This will be free to all participants. This excursion will start at 15:30.

The **old town** is built around the Venetian port and is also a relatively integral area where Venetian buildings and later Turkish elements compose a unique architectural style. Due to the historic center of Chania with its Venetian walls defining the borders between the old and new city and its ramparts, the city has been pronounced as preserved. It consists of five connected districts surrounding the Venetian port.

Its design was made by Venetian engineer Michelle Sammichelli. The **Lighthouse** is located at the end of the rock protecting the port from the north. It was built in 1570 by the Venetians and reconstructed in 1830 by the Egyptians and from there on preserves its current state.

On the east of Palea Poli is Splantzia (or Plaza) district built on the former Turkish district. Here you will see among others Aghii Anargiri church, the only Orthodox church which had the permission to operate during the period of the Venetian and Turkish occupations. You will also see the Sintrivani square.

Neoria (or Chiones) district on **the northeast side** is located in the area of the former port of the city and of the Venetian ship yards of 14th and 16th centuries from which it also took its name.

Kastelli district is in the center of Palea Poli (Old Town) west of Neoria. It is the exalted location of the Byzantine citadel where “palatso” (palace) of the Venetian commander and the lodgings of Pashas of Chania were later built. Venetians used to call the area Castello Vecchio.

On the southeast of the old city lies the Hebrew district or else Ovraika. It reminds us the times when the developing Hebrew community of Chania was obliged by the Venetians to move to a delimitated area called judeca where two synagogues were operating.

On the boarders of Ovraika, in Chalides Street, you will see the Folklore Museum of Chania and Aghios Fragkiskos church (14th century) which houses the Archeological Museum of Chania. On the north side is the Turkish bath (chamam). In the south side of Ovraika and on Skridlof Street lies the so called Stivanadika (from stivani, the Cretan boots). Among the shops selling leather items and souvenirs survive some traditional shoe ateliers.

Following your tour in the old town of Chania, you will re-board your coach for your transfer to the place where the Congress Dinner will be held.

Congress Dinner

Tuesday, 12 November 2013 at 20:30

The Congress Dinner will be hosted at “Nikolas” tavern. The dinner will comprise of sumptuous and tasteful dishes and we will be entertained with live music.

After the end of the dinner you will re-board your coach for the return transfer to the hotel.

Program at a Glance

Sunday 10 November 2013			
14:00-18:30	Registration		
18:30-18:45	Opening – *Imperial room* Welcome by the conference chairs Prof. K. S. Nikita and Prof. D. I. Fotiadis		
18:45-19:00	Welcome by the Rector of Technical University of Crete Prof. V. Digalakis		
19:00-19:30	Plenary Lecture: **Prof. Robert W. Williams,** *University of Tennessee Health ScienceCenter, Memphis, USA* **“Systems Genetics: Experimental and Computational Challenges”**		
19:30-20:00	Plenary lecture: **Mr. Anastasius Gavras,** *Member of the editorial board of the Eurescom, Germany* **“Emerging trends for decentralized e-health services in smart cities”**		
20:00-20:30	Presentation of achievement award to Prof. N. Bourbakis and Prof. Y. T. Zhang – *Imperial room*		
20:30-22:30	Welcome cocktail- *Bar “Galini”, Minoa Palace Resort & Spa*		
Monday 11 November 2013			
08:00-08:30	Invited lecture: **“An Overview of M-Health Medical Video Communication Systems”** **Prof. Constantinos S. Pattichis,** *University of Cyprus, Cyprus*		
08:30-10:00	**Session M.1.1** *Imperial 1 room*	**Session M.1.2** *Imperial 2 room*	**Session M.1.3** *Imperial 3 room*
10:00-10:30	Coffee Break – *Imperial Lobby*		
10:30-12:00	**Session M.2.1** *Imperial 1 room*	**Session M.2.2** *Imperial 2 room*	**Session M.2.3** *Imperial 3 room*
12:00-12:30	Invited lecture: **“Challenges and Opportunities in Cardiovascular Health Informatics”** **Prof. Yuan-Ting Zhang,** *Chinese University of Hong Kong, China*		
12:30-13:30	Buffet Lunch – *“Elia” restaurant*		
13:30-15:00	**Session M.3.1** *Imperial 1 room*	**Session M.3.2** *Imperial 2 room*	**Session M.3.3** *Imperial 3 room*
15:00-16:30	**Session M.4.1** *Imperial 1 room*	**Session M.4.2** *Imperial 2 room*	**Session M.4.3** *Imperial 3 room*
16:30-17:00	Coffee Break – *Imperial Lobby*		
17:00-19:00	**Satellite event – Panel discussion on knowledge-intensive entrepreneurship,** *Imperial room*		
19:00-20:30	**Session M.5.1** *Imperial 1 room*	**Session M.5.2** *Imperial 2 room*	**Session M.5.3** *Imperial 3 room*
21:00-23:00	Barbeque – *“Elia” restaurant*		

Tuesday 12 November 2013				
08:00-08:30	Invited lecture: **“Implantable Microsystems for the Management of Trauma”** **Prof. Anthony Guiseppi–Elie**, *Clemson University, USA*			
08:30-10:00	**Session T.1.1** *Imperial 1 room*	**Session T.1.2** *Imperial 2 room*	**Session T.1.3** *Imperial 3 room*	**Session T.1.4** *Imperial room*
10:00-10:30	Coffee Break – *Imperial Lobby*			
10:30-11:00	Invited lecture: **“Advances (Innovations) in Neurotechnology”** **Prof. Metin Akay,** *University of Houston, USA*			
11:00-12:30	**Session T.2.1** *Imperial 1 room*	**Session T.2.2** *Imperial 2 room*	**Session T.2.3** *Imperial 3 room*	**Satellite event** **Short seminar** **“From the lab to the market”** *Imperial room*
12:30-13:00	Invited lecture: **“Brain on a Chip: From Patterns to Circuits with Information Transfer”** **Prof. Bruce Wheeler,** *University of Florida, Gainesville, USA, IEEE EMBS President*			
13:00-14:00	Buffet Lunch– *“Elia” restaurant*			
14:00-15:30	**Session T.3.1** *Imperial 1 room*	**Session T.3.2** *Imperial 2 room*	**Session T.3.3** *Imperial 3 room*	**Session T.3.4** *Imperial room*
15:30-19:00	Excursion – *Old city of Chania*			
20:00-22:30	Congress Dinner – *“Nikolas” tavern*			
Wednesday 13 November 2013				
08:30-09:00	Invited lecture: **“Somatosensory Brain Machine Interfaces”** **Prof. Jose C. Principe,** *University of Florida, Gainesville, USA*			
09:00-10:30	**Session W.1.1** *Imperial 1 room*	**Session W.1.2** *Imperial 2 room*		**Session W.1.3** *Imperial 3 room*
10:30-11:00	Coffee Break – *Imperial Lobby*			
11:00-11:30	Invited lecture: **“Wellness, Disease and Public Health Informatics: Multidimensional Global Threats with Local Impact”** **Prof. Luis Kun**, Center for Hemispheric Defense Studies at the National Defense University, USA			
11:30-13:00	**Session W.2.1** *Imperial 1 room*	**Session W.2.2** *Imperial 2 room*	**Session W.2.3** *Imperial 3 room*	**Session W.2.4** *Imperial room*
13:00-13:30	Light Lunch – *Imperial Lobby*			
13:30-15:00	**Session W.3.1** *Imperial 1 room*	**Session W.3.2** *Imperial 2 room*		**Session W.3.3** *Imperial 3 room*
15:00-15:30	Closing remarks – Student Paper Competition Awards, *Imperial room*			

🟨	Algorithms, Modeling and Simulation of Bio-Sets
🟪	Bio-Imaging
🟪	Biological Systems and Models
🟩	Biomedical Data Engineering
🟦	Biomedical Image Processing, Analysis and Visualization
🟩	Biomedical Signal Processing
🟦	Bio-Ontology and Data Mining
🟦	Cardiovascular and Respiratory Systems Engineering
🟨	Clinical Engineering
🟥	Computer Assisted Intervention Systems
🟩	Data Visualization
🟨	Drug Discovery
🟦	Engineering Models in Bio-Medicine
🟥	Functional Genomics, Proteomics
🟧	Gene Expression Analysis & Bioinformatics Engineering
🟥	Identification and Classification of Genes
🟪	Intelligent Therapeutic & Diagnostic Systems
⬜	NeuorEngineering, Neuromuscular Systems and Rehabilitation Engineering
🟩	Satellite event
🟩	Sequence Search and Alignment & Systems Biology
⬜	Special Session
🟦	Workshop –ISMSR-13

*All plenary and invited lectures will be held at Imperial room of Imperial Congress Hall of Minoa Palace Resort and Spa hotel.

Satellite Event

Satellite Event on Innovation & Entrepreneurship

"Inspiring and enabling entrepreneurship – Bridging the gap between the lab and the marketplace"

Organized in cooperation with the Innovation & Entrepreneurship Unit of the National Technical University of Athens (NTUA)

The main aim of the satellite event is to instill an entrepreneurial spirit to the participants and support innovative business ideas by covering the principles of entrepreneurship and aspects of mentoring and assisting start-ups. The event consists of three parts:

1. Panel discussion on knowledge-intensive entrepreneurship.
2. Short seminar "From the lab to the market".
3. Individualized coaching meetings for researchers or research teams interested in converting their ideas into a new business concept.

Contributors

Johan Van den Bossche

- Co-founder & Manager of SO Kwadraat, a non-profit organization for supporting high-tech entrepreneurs and spin-offs.
- Serial Entrepreneur of high-tech start-ups.

Thérèse Schölvinck

- Director in Medical Technology at the European Patent Office.

Nikolaos Stergiopulos

- Professor of Biomedical Engineering at the École Polytechnique Fédérale de Lausanne.
- Founder & Director of Rheon Medical SA and Antlia SA.

Yannis Caloghirou

- Professor of Economics of Technology and Industrial Strategy at the NTUA.
- Head of Innovation & Entrepreneurship Unit of NTUA.

Ioanna Kastelli

- Coordinator of Innovation & Entrepreneurship Unit of NTUA.

Antonis Livieratos

- Consultant for the establishment & growth of high-tech companies at the Innovation & Entrepreneurship Unit of NTUA.

Maria-Teresa Arredondo Waldmeyer

- Professor of Telecommunications at the Universidad Politécnica de Madrid.

Metin Akay

- Professor of Biomedical Engineering at the University of Houston.

Costas Balas

- Professor at the Technical University of Crete.
-Winner of the Applied Research & Innovation Competition "Greece Innovates"

Panel discussion on knowledge-intensive entrepreneurship

17.00-17.20	**"The role of the academic lab in the innovation and development of clinically relevant medical technology"** Nikolaos Stergiopulos, École Polytechnique Fédérale de Lausanne, Switzerland
17.20-17.40	**“Competitive strength through patents in the medical area:** **- If you invented it, protect it** **- If they invented it, make sure you know about it”** Thérèse Schölvinck, European Patent Office, Netherlands
17.40-18.00	**“How to create your own high-tech company”** Johan Van den Bossche, SO Kwadraat, Belgium
18.00-18.20	**“Should I, Would I, Could I, and I did it. Creating new knowledge-intensive entrepreneurial ventures in Europe”** Yannis Caloghirou, National Technical University of Athens, Greece
18.20-19.00	**Round table** *Headed by* Yannis Caloghirou, National Technical University of Athens*,* Greece*, Contributors*

Metin Akay, University of Houston, USA
Maria-Teresa Arredondo Waldmeyer, Universidad Politécnica de Madrid, Spain
Costas Balas, Technical University of Crete, Greece
Ioanna Kastelli, National Technical University of Athens, Greece
Antonis Livieratos, National Technical University of Athens, Greexe
Thérèse Schölvinck, European Patent Office, Netherlands
Nikolaos Stergiopulos, École Polytechnique Fédérale de Lausanne, Switzerland
Johan Van den Bossche, SO Kwadraat, Belgium

Short seminar “From the lab to the market”

The seminar will comprise short interventions and interaction on the following topics:

- Market intelligence especially in B2B transactions
- From knowledge to practice
- Intellectual property protection with emphasis on the field of bioinformatics and bioengineering
- Financing innovation
- Business models
- The founding team of the new venture
- Managing risk

During this seminar the contributors intend to discuss with the participants on specific issues of their interest.

After the seminar, there will be possibility for participants to have individual discussion with the experts on research ideas that might be transformed into business ideas.

Contributors
Thérèse Schölvinck, European Patent Office, Netherlands
Johan Van den Bossche, SO Kwadraat, Belgium
Yannis Caloghirou, National Technical University of Athens, Greece
Ioanna Kastelli, National Technical University of Athens, Greece
Antonis Livieratos, National Technical University of Athens, Greece

6th IEEE International Symposium on Monitoring and Surveillance Research (ISMSR): Healthcare and BioInformatics

Aim & Scope

The ISMSR actually is the 6th annual event and is the continuation of the IEEE International Symposium on Research on Assistive Technologies (2007) and the Assistive and Monitoring Technologies tracks from the IEEE Conferences (TAI, BIBE, IISA) 2008-2012. The annual IEEE International Symposium on Monitoring & Surveillance Research (ISMSR) provides a major international forum where the creation and exchange of ideas related to smart homes, ambient assistive living, and monitoring and surveillance research are fostered among academia, industry, and government agencies. The symposium facilitates the cross fertilization of these ideas and promotes their transfer into practical tools, for developing intelligent systems and pursuing monitoring and surveillance applications, like Bioinformatics and Bioengineering. The ISMSR encompasses all technical aspects of specifying, developing and evaluating the theoretical underpinnings and applied mechanisms of the Monitoring and Surveillance based components of computer tools (i.e. algorithms, architectures and languages), smart devices and environments, and advanced sensors.

Workshop Sessions

Session M.1.3: *Healthcare Monitoring Technologies and Methods*

Chair: *Prof. Nikolaos Bourbakis*

Monday 11 November 2013

08:30-10:00 am

Room: *Imperial 3*

Session M.2.3: *Computational Oncology: From mathematical models to clinical practice*

Chair: *Prof. Michalis Zervakis*

Monday 11 November 2013

10:30-12:00 am

Room: Imperial 3

Session M.2.3 is supported by the project “YPERThEN”, which is an INTERREG 2007-2013 project, funded by National Strategic Reference Framework (NSRF) and funds from Greece and Cyprus

IJMSR special issue

Extended versions of the best papers of the conference will be invited for publication in a special issue of the International Journal on Monitoring and Surveillance Research: Healthcare and Safety (IJMSR).

Awards

Sunday 10 November 2013

20:00 Presentation of achievement award to Prof. N. Bourbakis

In recognition of his valued contribution to the field of Visually Impaired and Blind Information Technologies

20:15 Presentation of achievement award to Prof. Y. T. Zhang

In recognition of his valued contribution to Biomedical Health Informatics

Chairs: *Prof. Konstantina S. Nikita, Prof. Dimitrios I. Fotiadis*

Wednesday 13 November 2013

14:30 Student Paper Competition Awards

The five finalists of the competition will receive commemorative and monetary awards. The sponsor of the awards is Biological and Artificial Intelligence Foundation - BAIF. The winners will be also invited to submit extended versions of their papers in journal special issues on topics related to the conference.

Chair: *Prof. George Spyrou*

Plenary Lectures

“Advances (Innovations) in Neurotechnology ”

Tuesday 12 November 2013

10:30-11:00

Imperial room

Chair: Prof. Dimitrios Koutsouris

Prof. Metin Akay
Founding Chair, John S Dunn Endowed Chair Professor,
Department of Biomedical Engineering, Cullen College of
Engineering, University of Houston, Houston, TX, USA

Abstract

Neural Engineering is a new discipline which unites engineering, computer science, physics, chemistry, and mathematics with cellular, molecular, cognitive and behavioral neurosciences, to understand the organizational principles and underlying mechanisms of the biology of neural systems, and to study the behavior dynamics and complexities of neural systems in nature. Therefore, it deals with many aspects of basic and clinical problems associated with neural dysfunction including the representation of sensory and motor information, the electrical stimulation of the neuromuscular system to control the muscle activation and movement, the analysis and visualization of complex neural systems at multi-scale from the single-cell and to the system levels to understand the underlying mechanisms, the development of novel electronic and photonic devices and techniques for experimental probing, the neural simulation studies, and the design and development of human-machine interface systems and artificial vision sensors and neural prosthesis to restore and enhance the impaired sensory and motor systems and functions from gene to system.

Furthermore, the neuroscience has become more quantitative and information-driven science since emerging implantable and wearable sensors from macro to nano and computational tools facilitate collection and analysis of vast amounts of neural data. Complexity analysis of neural systems provides physiological knowledge for the organization, management and mining of neural data by using advanced computational tools since the neurological data are inherently complex and non-uniform and collected at multiple temporal and spatial scales. The investigations of complex neural systems and processes require an extensive collaboration between biologists, mathematicians, physicists, computer

scientists and engineering to improve our understanding of complex neurological process from system to gene.

To highlight this emerging discipline, we devote this talk to the recent advances in neural engineering.

Curriculum Vitae

Metin Akay received his B.S. and M.S. in Electrical Engineering from the Bogazici University, Istanbul, Turkey in 1981 and 1984, respectively and a Ph.D. degree from Rutgers University in 1990. He is currently the founding chair of the new Biomedical Engineering Department and the John S. Dunn professor of biomedical engineering at the University of Houston. He has played a key role in promoting biomedical education in the world by writing and editing several books, editing several special issues of prestigious journals, including the Proc of IEEE, and giving several keynote and plenary talks at international conferences, symposiums and workshops regarding emerging technologies in biomedical engineering.

He is the founding editor-in-chief of the Biomedical Engineering Book Series published by the Wiley and IEEE Press and the Wiley Encyclopedia of Biomedical Engineering. He is also the editor of the Neural Engineering Handbook published by Wiley/IEEE Press and the first steering committee chair of the IEEE Trans on Computational Biology and Bioinformatics.

He established the IEEE EMBS Special Topic Conference on Neural Engineering. He is also the chair of the IEEE EMBS Neuroengineering Technical Committee. He was the program chair of the International IEEE EMBS 2001 and the co-chair of the International IEEE EMBS 2006 and the program co-chair of the International IEEE EMBS 2011 and the IEEE EMBS Point-of-Care Health Technologies (POCHT) 2013.

He currently serves on the advisory board of several international journals including the IEEE T-BME, IEEE T-ITIB, Smart Engineering Systems etc. and furthermore serves on several NIH and NSF review panels

Dr. Akay is a recipient of the IEEE EMBS Early Career and Service awards as well an IEEE Third Millenium Medal and is a fellow of IEEE, the Institute of Physics (IOP), the American Institute of Medical Biological Engineering(AIMBE) and the American Association for the Advancement of Science (AAAS). His Neural Engineering and Informatics Lab is interested in developing an intelligent wearable system for monitoring motor functions in Post-Stroke Hemiplegic Patients and detecting coronary artery disease. In addition, his lab is currently investigating the effect of nicotine on the dynamics of ventral tegmental area (VTA) dopamine neural networks.

“Implantable Microsystems for the Management of Trauma”

Tuesday 12 November 2013

08:00-08:30

Imperial room

Chair: Prof. Dimitrios Lymberopoulos

Prof. Anthony Guiseppi–Elie
Sc.D., FAIMBE Professor,
Clemson University, USA

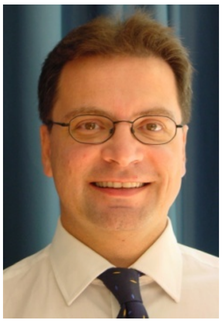
Abstract

Continued high morbidity and complications due to trauma related hemorrhage underscores the importance of efforts to fully understand the temporal progression of molecular physiologic events needed to bring life-saving changes to practice. The current state of trauma diagnostics emphasizes vital signs and stat metabolic biomarkers. Tachycardia and hypotension are markers of hemorrhagic shock in decompensated trauma patients. Base deficit has been predicative of injury severity at hospital admission. Tissue oxygen saturation has been predicative of onset of multiple organ dysfunction syndrome (MODS). Blood potassium levels increase with onset of hemorrhagic shock. Lactate is a surrogate for tissue hypoxia and its clearance predicts mortality. Insulin resistance and attendant triage glucose measurements have been shown to be specific in predicting major injuries. No vital sign has yet to be proven effective as an independent predictor of trauma severity. Implantable point-of-care (POC) analytical microsystems are being developed for use by first responders to allow for rapid, continual monitoring of glucose and lactate via dual responsive amperometric enzyme biosensors, tissue acidosis via impedimetry and VO2 via voltammetry. Minimally invasive multi-analyte monitoring biochips have the potential to explore areas still unexplored in the realm of trauma physiology.

Curriculum Vitae

Anthony Guiseppi-Elie is Professor of Chemical and Biomolecular Engineering, Bioengineering, Electrical and Computer Engineering and Director of the Center for Bioelectronics, Biosensors and Biochips at Clemson University. He is Founder and Scientific Director of ABTECH Scientific, Inc., a near-patient biomedical diagnostics company. He holds the Sc.D. in materials science and engineering from MIT, the M.Sc. in chemical engineering from the University of Manchester Institute of Science and Technology (UMIST) and the B.Sc. (First Class Honors) with majors in Analytical and Applied Chemistry from the University of the West Indies (UWI). His research interests are in engineered bioanalytical microsystems in the service of human health and medicine. Dr. Guiseppi-Elie has published over 120 archival scientific papers (2369 citations, h-factor = 26), 31 book or proceedings chapters, holds 8 US and foreign patents, has given in excess of 200 invited lectures/colloquia, and has co-organized and lead 30 national and international scientific workshops, symposia and conferences. Prof. Guiseppi is an Associate Editor of Biomedical Microdevices and a member of the editorial boards of Biomedical Microdevices, The Journal of Bioactive and Compatible Polymers, NanoBiotechnology, Applied Biochemistry and Biotechnology . Dr. Guiseppi is a Fellow of AIMBE, senior member of IEEE, a lifetime Member of AIChE and holds memberships in RSC, AAAS, ACS, MRS and BMES. At Clemson University Prof. Guiseppi teaches engineering materials, biological transport phenomena, biomolecular engineering, biosensors and bioelectronics, and nanobiotechnology.

“Emerging trends for decentralized e-health services in smart cities”



Sunday 10 November 2013

19:30-20:00

Imperial room

Chair: Prof. Dimitrios I. Fotiadis

Mr. Anastasius Gavras
Steering board member of the FI-PPP
Member of the editorial board of the Eurescom, Germany

Abstract

Societies globally are undergoing fundamental and unprecedented demographic changes. Similarly cities are experiencing intrinsic structural changes. Today many nations in Europe and worldwide are facing the impact of these challenges that in some cases exhibit interactions that amplify the effects. Governments and local authorities are seeking for solutions by setting policies to mitigate the anticipated effects. In some cases information and communications technologies (ICT) can support such policies by providing the infrastructure for the implementation and provisioning of various services to citizens in an effective and cost efficient way and at the same time enable citizen participation. Among various dimensions that typically are associated with smart cities, like mobility, environment, living, etc. the integration of health care is a primary objective since the cost of health care is currently increasing faster than the GDP in most countries. Europe has mobilized a significant part of its industry in a Public-Private-Partnership on Future Internet (FI-PPP), which is a European program for Internet-enabled innovation. The FI-PPP will accelerate the development and adoption of Future Internet technologies in Europe, advance the European market for smart infrastructures, and increase the effectiveness of business processes through the Internet.

In this context the FI-STAR project establishes early trials of services and applications in the health care sector by building on top of Future Internet Technologies developed in the program. The project's ambition is to augment smart cities infrastructures by creating a sustainable ecosystem for all user groups in the global health care and adjacent markets based on FI-PPP specifications. FI-STAR is a unique opportunity to deliver standardized and certified software including a safe, secure and resilient platform, taking advantage of all Cloud Computing benefits and guaranteeing the protection of sensitive and personal data.

The presentation will provide an insight on the current status and the anticipated future trends for decentralized e-health services in smart cities.

Curriculum Vitae

Anastasius Gavras has more than 20 years of professional experience in academic and industry research. He joined Eurescom, the leading organization for managing collaborative R&D in telecommunications, more than 12 years ago as program manager, focusing on the areas of management of networks & systems, security and middleware. In these areas he has managed a large number of studies and projects on topics which are of concern to the Eurescom member community of European telecom network operators and the European telecom industry at large. He has served as coordinator of several RTD projects under the European framework programs and has experience in standardization among others in OMG and ITU-T for which he has served as rapporteur.

His current interests are large scale testbed federations for enabling future Internet research and experimentation among others in the context of the Public-Private Partnership on Future Internet (FI-PPP). In the context of the FI-PPP he is the project co-ordinator of an early trial project in the health sector. Furthermore he is interested in innovation on top of future Internet platforms and the evolution of the future networks in general. He is a steering board member of the FI-PPP and is actively involved from their inception, both in the Future Internet Assembly (FIA) and the Future Internet Research and Experimentation (FIRE) initiative. He is author or co-author of several papers and articles in the area and is co-editor of all four FIA books so far. He is member of the editorial board of the Eurescom mess@ge magazine and has authored several articles for the magazine, typically with a techno-socio-economic dimension.

“Wellness, Disease and Public Health Informatics: Multidimensional Global Threats with Local Impact”

Wednesday 13 November 2013

11:00-11:30

Imperial room

Chair: Prof. Manolis Tsiknakis

Prof. Luis Kun
IEEE Fellow - Distinguished Visitor CS / SSIT William Perry, Center for Hemispheric Defense Studies at the National Defense University, USA

Abstract

As national economies around the world struggle and society realizes that wellness may be a better cost-effective way to deal with healthcare; prevention of disease will certainly become a center of attention. Aside from genetics, at the macro level, Public Health in particular, offers many new avenues for biomedical engineers. Information is key and due to our "islands of excellence", the perception we have under different crisis situations, does not allow us to reach real solutions to complex problems such as human health. Because of it I advocate for an interoperability among trans-disciplines, multi-disciplines and inter-disciplines. This approach allows us to avoid getting solutions that focus on partial knowledge of the problem and therefore getting a solution that does address all parts of an "interdependent" system. This type of complex situations cannot afford wrong decisions since it can ruin an individual's life or a nation's security, many times through irreversible damage. The information we daily receive including and related to diseases, cures, and accidents influences our perceptions. In turn these perceptions influence greatly decision making and because of those many experts that specialize in a very deep but yet narrow field, outcomes of their actions may create a bigger problem. From a worldwide perspective, everything is connected and yet disconnected. This translates into a very high cost and from a futuristic vision implies that the biggest problems society will face relate to fulfill necessities for access to clean water, food, medications and energy. A holistic systems approach is needed and proposed because of the global economy, where data mining, Knowledge Management and Geographical Information Systems are some of the emerging tools with great impact.

Curriculum Vitae

Luis Kun is IEEE-USA Founding Chair of the: Electronic Health Record and High Performance Computers and Communications WG; the Bioterrorism and Homeland Security WG; and the

Critical Infrastructure Protection Committee. As a Distinguished Fellow at the CDC he wrote the IT Strategic Vision for the National Immunization Program; he was also the Senior IT advisor for the Agency for Healthcare Policy and Research highly responsible for the Telemedicine portion of the Balanced Budget (for homecare of the elderly) signed by President Clinton in August 1997. He worked for IBM for 14 years where he developed the first health PC applications, and was involved on telemedicine, PACS, Point of Care and Expert Systems. Luis Kun is a Fellow of IEEE and the American Institute of Medical and Biological Engineering. He is on the Board of many Committees and Journals and is the Editor in Chief of Springer's Journal on Health and Technology. He was on the Board of Governors of IEEE Computer Society and is on the BOG of IEEE Society for Social Implications of Technology and the International Federation of Medical and Biological Engineering (IFMBE). Luis Kun received his BSEE, MSEE and Ph.D. in Biomedical Engineering from the University of California at Los Angeles (UCLA).

“An Overview of M-Health Medical Video Communication Systems”

Monday 11 November 2013

08:00-08:30

Imperial room

Chair: Prof. Michalis Zervakis

Prof. Constantinos S. Pattichis
Department of Computer Science,
University of Cyprus, Cyprus

Abstract

Significant technological advances over the past decade have led m-health systems and services to a remarkable growth. It is anticipated that such systems and services will soon be established in standard clinical practice. M-health medical video communication systems progression has been primarily driven by associated advances in video coding and wireless networks technologies. Responsive, reliable, and of high-diagnostic quality systems are now feasible, and build on compression ratios and error resilience tools found in current state-of-the-art video coding standards, linked with low-delay and high-bandwidth communications facilitated by new wireless systems. To achieve this however, these systems need to be diagnostically driven. In other words, both encoding and transmission need to adapt to the underlying medical video modality's properties, for maximizing the communicated video's clinical capacity. Moreover, the proper mechanisms should be developed that will guarantee the quality of the transmitted clinical content. Current video quality assessment (VQA) algorithms are unsuccessful to replicating clinical evaluation performed by the relevant medical experts. Clearly, there is a demand for new clinical VQA metrics. This lecture reviews medical video communication systems. It highlights past approaches and focuses on current design trends and future challenges. It provides an insight to the most prevailing diagnostically driven concepts and the challenges associated with each system component, including pre-processing, encoding, wireless transmission, and quality assessment. It discusses how exploiting high efficiency video coding (HEVC) standard, together with the emergence of 4G wireless networks, is expected to deliver the m-health medical video communications systems that will rival in hospital examinations. The latter, linked clinical VQA that will correlate with clinical ratings is expected to aid the adoption of such systems and services in daily clinical practice.

Curriculum Vitae

He is currently Professor with the Department of Computer Science of the University of Cyprus. His research interests include ehealth and mhealth, medical imaging, biosignal analysis, life sciences informatics, and intelligent systems. He has published 78 refereed journal and 186 conference papers, and 27 chapters in books in these areas. He is Co-Editor of the books M-Health: Emerging Mobile Health Systems, and of the Ultrasound and Carotid Bifurcation Atherosclerosis, published by Springer in 2006, and 2012 respectively. He was Guest Co-Editor of 11 journal Special Issues including the more recent ones on Atherosclerotic Cardiovascular Health Informatics, and Citizen Centered e-Health Systems in a Global Health-care Environment, of the IEEE Trans. on Information Technology in Biomedicine. He was General Co-Chairman of the IEEE 12th International Conference on BioInformatics and BioEngineering (BIBE2012), and the IEEE Information Technology in Biomedicine (ITAB09). Moreover, he serves as Distinguished Lecturer of the IEEE EMBS, an Associate Editor of the IEEE Journal of Biomedical and Health Informatics, and on the Editorial Board of the Journal of Biomedical Signal Processing and Control. He is a Fellow of IET, and Senior Member of IEEE.

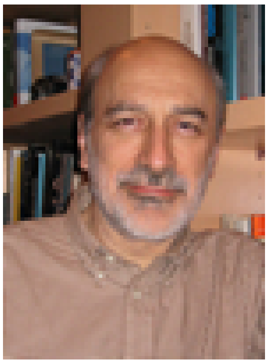
“Somatosensory Brain Machine Interfaces”

Wednesday 13 November 2013

08:30-09:00

Imperial room

Chair: Prof. Aristotelis Chatziioannou



Prof. Jose C. Principe
Computational NeuroEngineering Laboratory
University of Florida, Gainesville, USA

Abstract

In the future use of Brain Machine Interfaces (BMIs) it will be important to bring to the subject the feeling of touch when the robotic device grabs an object in the external world under the brain control of the subject. We are now developing the modelling and signal processing infrastructure to implement a somatosensory BMI by stimulating the Thalamus and producing in the primary sensorymotor cortex a response that mimics the normal stimulation felt by the subject. This talk will present the adaptive inverse control scheme and the spike kernel models that we are developing and some preliminary results.

Curriculum Vitae

Jose C. Principe is Distinguished Professor of Electrical and Biomedical Engineering at the University of Florida, Gainesville, where he teaches advanced signal processing and machine learning. He is BellSouth Professor and Founding Director of the University of Florida Computational Neuro-Engineering Laboratory (CNEL). His research interests are centered in advanced signal processing and machine learning, Brain Machine Interfaces and the modeling and applications of cognitive systems. He has authored 5 books and more than 200 publications in refereed journals and book chapters, and 450 conference papers. He has directed 72 Ph.D. dissertations and 67 Master theses. Dr. Principe is an IEEE, AIMBE and IAMBE Fellows a recipient of the INNS Gabor Award, the IEEE Neural Network Pioner Award, the Engineering in Medicine and Biology Society Career Achievement Award, the IEEE Computational Intelligence Society Neural Network Pioneer Award, and Honorary doctor degrees from Universita Mediterranea, Italy, University of Maranhao Brasil, and Aalto University, Finland. He is Editor in Chief of the IEEE Reviews on Biomedical Engineering, Past Editor-in-Chief of the IEEE Transactions on Biomedical Engineering, current ADCOM member of the IEEE CIS society, IEEE Biometrics Council, and IEEE BME society, member of the Technical Committee on Machine Learning for Signal Processing of the IEEE Signal Processing Society; member of the College of Fellows of the International Neural Network Society, and

Past President of the INNS. He is also a former member of the Scientific Board of the Food and Drug Administration.

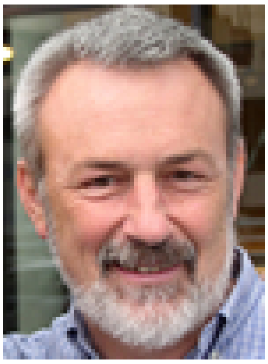
“Brain on a Chip: From Patterns to Circuits with Information Transfer”

Tuesady 12 November 2013

12:30-13:00

Imperial room

Chair: Prof. Konstantina S. Nikita



Prof. Bruce Wheeler
Department of Biomedical Engineering,
University of Florida, Gainesville, USA
IEEE EMBS President

Abstract

The wild idea that nerve cells grown in culture could have reliable computational function, while still a wild idea, is closer to reality than is reasonable to expect, thanks to applications of both engineering and applied biology. The metaphor works both ways: applications of more traditional engineering technologies - signal processing, electronics, microlithography, materials science - make possible the controlled growth, recording, and stimulation of nerve cells. In turn the goal is to design, construct, test, and utilize - in short to engineer - a working biological construct. This work has progressed to where we are constructing circuits using microtunnels that mimic the classic memory circuit of the hippocampus.

Collaborator: Dr. GJ Brewer, SIU School of Medicine, Springfield IL. Support: NIH.

Curriculum Vitae

Bruce Wheeler is a Professor in the Pruitt Family Department of Biomedical Engineering at the University of Florida. For four years he served as the Acting Department Chair and was co-author of the new undergraduate degree program. From 1980 to 2008 he was with the University of Illinois at Urbana-Champaign, including Professor and Founding and Interim Department Head of the Bioengineering Department. He was also a Professor of Electrical and Computer Engineering and the Beckman Institute, a former Associate Head of ECE, and a former chair of the Neuroscience Program. He was the Editor in Chief of the IEEE Transactions on Biomedical Engineering and is now President of the IEEE Engineering in Medicine and Biology Society. He is a Fellow of the IEEE and AIMBE. He received the B.S. degree from MIT and later the M.S. and Ph.D. in Electrical Engineering from Cornell. Prof. Wheeler's research interests lie in the application of electrical engineering methodologies, signal processing and microfabrication, to the study of the nervous system, including the microlithographic control of the patterns of growth of neurons in vitro so as to permit stimulation and recording with microelectrode arrays. Hopefully this work will lead to better understanding of the behavior of small populations of neurons and lead to better insights into the functioning of the brain. He also has had involvement in algorithm development for directional hearing aids.

“Systems Genetics: Experimental and Computational Challenges”

Sunday 10 November 2013

19:00-19:30

Imperial room

Chair: Prof. Dimitrios I. Fotiadis

Prof. Robert W. Williams
UT-Oak Ridge National Laboratory Chair in Computational Genomics, Center for Integrative and Translational Genomics, Department of Anatomy and Neurobiology, University of Tennessee Health Science Center, Memphis USA

Abstract

The analysis of human disease has profited enormously from systematic application of reductionist methods. But as we learn more about biological systems, we realize that health and disease are due to complex networks of interactions across multiple levels. Simple systems often do not provide robust results or reliable predictions. Systems genetics is a new hybrid of genetics and systems biology that models the consequences of genetic variation and the impact of environmental perturbations on biological processes and disease risk.

In this talk I describe key experimental and computational systems needed for systems genetics. Experimental and replicable populations of isogenic lines of mice that incorporate the same level of genetic complexity as humans are a key requirement. These new murine Reference Populations or families promise to revolutionize our ability to deliver personalized and predictive health care to humans over the next 100 years. Constructing and testing complex biological models is a computational and sociological challenge. I will review some of the latest progress we and other groups are making on building open on-line computational services for systems genetics.

Curriculum Vitae

Robert W. Williams received a Ph.D. in physiology at UC Davis and did postdoctoral work in neurobiology at Yale. He is the Director of the Center for Integrative and Translational Genomics and holds the UT Oak Ridge National Laboratory Governor's Chair in Computational Genomics. Williams is a past president of the International Society for Behavioural and Neural Genetics and founding director of the Complex Trait Community (www.complextrait.org). He is editor-in-chief of Frontiers in Neurogenomics, and serves on the editorial boards of Genes, Brain & Behavior, Neuroinformatics, Mammalian Genome, Molecular Vision, European Journal of Anatomy, Alcohol, BiomedCentral Neuroscience, the Journal of Biomedical Discovery and Collaboration, and Behavior Genetics. One of Williams' more notable recent contributions is in the field of systems biology and systems genetics. He and his research group have built GeneNetwork (www.genenetwork.org), an online resource and data analysis toolset used widely by the genetics and molecular biology research communities.

“Challenges and Opportunities in Cardiovascular Health Informatics”

Monday 11 November 2013

12:00-12:30

Imperial room

Chair: Prof. Konstantina S. Nikita

Prof. Yuan-Ting Zhang
Director of Joint Research Center for Biomedical Engineering
at EE,the Chinese University of Hong Kong, Hong Kong, China.
Director of the Key Lab for Health Informatics of Chinese
Academy of Sciences (HICAS) at SIAT, Shenzhen, China.

Abstract

“Advance health informatics” has been identified by the US National Academy of Engineering as one of 14 grand challenges for engineers in the 21st century. Health informatics deals with systematically the acquisition, transmission, processing, storage, retrieval, and use of information for human health. It can greatly enhance the quality, efficiency and cost-effectiveness of medical care and rapidly provide the response to widespread public health emergencies. Information acquisition is considered as the first crucial step in health informatics. This talk will discuss the challenges and opportunities in cardiovascular health informatics with the focus on the aspects of unobtrusive and wearable medical devices. The development of an unobtrusive and wearable cuff-less blood pressure device will be used as an example to illustrate ways of addressing some of these challenges. The potential applications for the unobtrusive monitoring of vulnerable patients with acute cardiovascular diseases will be examined. Future prospects such as flexible electronics for unobtrusive and wearable medical devices will also be presented.

Curriculum Vitae

Dr. Yuan-Ting Zhang is currently the Director of Joint Research Center for Biomedical Engineering and Professor of Department of Electronic Engineering at the Chinese University of Hong Kong (CUHK), Hong Kong, China. He serves concurrently the Director of the Key Lab for Health Informatics of the Chinese Academy of Sciences (HICAS) at SIAT, Shenzhen, China. He is the first Head of the Division of Biomedical Engineering at CUHK and the founding Director of the CAS-SIAT Institute of Biomedical and Health Engineering. Dr. Zhang was elected to the AdCom of IEEE Engineering in Medicine and Biology Society (EMBS) in 1999 and became previously the Vice-President of the IEEE-EMBS in 2000. He served as the Technical Program Chair and the General Conference Chair of the 20th and 27th IEEE-EMBS Annual International Conferences in 1998 and 2005, respectively. He also served on IEEE

Medal on Innovations in Healthcare Technology Award Committee and IEEE Fellow Elevation Committee. He severed on the editorial boards of several international journals in biomedical engineering such as the Editor-in-Chief of IEEE Transactions on Information Technology in Biomedicine (T-ITB). Dr. Zhang serves currently on the Fellow Membership Committee of the International Academy of Medical and Biological Engineering, IEEE-EMBS Technical Committee on Information Technology in Biomedicine, HK-ITC Projects Assessment Panel, , the IEEE-EMBS Summer School Steering Committee, the BSN Steering Committee, and the Editor-in-Chief of IEEE Journal of Biomedical and Health Informatics (J-BHI) which was retitled from T-ITB in Jan., 2013. Dr. Zhang's current research interests include wearable medical devices, body sensor networks, physiological modeling, neural engineering, cardiovascular health informatics, and m-u-p-Heath technologies. He has authored and co-authored over 400 scientific publications in BME and filed over 30 patents, some of which have been successfully licensed for commercialization. His research work has won him and his students/teams numerous honors/awards including the best journal paper awards from IEEE-EMBS, best conference paper awards from IFMBE, and the Grand Award in e-Health at the Asia-Pacific ICTAAC in Melbourne in 2009. He is the recipient of the IEEE-EMBS outstanding service award in 2006. Dr. Zhang holds the fellowships from the International Academy of Medical and Biological Engineering (IAMBE), the Institute of Electrical and Electronics Engineers (IEEE), and the American Institute of Medical and Biological Engineering (AIMBE) in recognition of his outstanding contributions to the development of wearable medical devices and mobile health technologies. Dr. Zhang completed his undergraduate and Master Degree studies in 1976 and 1981, respectively, in telecommunication from Department of Electronics of Shandong University and was conferred a Ph.D. in electrical engineering at the Institute of Bioengineering from the University of New Brunswick in 1990.

Topics Table

TOPIC	MONDAY 11 NOVEMBER, 2013					TUESDAY 12 NOVEMBER, 2013			WEDNESDAY 13 NOVEMBER, 2013		
	08:30 - 10:00	10:30 - 12:00	13:30 - 15:00	15:00 - 16:30	19:00 - 20:30	08:30 - 10:00	11:00 - 12:30	14:00 - 15:30	09:00 - 10:30	11:30 - 13:00	13:30 - 15:00
Advanced Concepts in Endoscopic Imaging and Engineering				▨							
Algorithms, Modeling and Simulation of Bio-Sets					▨						
Bio-Imaging				▨	▨						
Biological Systems and Models							▨				
Biomedical Data Engineering								▨			▨
Biomedical Image Processing, Analysis and Visualization						▨		▨			
Biomedical Signal Processing			▨						▨	▨	
Bio-Ontology and Data Mining			▨								
Cardiovascular and Respiratory Systems Engineering									▨		
Clinical Engineering										▨	
Computational BioEngineering		▨	▨								

TOPIC	MONDAY 11 NOVEMBER, 2013					TUESDAY 12 NOVEMBER, 2013			WEDNESDAY 13 NOVEMBER, 2013		
	08:30 - 10:00	10:30 - 12:00	13:30 - 15:00	15:00 - 16:30	19:00 - 20:30	08:30 - 10:00	11:00 - 12:30	14:00 - 15:30	09:00 - 10:30	11:30 - 13:00	13:30 - 15:00
		▨	▨								
Computer Assisted Intervention Systems		▨									
Data Visualization								▨			
Drug Discovery					▨						
Engineering Models in Bio-Medicine				▨							▨
Functional Genomics, Proteomics								▨			
Gene Expression Analysis Bioinformatics Engineering						▨			▨	▨	
Identification and Classification of Genes							▨				
Intelligent Therapeutic & Diagnostic Systems										▨	
NeuorEngineering, Neuromuscular Systems and Rehabilitation Engineering	▨										▨
Porting Bio and Health Informatics to the Cloud	▨										
Risk Analysis and Prediction in						▨					

TOPIC	**MONDAY 11 NOVEMBER, 2013**					**TUESDAY 12 NOVEMBER, 2013**			**WEDNESDAY 13 NOVEMBER, 2013**		
	08:30 - 10:00	**10:30 - 12:00**	**13:30 - 15:00**	**15:00 - 16:30**	**19:00 - 20:30**	**08:30 - 10:00**	**11:00 - 12:30**	**14:00 - 15:30**	**09:00 - 10:30**	**11:30 - 13:00**	**13:30 - 15:00**
Cardiovascular Applications						▨					
Sequence Search and Alignment & Systems Biology						▨					
The Digital Patient concept: Vision and Early Demonstrations							▨				

TechnicalProgram

SUNDAY, 10 NOVEMBER 2013

14:00-18:30	Registration

18:30-18:45	Opening – *Imperial room* Welcome by the conference chairs Prof. K. S. Nikita and Prof. D. I. Fotiadis

18:45-19:00	Welcome by the Rector of Technical University of Crete Prof. V. Digalakis *Imperial room*

19:00-19:30	Plenary Lecture: **Prof. Robert W. Williams,** *University of Tennessee Health ScienceCenter, Memphis, USA* **“Systems Genetics: Experimental and Computational Challenges”** ***Chair:*** *Prof. Dimitrios I. Fotiadis*

19:30-20:00	Plenary lecture: **Mr. Anastasius Gavras,** *Member of the editorial board of the Eurescom, Germany* **“Emerging trends for decentralized e-health services in smart cities”** ***Chair:*** *Prof. Dimitrios I. Fotiadis*

20:00-20:30	Presentation of achievement award to Prof. N. Bourbakis and Prof. Y. T. Zhang *Imperial room*

20:30-22:30	Welcome cocktail- *Bar “Galini”, Minoa Palace Resort & Spa* 

MONDAY, 11 NOVEMBER 2013

Imperial room **08:00-08:30**	Invited lecture: **"An Overview of M-Health Medical Video Communication Systems"** **Prof. Constantinos S. Pattichis,** *University of Cyprus, Cyprus* ***Chair:*** *Prof. Michalis Zervakis*

Session M.1.1 - Imperial 1 room: 08:30-10:00

Special Session #2 - Porting Bio and Health Informatics to the Cloud

Chair: *Christoph Thuemmler*

M.1.1.1 - A Profile-based Trust Management Scheme for Ubiquitous Healthcare Environment

Georgia Athanasiou, Georgios Mantas, Maria-Anna Fengou, Dimitrios Lymberopoulos

M.1.1.2 - Creating dynamic and customized fetal growth curves using cloud computing

Mario Bochicchio, Antonella Longo, Lucia Vaira, Antonio Malvasi, Andrea Tinelli

M.1.1.3 - CloudStudy: A Cloud-Based System for Supporting Multi-Centre Studies

Amalia Tsafara, Christos Tryfonopoulos, Spiros Skiadopoulos

M.1.1.4 - An architecture for designing Future Internet (FI) applications in sensitive domains: Expressing the Software to data paradigm by utilizing hybrid cloud technology

Stelios Sotiriadis, Euripides Petrakis, Stefan Covaci, Paolo Zampognaro, Eleni Georga, Christoph Thuemmler

Session M.1.2 – Imperial 2 room: 08:30-10:00

NeuorEngineering, Neuromuscular Systems and Rehabilitation Engineering

Chair: *Athanasios Bibas*

M.1.2.1 - Controlling Variability of Air-Pulses to Determine the Thresholds of Laryngeal-Pharyngeal Reflexes by a Novel Device

Luis F Giraldo, Mauricio Agudelo, Mario Arbulu, Felipe Ortiz, Javier Burguete, Secundino Fernandez

M.1.2.2 - Quering Functional Brain Connectomics to Discover Consistent Subgraph Patterns

Nantia Iakovidou, Stavros Dimitriadis, Nikos Laskaris, Kostas Tsichlas

M.1.2.3 - Design and Simulation of Wheel-chaired Elliptical Stepping Exercise for Stroke Rehabilitation

Saiful Zaimy Yahaya, Zakaria Hussain, Rozan Boudville

M.1.2.4 - A system for optically controlling neural circuits with very high spatial and temporal resolution

Chethan Pandarinath, Eric Carlson, Sheila Nirenberg

M.1.2.5 - Towards an Overall 3-D Vector Field Reconstruction via Discretization and a Linear Equations System

Chrysa Papadaniil, Leontios Hadjileontiadis

Session M.1.3- Imperial 3 room: 08:30-10:00

Workshop – ISMSR-13

Healthcare Monitoring Technologies and Methods

Chair: *Nikolaos Bourbakis*

M.1.3.1 -TeleCare of Mental Disorders by Applying Semantic Web Technology

Chryssa Thermolia, Ekaterini Bei, Euripides Petrakis

M.1.3.2 - Microstate analysis of the EEG using Local Global graphs

Kostas Michalopoulos, Nikolaos Bourbakis

M.1.3.3 - A Low-Cost Embedded Real-Time 3D Stereo Matching System for Surveillance Applications

Georgia Rematska, Kyprianos Papadimitriou, Apostolos Dollas

M.1.3.4 - The MobiFall Dataset: An Initial Evaluation of Fall Detection Algorithms Using Smartphones

George Vavoulas, Matthew Pediaditis, Emmanouil Spanakis, Manolis Tsiknakis

M.1.3.5 - A wearable Ultrasound multi-transducer array system for Abdominal Organs Monitoring

Michael Tsakallakis, Nikolaos Bourbakis

M.1.3.6 - A Single Chip Solution for Pulse Transmit Time Measurement

Sasa Knezevic, Radovan Stojanovic

Imperial Lobby **10:00-10:30**	Coffee Break 

Session M.2.1 – Imperial 1 room: 10:30-12:00

Computer Assisted Intervention Systems

Chair: *Christos Schizas*

M.2.1.1 - Electronic Health Record: Facilitating the Coding Process

Harris Soteriades, Kleanthis Neokleous, George Tsouloupas, Antonis Jossif, Schizas Christos

M.2.1.2 - Towards Efficient and Secure in-Home Wearable Insomnia Monitoring and Diagnosis System

Sana Tmar-Ben Hamida, Elyes Ben Hamida, Beena Ahmed, Adnan Abu-Dayya

M.2.1.3 - Guided Physical Exercise of Cardiac Patients during Rehabilitation: Adherence and Changes in Physiological Variables

Hilkka Runtti, Dimitris Filos, Mark van Gils, Ioanna Chouvarda, Anita Honka, Juha Pärkkä

M.2.1.4 - Ef-Zin: A hybrid framework for ubiquitous management of comorbidity and multimorbidity in chronic diseases.

Foteini Andriopoulou, Konstantinos Birkos, Dimitrios Lymberopoulos

M.2.1.5 - Detection of occlusal caries based on digital image processing

Georgia Koutsouri, Elias Berdouses, Evanthia Tripoliti, Constantine Oulis, Dimitrios Fotiadis

M.2.1.6 - On the Use of Smartphones for Detecting Obstructive Sleep Apnea

Mamoun Al-Mardini, Fadi Aloul, Assim Sagahyroon, Luai Al-Husseini

Session M.2.2 – Imperial 2 room: 10:30-12:00

Special Session #3 - Computational BioEngineering

Chair: *Nenad Filipovic*

M.2.2.1 - Multivariate Discriminant Analysis of Multiparametric Brain MRI to Differentiate High Grade and Low Grade Gliomas - A Computer-Aided Diagnosis Development Study

Füsun Çıtak Er, Zeynep Firat, Ilhami Kovanlikaya, Ugur Ture, Esin Ozturk Isik

M.2.2.2 - Blind Recovery of Cardiac and Respiratory Sounds Using Non-negative Matrix Factorization & Time-Frequency Masking

Ghafoor Shah, Constantinos Papadias

M.2.2.3 - Graph-theoretic analysis of scalp EEG brain networks in epilepsy - the influence of montage and volume conduction

Manolis Christodoulakis, Avgis Hadjipapas, Eleftherios Papathanasiou, Maria Anastasiadou, Savvas Papacostas, Georgios Mitsis

M.2.2.4 - Experimental and Numerical Investigation of Electromagnetic Field at Different Cancer Cell Lines

Nenad Filipovic, Tijana Djukic, Milos Radovic, Danijela Cvetkovic, Snezana Markovic, Branislav Jeremic

M.2.2.5 - Application of Data Mining Algorithms for Mammogram Classification

Milos Radovic, Marina Djokovic, Aleksandar Peulic

M.2.2.6 - Estimation of Blood Pressure Levels from Reflective Photoplethysmograph using Smart Phones

Aishwarya Visvanathan, Aniruddha Sinha, Arpan Pal

Session M.2.3 – Imperial 3 room: 10:30-12:00

Workshop-ISMSR-13

Computational Oncology: From mathematical models to clinical practice

Chair: *Michalis Zervakis*

M.2.3.1 - Towards in-vivo Validation of Computational (in silico) Models of Tumor Growth

V. Sakkalis

M.2.3.2 - Computational Development Models in the Micro-Environment of Cancer

M. Papadogiorgaki

M.2.3.3 - Improving Personalized Therapy Assessment in Cancer Patients based on MRI Image Analysis

K. Marias

M.2.3.4 - Stochastic Approaches for Personalized Modeling of Cancer

G. Mitsis

M.2.3.5 - On the use of Computational Models in Clinical Practice

P. Koliou

Open Discussion

Imperial room **12:00-12:30**	Invited lecture: **“Challenges and Opportunities in Cardiovascular Health Informatics”** **Prof. Yuan-Ting Zhang,** *Chinese University of Hong Kong, China* ***Chair:*** *Prof. Konstantina S. Nikita*

“Elia” restaurant **12:30-13:30**	Buffet Lunch 

Session M.3.1 – Imperial 1 room: 13:30 -15:30

Bio-Ontology and Data Mining

Chair: *Dimitrios Lymberopoulos*

M.3.1.1 -OnTheFly 2.0: A service to automatically annotate files and extract biological information.

Evangelos Pafilis, Georgios A. Pavlopoulos, Venkata P. Satagopam, Nikolas Papanikolaou, Heiko Horn, Christos Arvanitidis, Lars Juhl Jensen, Reinhard Schneider, Ioannis Iliopoulos

M.3.1.2 - Enhanced Probabilistic Latent Semantic Analysis with Weighting Schemes to Predict Genomic Annotations

Pietro Pinoli, Davide Chicco, Marco Masseroli

M.3.1.3 - Modified Free Energy Model to improve RNA secondary structure prediction with pseudoknots

Kwok-Kit Tong, Kwan-Yau Cheung, Kin-Hong Lee, Kwong-Sak Leung

M.3.1.4 - Classification of RNAs with Pseudoknots using k-mer Occurrences Count as Attributes

Kwan-Yau Cheung, Kwok-Kit Tong, Kin-Hong Lee, Kwong-Sak Leung

M.3.1.5 - Integrative Warehousing of Biomolecular Information to Support Complex Multi-Topic Queries for Biomedical Knowledge Discovery

Arif Canakoglu, Marco Masseroli, Stefano Ceri, Luca Tettamanti, Giorgio Ghisalberti, Alessandro Campi

Session M.3.2 – Imperial 2 room: 13:30 -15:30

Special Session #3 - Computational BioEngineering

Chair: *Nenad Filipovic*

M.3.2.1 - SIFEM Project: Semantic Infostructure interlinking an open source Finite Element tool and libraries with a model repository for the multi-scale Modelling of the inner-ear

Christos Bellos, Athanasios Bibas, Dimitrios Kikidis, Steve Elliott, Stefan Stenfelt, Ratnesh Sahay, Konstantina Nikita, Dimitrios Koutsouris, Dimitrios Fotiadis

M.3.2.2 - SIFEM Project: Finite Element Modeling of the Cochlea

Velibor Isailovic, Milica Obradovic, Dalibor Nikolic, Igor Saveljic, Nenad Filipovic

M.3.2.3 - Modeling of Abdominal Aorta Aneurism Rupture by using Experimental Bubble Inflation Test

Igor Koncar, Dalibor Nikolic, Suzana Pantovic, Mirko Rosic, Nikola Mijailovic, Nikola Ilic, Marko Dragas, Zivan Maksimovic, Lazar Davidovic, Nenad Filipovic

M.3.2.4 - Multi-process Dynamic Modeling of Tumor-specific Evolution

Achilleas Achilleos, Charalambos Loizidis, Marios Hadjiandreou, Triantafyllos Stylianopoulos, Georgios D. Mitsis

M.3.2.5 - Towards a Semantic Representation for Multi-Scale Finite Element Biosimulation Experiments

Andre Freitas, Margaret Jones, Kartik Asooja, Christos Bellos, Steve Elliott, Stefan Stenfelt, Panagiotis Hasapis, Christos Georgousopoulos, Torsten Marquardt, Stefan Decker, Ratnesh Sahay

M.3.2.6 - Modeling Atherosclerotic Plaque Growth: A Case Report Based on a 3D Geometry of Left Coronary Arterial Tree from Computed Tomography

Antonis I. Sakellarios, Panagiotis Siogkas, Lambros Athanasiou, Themis Exarchos, Michail Papafaklis, Christos Bourantas, Katerina Naka, Lampros Michalis, Nenad Filipovic, Oberdan Parodi, Dimitrios Fotiadis

Session M.3.3 – Imperial 3 room: 13:30 -15:30

Biomedical Signal Processing

Chair: *Nizamedin Aydin*

M.3.3.1 - A new approach to adaptive noise cancellation in synthetic auditory evoked potentials

Nurettin Acir, Engin Cemal Mengus

M.3.3.2 - Denoising Simulated EEG Signals: A Comparative Study of EMD, Wavelet Transform and Kalman Filter

Christos Salis, Anastasios Malissovas, Paschalis Bizopoulos, Alexandros Tzallas, Panagiotis Angelidis, Dimitrios Tsalikakis

M.3.3.3 - TRS-TMS: an EEGLAB plugin for the reconstruction of onsets in EEG-TMS datasets

Sara Petrichella, Luca Vollero, Florinda Ferreri, Giulio Iannello

M.3.3.4 - Unsupervised Approach for Measurement of Cognitive Load using EEG Signals

Diptesh Das, Debatri Chatterjee, Aniruddha Sinha

M.3.3.5 - EEG Epileptic Seizure Detection using k-Means Clustering and Marginal Spectrum based on Ensemble Empirical Mode Decomposition

Paschalis Bizopoulos, Dimitrios Tsalikakis, Alexandros Tzallas, Dimitrios Koutsouris, Dimitrios Fotiadis

M.3.3.6 - Synchronization coupling investigation using ICA cluster analysis in resting MEG signals in Reading Difficulties

Marios Antonakakis, Giorgos Giannakakis, Manolis Tsiknakis, Sifis Micheloyannis, Michalis Zervakis

Session M.4.1 – Imperial 1 room: 15:00-16:30

Bio-Imaging

Chair: *Dimitris Maroulis*

M.4.1.1 - EEG Identification of a localized 1-D neuronal excitation

George Dassios, Konstantia Satrazemi

M.4.1.2 - Analysis of errors and bounds in Electroencephalography

George Dassios, Michael Doschoris, Fotini Kariotou, Vasiliki Christina Panagiotopoulou

M.4.1.3 - The Influence of Surface Deformations on EEG Recordings

George Dassios, Michael Doschoris, George Fragoyannis

M.4.1.4 - 2D-GE Spot Detection Combining Multidirectional Texture and Spatial Intensity Cues

Eleni Zacharia, Eirini Kostopoulou, Dimitris Maroulis, Nicholas P. Anagnou, Kalliopi I. Pappa

M.4.1.5 - Local focus-tolerant image descriptors for classification of biological particles

Nefeli Vassiliki Politi-Stergiou, Ilias Theodorakopoulos, George Economou

M.4.1.6 - Improving Image Quality in Dual Energy CT by Edge-Enhancing Diffusion Denoising

Andreas Petropoulos, Georgios Vlachopoulos, Spyros Skiadopoulos, Anna Karahaliou, Lena Costaridou

Session M.4.2 – Imperial 2 room: 15:00-16:30

Special Session #5 - Advanced Concepts in Endoscopic Imaging and Engineering

Co-Chairs: *Dimitris K. Iakovidis, Anastasios Koulaouzidis*

M.4.2.1 - Towards a Multimodal Wireless Video Capsule for the Early Detection of Cancerous Polyps

Olivier Romain, Aymeric Histace, Juan Silva, Jad Ayoub, Bertrand Granado

M.4.2.2 - Capsule Endoscope Localization based on Visual Features

Dimitris Iakovidis, Evaggelos Spyrou, Dimitris Diamantis, Ilias Tsiompanidis

M.4.2.3 - Efficient Homography-Based Video Visualization for Wireless Capsule Endoscopy

Dimitris Iakovidis, Evaggelos Spyrou, Dimitris Diamantis

M.4.2.4 - Operation of Ingestible Antennas along the Gastrointestinal Tract: Detuning and Performance

Konstantinos Psathas, Anastasis Keliris, Asimina Kiourti, Konstantina Nikita

M.4.2.5 - A Comparison of Color Correction Algorithms for Endoscopic Cameras

Ioannis Constantinou, Marios Neofytou, Vasilis Tanos, Marios Pattichis, Christodoulos Christodoulou, Constantinos Pattichis

Session M.4.3 – Imperial 3 room: 15:00-16:30

Engineering Models in Bio-Medicine

Chair: *Carmelina Ruggiero*

M.4.3.1 - The Effects of Synthetic Azurocidin Peptide Analogue on Staphylococcus Aureus Bacterium

Jie Hu, Pantea Peidaee, Eltaher Elshagmani, Taghrid Istivan, Elena Pirogova

M.4.3.2 - Identification the Shape of Biconcave Red Blood Cells Using Histogram of Oriented Gradients and Covariance Features

George Apostolopoulos, Stefanos Tsinopoulos, Evaggelos Dermatas

M.4.3.3 - Feasibility Study on Serviced-based Method of Data Acquisition for Human Signal Molecule Profiling Database

Xinyan Zhao, Tao Dong

M.4.3.4 - 3D Printing: Basic concepts Mathematics and Technologies

Athanasios Anastasiou, Charalampos Tsirmpas, Alexandros Rompas, Kostas Giokas, Dimitris Koutsouris

M.4.3.5 - Polyelectrolyte Multilayer Coatings for Implant Osseointegration

Massimo Giulianelli, Roberta Ferretti, Laura Pastorino, Carmelina Ruggiero

Imperial Lobby **16:30-17:00**	Coffee Break 

Imperial room **17:00-19:00**	**Satellite event** **Panel discussion on knowledge-intensive entrepreneurship**

Session M.5.1 – Imperial 1 room: 19:00-20:30

Drug Discovery

Chair: *Dimitrios Koutsouris*

M.5.1.1 - An Isometry-Invariant Spectral Approach for Protein-Protein Docking

Dela De Youngster, Eric Paquet, Herna Lydia Viktor, Emil Petriu

M.5.1.2 - Drug Screening with Elastic-Net Multiple Kernel Learning

Kitsuchart Pasupa, Zakria Hussain, John Shawe-Taylor, Peter Willett

M.5.1.3 - A Fast Point Pattern Matching Algorithm for Robust Spatially Addressable Bead Encoding

Abhik Datta, Adams Wai-Kin Kong, Soumita Ghosh, Dieter Trau

M.5.1.4 - Implementation of Reversible Multiplier Circuit Using Deoxyribonucleic Acid

Ankur Sarker, Mohd. Istiaq Sharif, Tanvir Ahmed, Md. Atiqur Rahman, S. M. Mahbubur Rashid, Hafiz Md. Hasan Babu

Session M.5.2 – Imperial 2 room: 19:00-20:30

Algorithms, Modeling and Simulation of Bio-Sets

Chair: *Dimitrios Fotiadis*

M.5.2.1 - Biologically Inspired Near Extinct System Reconstruction

Athanasios Bibas, George Spanoudakis, Christos Bellos, Dimitrios Fotiadis, Dimitrios Koutsouris

M.5.2.2 - A Discrete Optimization Approach for SVD Best Truncation Choice based on ROC Curves

Davide Chicco, Marco Masseroli

M.5.2.3 - Studying the correlation between the extracellular environment geometry and the diffusion processes

Pantelis Ampatzoglou, Maria Hadjinicolaou

M.5.2.4 - Identification and correction of substitution errors in Moleculo long reads

Jared Price, Judson Ward, Joshua Udall, Quinn Snell, Mark Clement

M.5.2.5 - Short-term vs. Long-term Analysis of Diabetes Data: Application of Machine Learning and Data Mining Techniques

Eleni Georga, Vasilios Protopappas, Stavroula Mougiakakou, Dimitrios Fotiadis

Session M.5.3– Imperial 3 room: 19:00-20:30

Bio-Imaging

Chair: *George Spyrou*

M.5.3.1 - Segmentation of Enhanced Depth Imaging Optical Coherence Tomography Images Using Wavelet Based Graph Cut Algorithm

Hajar Danesh, Raheleh Kafieh, Hossein Rabbani

M.5.3.2 - A Level Set Based Method for Lung Segmentation in CT Images

Shiva Azimi, Hossein Rabbani

M.5.3.3 - The Use of Real-Time MRI Techniques for Imaging an Extended Field of View in Magnetic Resonance Angiography

Stephen Riederer, Casey Johnson, Paul Weavers

M.5.3.4 - Modeling of Solitary Pulmonary Nodules in PET/CT images using Monte Carlo Methods

George Tzanoukos, Anastasios Gaitanis Alexandros Georgakopoulos, Achilleas Chatziioannou, Sofia Chatziioannou, George Spyrou

M.5.3.5 - Comparison of EIT Reconstruction Techniques Applied to IMPETOM

Eduardo Santos, Franco Simini

M.5.3.6 - Evaluation of Modified Median Root Prior on a myocardium study, using realistic PET/MR data

Konstantinos Karaoglanis, Anastasios Gaitanis, Charalampos Tsoumpas

“Elia” restaurant 21:00-23:00	Barbeque	

TUESDAY, 12 NOVEMBER 2013

Imperial room **08:00-08:30**	Invited lecture: **“Implantable Microsystems for the Management of Trauma”** **Prof. Anthony Guiseppi–Elie**, *Clemson University, USA* ***Chair:*** *Prof. Dimitrios Lymberopoulos*

Session T.1.1 – Imperial 1 room: 08:30-10:00

Special Session #1 - Risk Analysis and Prediction in Cardiovascular Applications

Co-Chairs: *Renata Guarneri, Claudio Silvestro*

T.1.1.1 - The RT3S Project – An Introduction

Gabriele Dubini, Maria Renata Guarneri, Gordon Clapworthy, Nassos Katsaounis, Patricia Lawford, Euripides Petrakis, Michel Rochette, Claudio Silvestro, Debora Testi

T.1.1.2 - Real Time Prediction of the Fatigue Behavior of Peripheral Stents

Francesco Migliavacca, Michel Rochette, Florent Petiot, Christelle Biochon, Elena Dordoni, Gabriele Dubini, Giancarlo Pennati, Lorenza Petrini

T.1.1.3 - Reconstruction method of a stented coronary bifurcation model for fluid dynamic numerical analyses from optical coherence tomography images

Claudio Chiastra, Eros Montin, Francesco Burzotta, Luca Mainardi, Francesco Migliavacca

T.1.1.4 - AimaSimul: a software tool to plan stent positioning in peripheral arteries and evaluate the associated fatigue fracture risk

Debora Testi, Nigel J. B. McFarlane, Hui Wei, Youbing Zhao, Gordon J. Clapworthy, Desmond M. Ryan, Patricia Lawford

T.1.1.5 - Crafting Vascular Medicine Training Scenarios: The RT3S Authoring Tool

Evanthia Tripoliti, Ioannis Pappas, Euripides Petrakis, Josep Maria Sans

T.1.1.6 - Application of Decisional Models to the Health-Economic Assessment of New Interactive Clinical Software

Claudio Silvestro, Jonathan Michaels, Spiridoula Dimou, Evanthia Tripoliti, Euripides Petrakis

Session T.1.2 – Imperial 2 room: 08:30-10:00

Gene Expression Analysis & Bioinformatics Engineering

Chair: *Michalis Zervakis*

T.1.2.1 - A Generic Framework for the Elicitation of Stable and Reliable Gene Expression Signatures

Nick Chlis, Stelios Sfakianakis, Ekaterini Bei, Michalis Zervakis

T.1.2.2 -QLZCClust: Quaternary Lempel-Ziv Complexity based Clustering of the RNA-seq Read Block Segments

Ashis Kumer Biswas, Jean X. Gao

T.1.2.3 - Reconstructing Phylogenetic Network with ReTF algorithm (Rearranging Transcriptional Factor)

Shamita Malik, Dolly Sharma

T.1.2.4 - Inference of a robust diagnostic signature in the case of Melanoma: Gene Selection by Information Gain and Gene Ontology Tree Exploration

Ioannis Valavanis, Konstantinos Moutselos, Ilias Maglogiannis, Aristotelis Chatziioannou

T.1.2.5 - Feature Identification and Reduction for Improved Generalization Accuracy in Secondary-Structure Prediction

Seeley Matt, Mark Clement, Quinn Snell

Session T.1.3 – Imperial 3 room: 08:30-10:00

Sequence Search and Alignment & Systems Biology

Chair: *Aristotelis Chatziioannou*

T.1.3.1 - Some Results on Topological Colored Motifs in Metabolic Networks

Elói Araújo, Marco Aurélio Stefanes

T.1.3.2 - Prediction of Enzymatic Activity of Proteins Based on Structural and Functional Domains

Theodoros Koutsandreas, Eleftherios Pilalis, Aristotelis Chatziioannou

T.1.3.3 - Fast search of locally repetitive elements based on auto-correlation property in genome

Kyung-Seop Shin, Byung-Chang Chung, Woo-Chan Kim, Dong-Ho Cho

T.1.3.4 - A Comparison of Community Identication Algorithms for Regulatory Network Motifs

Douglas Oliveira, Marco Carvalho

T.1.3.5 - A Synthetic Biology Approach to the Realization of Embedded Feedback Controllers for Chemical Reaction Networks

Carlo Cosentino, Mariaconcetta Bilotta, Alessio Merola, Francesco Amato

Session T.1.4 – Imperial room: 08:30-10:00

Biomedical Image Processing, Analysis and Visualization

Chair: *Ilias Maglogiannis*

T.1.4.1 - Segmentation and Recognition of Multi-Food Meal Images for Carbohydrate Counting

Marios Anthimopoulos, Joachim Dehais, Peter Diem, Stavroula Mougiakakou

T.1.4.2 - Human Segmentation and Pose Recognition in Fish-eye Video for Assistive Environments

Kostas Delibasis, Theodosios Goudas, Vassilios Plagianakos, Ilias Maglogiannis

T.1.4.3 - HEp-2 Cells Classification Using Locally Aggregated Features Mapped in the Dissimilarity Space

Dimitrios Kastaniotis, Ilias Theodorakopoulos, George Economou, Spiros Fotopoulos

T.1.4.4 - A Scheme for X-ray Medical Image Denoising using Sparse Representations

Evmorfia Adamidi, Evangelos Vlachos, Aris Dermitzakis, Kostas Berberidis, Nicolas Pallikarakis

T.1.4.5 - A Comparison of Ultrasound Intima Media Thickness Measurements of the Left and Right Common Carotid Artery

Christos Loizou, Constantinos Pattichis, Niki Georghiou, Maura Griffin, Andrew Nicolaides

T.1.4.6 - Image registration of follow-up examinations in digital dermoscopy

Christos Nikolaos E. Anagnostopoulos, Dimitrios Vergados, Panagiotis Mintzias

Imperial Lobby **10:00-10:30**	Coffee Break – *Imperial Lobby*

Imperial room **10:30-11:00**	Invited lecture: “Advances (Innovations) in Neurotechnology” **Prof. Metin Akay,** *University of Houston, USA* ***Chair:*** *Prof. Dimitrios Koutsouris*

Session T.2.1 – Imperial 1 room: 11:00-12:30

Special Session #4 - The Digital Patient concept: Vision and Early Demonstrations

Co-Chairs: *Feng Dong, Manolis Tsiknakis*

T.2.1.1- "Digital Patients and their impact on Healthcare"
Roderick Tooher

T.2.1.2 - Exploitation of patient avatars towards stratified medicine through the development of in silico clinical trials approaches

Marios Spanakis, Efrosini Papadaki, Apostolos Karantanas, Thomas G. Maris, Dimitris Kafetzopoulos, Vaggelis Sakkalis, Konstantinos Marias

T.2.1.3 - Designing a digital patient avatar in the context of the MyHealthAvatar project initiative

Evaggelia Maniadi, Haridimos Kondylakis, Emmanouil G. Spanakis, Marios Spanakis, Manolis Tsiknakis, Kostas Marias, Feng Dong

T.2.1.4 - A Virtual Individual’s Model Based on Facial Expression Analysis: a Non-Intrusive Approach for Wellbeing Monitoring and Self-Management

Franco Chiarugi, Eirini Christinaki, Sara Colantonio, Giuseppe Coppini, Paolo Marraccini, Matthew Pediaditis, Ovidio Salvetti, Manolis Tsiknakis

T.2.1.5 - A Scalable Data Repository for Recording Self-Managed Longitudinal Health Data of Digital Patients

Xia Zhao, Youbing Zhao, Nikolaos Ersotelos, Dina Fan, Enjie Liu, Gordon Clapworthy, Feng Dong

T.2.1.6 - A Cross-platform Approach for Treatment of Amblyopia

Hui Wei, Youbing Zhao, George Saleh, Feng Dong, Gordon Clapworthy, Xujiong Ye

Session T.2.2 – Imperial 2 room: 11:00-12:30

Identification and Classification of Genes

Chair: *Michalis Zervakis*

T.2.2.1 - Candidate Biomarkers for Response to Tamoxifen in Breast Cancer metastatic patients

Claudia Cava, Gloria Bertoli, Italo Zoppis, Giancarlo Mauri, Maria Carla Gilardi, Isabella Castiglioni

T.2.2.2 - Automated Selection of Differentially Methylated Regions in Microarray Data

Pavlos Antoniou, Spiros Michalakopoulos, Elisavet Papageorgiou, Philippos Patsalis, Carolina Sismani

T.2.2.3 - Towards an Integrated Framework for Clinico-Biological Data Management and Analysis: the Case of Chronic Lymphocytic Leukemia

Evangelia Minga, Athanasios Gkoufas, Anna Vardi, Evangelia Stalika, Anastasia Hadzidimitriou, Kostas Stamatopoulos, Nicos Maglaveras, Ioanna Chouvarda

T.2.2.4 - Identifying Gender Independent Biomarkers Responsible for Human Muscle Aging Using Microarray Data

Emmanouil Sifakis, Ioannis Valavanis, Olga Papadodima, Aristotelis Chatziioannou

T.2.2.5 - Hierarchical Multi-Label Gene Function Prediction using Adaptive Mutation in Crowding Niching

Mina Moradi Kordmahalleh, Abdollah Homaifar, Dukka KC

Session T.2.3 – Imperial 3 room: 11:00-12:30

Biological Systems and Models

Chair: *Konstantina Nikita*

T.2.3.1 - A Model-Based Retrospective Analysis of the Fixed-Ratio Oscillometric Blood Pressure Measurement

Rein Raamat, Kersti Jagomagi, Jaak Talts, Jana Kivastik

T.2.3.2 - Accelerated MR Physics Simulations on multi-GPU systems

Christos Xanthis, Ioannis Venetis, Anthony Aletras

T.2.3.3- A Lumped Parameter Model for the Analysis of the Motion of the Muscles of the Lower Limbs under Whole-Body Vibration

Francesco Amato, Paolo Bifulco, Mario Cesarelli, Domenico Colacino, Carlo Cosentino, Antonio Fratini, Alessio Merola, Maria Romano

T.2.3.4 - A Mathematical Model for Secondary Structure in Proteins

Alexey Nikolaev, Saad Mneimneh

T.2.3.5 - Support vector-based fuzzy system for the prediction of mouse class I MHC peptide binding affinity

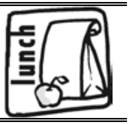
Volkan Uslan, Huseyin Seker

T.2.3.6 - A bioinformatics approach for investigating the determinants of Drosha processing

Nestoras Karathanasis, Ioannis Tsamardinos, Panayiota Poirazi

Imperial room **11:00-12:30**	**Satellite event** **Short seminar "From the lab to the market"**

Imperial room **12:30-13:00**	Invited lecture: **"Brain on a Chip: From Patterns to Circuits with Information Transfer"** **Prof. Bruce Wheeler,** *University of Florida, Gainesville, USA, IEEE EMBS President* ***Chair:*** *Prof. Konstantina S. Nikita*

"Elia" restaurant **13:00-14:00**	Buffet Lunch 

Session T.3.1 – Imperial 1 room: 14:00-15:30

Biomedical Image Processing, Analysis and Visualization

Chair: *Huseyin Seker*

T.3.1.1 - Gradient cumulative filtering to detect MRI thermometry artifacts

Juha Kortelainen, Juha Koikkalainen, Julius Koskela, Gösta Ehnholm

T.3.1.2 - Resting state and task related fMRI in small cell lung cancer patients

Konstantinos Bromis, Irene Karanasiou, George Matsopoulos, Errikos Ventouras, Nikolaos Uzunoglu, Georgios Mitsis, Eustratios Karavasilis, Matilda Papathanasiou, Nikolaos Kelekis, Vasileios Kouloulias

T.3.1.3 - Variations on breast density and subtlety of the findings require different computational intelligence pipelines for the diagnosis of clustered microcalcifications

Ioannis Andreadis, George Spyrou, Panos Ligomenides, Konstantina Nikita

T.3.1.4 - Generation of clustered microcalcifications' atlases for benign and malignant cases

Ioannis Andreadis, George Spyrou, Panos Ligomenides, Konstantina Nikita

T.3.1.5 - Performance Evaluation of Clustering Algorithms on Microcalcifications as Mammography Findings

Emmanouil Ikonomakis, George Spyrou, Panos Ligomenides, Michael Vrahatis

T.3.1.6 - Investigation of AM-FM Methods for Mammographic Breast Density Classification

Styliani Petroudi, Ioannis Constantinou, Chryso Tziakouri, Marios Pattichis, Constantinos Pattichis

Session T.3.2 – Imperial 2 room: 14:00-15:30

Functional Genomics, Proteomics

Co-Chairs: *Costas Papaloukas, Dimitrios Vergados*

T.3.2.1 - Impacts of the Different Spline Orders on the B-spline Association Estimator

Zeyneb Kurt, Nizamedin Aydin, Gökmen Altay

T.3.2.2 - Identification of signaling pathways related to drug efficacy in hepatocellular carcinoma via integration of phosphoproteomic, genomic and clinical data

Ioannis N Melas, Douglas A Lauffenburger, Leonidas G Alexopoulos

T.3.2.3 - Novel Biomarkers Discovery for HBV and HCV Monitoring Through Protein Interaction Networks Analysis

Thomas Simos, Costas Papaloukas, George Thyphronitis, Urania Georgopoulou

T.3.2.4 - Toll-like Receptor Structural Determinants: Variability Analysis by Digital Signal Processing Methods

Norbert Maggi, Patrizio Arrigo, Carmelina Ruggiero

T.3.2.5 - HRelief: A new algorithm relief hybrid for biological motifs selection

Faouzi Mhamdi, Hanen Mhamdi

Session T.3.3 – Imperial 3 room: 14:00-15:30

Data Visualization

Chair: *George Spyrou*

T.3.3.1 - Implementing Patient Recruitment on EURECA Semantic Integration Platform through a Groovy Query Engine

Brecht Claerhout, Kristof De Schepper, David Perez-Rey, Raul Alonso-Calvo, Jasper van Leeuwen, Anca Bucur

T.3.3.2 - A user interface design for a patient oriented digital patient

Nikolaos Ersotelos, Xia Zhao, Youbing Zhao, Enjie Liu, Gordon Clapworthy, Feng Dong

T.3.3.3 - Weighted Committee-Based Structure Learning for Microarray Data

Hasna Njah, Salma Jamoussi

T.3.3.4 -WebGL-based Interactive Rendering of Whole Body Anatomy for Web-oriented Visualisation of Avatar-centered Digital Health Data

Youbing Zhao, Xia Zhao, Nikolaos Ersotelos, Feng Dong, Enjie Liu, Gordon Clapworthy

Session T.3.4 – Imperial room: 14:00-15:30

Biomedical Data Engineering

Chair: *Panagiotis Bamidis*

T.3.4.1 - Clinical Decision Support Framework for Validation of Multiscale Models and Personalization of Treatment in Oncology

Anca Bucur, Jasper van Leeuwen, Traian Cristian Cirstea, Norbert Graf

T.3.4.2 - Molecular Clustering via Knowledge Mining from Biomedical Scientific Corpora

Panagiotis Hasapis, Dimitrios Ntalaperas, Christos Kannas, Aristos Aristodimou, Dimitrios Alexandrou, Thanassis Bouras, Athos Antoniades, Christos Georgousopoulos, Constantinos Pattichis, Andreas Constantinou

T.3.4.3 - Decision Tree Induction to Prediction of Prognosis in Severe Traumatic Brain Injury of Brazilian Patients from Florianopolis City

Merisandra Garcia, Ruano Pereira, Evandro Martins, Fernando Azevedo

T.3.4.4 -TeleRehabilitation: a novel service oriented platform to support Tele-Supervised rehabilitation programs for ICU patients

Nikolas Stylianides, Andreas Papadopoulos, Ioannis Constantinou, Loizos Loizou, Marios Dikaiakos, Theodoros Kyprianou

T.3.4.5 - In silico study of mechanical stresses at the cellular level during tissue development

Anne Jeannin-Girardon, Pascal Ballet, Vincent Rodin

T.3.4.6 - "Meleti" Speech and Language Development Support System

Efthyvoulos Kyriacou, Marina Charalambous, Charalambos Theodorou, Christos Iliophotou, George Hadjichristofi, Maria Ioannou

15:30-19:00	Excursion – Old city of Chania 

20:00-22:30	Congress Dinner – "Nikolas" tavern 

WEDNESDAY, 13 NOVEMBER 2013

Imperial room **08:30-09:00**	Invited lecture: **“Somatosensory Brain Machine Interfaces”** **Prof. Jose C. Principe,** *University of Florida, Gainesville, USA* ***Chair:*** *Prof. Aristotelis Chataziioannou*

Session W.1.1 – Imperial 1 room: 09:00-10:30

Gene Expression Analysis & Bioinformatics Engineering

Co-Chairs: *Aristotelis Chatziioannou, Dimitrios Vergados*

W.1.1.1 - Ensemble learning and hierarchical data representation for microarray classification

by Mattia Bosio, Pau Bellot, Philippe Salembier, Albert Oliveras-Vergés

W.1.1.2 - Stability of feature selection algorithms for classification in high-throughput genomics datasets

Panagiotis Moulos, Ioannis Kanaris, Gianluca Bontempi

W.1.1.3 - Frequent Weighted Itemset Mining from Gene Expression Data

Elena Baralis, Luca Cagliero, Tania Cerquitelli, Silvia Chiusano, Paolo Garza

W.1.1.4 - A Kernel SVM Algorithm to Detect Mislabeled Microarrays in Human Cancer Samples

Manuel Martín-Merino

W.1.1.5 - Similarity and Dissimilarity of Whole Genomes using Intuitionistic Fuzzy Logic

Subhram Das, D. K. Bhattacharya

Session W.1.2 – Imperial 2 room: 09:00-10:30

Cardiovascular and Respiratory Systems Engineering

Chair: *Francesco Migliavacca*

W.1.2.1 -Multiscale motion analysis of the carotid artery wall from B-mode ultrasound: investigating the optimal wavelet parameterization

Nikolaos Tsiaparas, Aimilia Gastounioti, Spyretta Golemati, Konstantina Nikita

W.1.2.2 - Modeling stent deployment in realistic arterial segment geometries: the effect of the plaque composition

Georgia Karanasiou, Antonis Sakellarios, Evanthia Tripoliti, Euripides Petrakis, Michalis Zervakis, Francesco Migliavacca, Gabriele Dubini, Elena Dordoni, Lambros Michalis, Dimitrios Fotiadis

W.1.2.3 - Identification of scalp blood flow in NIRS data based on Granger causality

Masako Sugai, Masaharu Adachi

W.1.2.4 - Low-power Hardware Implementation of Noise Tolerant Heart Rate Extractor for a Wearable Monitoring System

Shintaro Izumi, Masanao Nakano, Ken Yamashita, Takahide Fujii, Hiroshi Kawaguchi, Masahiko Yoshimoto

W.1.2.5 - Computational Study of Particle Deposition in Patient Specific Geometries

Marika Pilou, Anastasios Skiadopoulos, Evangelos Makris, Panagiotis Neofytou, Christos Housiadas

Session W.1.3 – Imperial 3 room: 09:00-10:30

Biomedical Signal Processing

Chair: *Konstantina Nikita*

W.1.3.1 - An Information Theoretic Approach to Classify Cognitive States Using fMRI

Itir Onal, Mete Ozay, Orhan Firat, Ilke Oztekin, Fatos T. Yarman Vural

W.1.3.2 - Resting State fMRI Analysis using a Spatial Regression Mixture Model

Vangelis P. Oikonomou, Konstantinos Blekas, Loukas Astrakas

W.1.3.3 - Developing a Simulator for Multispectral Optoacoustic Tomography

Efthymios Maneas, Stratis Tzoumas, Vasilis Ntziachristos, George Spyrou

W.1.3.4 -Spatio-Spectral Analysis of ECoG Signals during Voice Activity

Vasileios Kanas, Iosif Mporas, Heather Benz, Kyriakos Sgarbas, Nathan Crone, Anastasios Bezerianos

W.1.3.5 - LBP-Based Ear Recognition

Nazmeen Bibi Boodoo-Jahangeer, Sunilduth Baichoo

Imperial Lobby **10:30-11:00**	Coffee Break 

Imperial room **11:00-11:30**	Invited lecture: **“Wellness, Disease and Public Health Informatics: Multidimensional Global Threats with Local Impact”** **Prof. Luis Kun**, Center for Hemispheric Defense Studies at the National Defense University, USA ***Chair:*** *Prof. Manolis Tsiknakis*

Session W.2.1 – Imperial 1 room: 11:30-13:00

Gene Expression Analysis & Bioinformatics Engineering

Chair: *Georgios Potamias*

W.2.1.1 - Integrative Transcriptomic Analysis of Two Cell Lines elucidates the Architecture of Endoplasmic Reticulum Stress Signaling in Glioblastoma

Aristotelis Chatziioannou, Olga Papadodima, Nicolas Dejeans, Eric Chevet

W.2.1.2 - Enhancing the Performance of a Microarray Gridding Algorithm via GPU Computing Techniques

Stamos Katsigiannis, Eleni Zacharia, Dimitris Maroulis

W.2.1.3 -Bonferroni correction hides significant motif combinations

Aika Terada, Jun Sese

W.2.1.4 - Experimental Model Construction and Validation of the ErbB Signaling Pathway

Kalliopi Kalantzaki, Leyteris Koumakis, Ekaterini Bei, Michalis Zervakis, Georgios Potamias, Dimitrios Kafetzopoulos

W.2.1.5 - Prioritized Functional Analysis of Biological Experiments Using Resampling and Noise Control Methodologies

Eleftherios Pilalis, Aristotelis Chatziioannou

Session W.2.2 – Imperial 2 room: 11:30-13:00

Intelligent Therapeutic & Diagnostic Systems

Chair: *Anca Bucur, Costas Balas*

W.2.2.1 - Rectangular Patch Antenna on Split-ring Resonators Substrate for THz Brain Imaging: Modeling and Testing

Maria Koutsoupidou, Irene Karanasiou, Nikolaos Uzunoglu

W.2.2.2 - Towards Generalized Nuclear Segmentation in Histological Images

Abhishek Vahadane, Amit Sethi

W.2.2.3 - A New Modality for Quantitative Evaluation of Parkinson's Disease: In-Air Movement

Peter Drotar, Jiri Mekyska, Irena Rektorova, Lucia Masarova, Zdenek Smekal, Marcos Zanuy

W.2.2.4 - Food Volume Computation for Self Dietary Assessment Applications

Joachim Dehais, Sergey Shevchik, Peter Diem, Stavroula Mougiakakou

W.2.2.5 - A Hybrid Genetic Algorithm for the Selection of the Critical Features for Cardiovascular Complications Prognosis in Type 2 Diabetic Patients

Kalliopi Dalakleidi, Konstantia Zarkogianni, Vassilios Karamanos

Session W.2.3 – Imperial 3 room: 11:30-13:00

Clinical Engineering

Chair: *Maria Tereza Arredondo*

W.2.3.1 - Guidelines for the economic analysis of a telematic platform for Parkinson's disease monitoring

Jorge Cancela, Maria T Arredondo, Olivia Hurtado

W.2.3.2 - Preliminary Study on Optical Feature Detection for Head Tracking in Radiation Therapy

Tobias Wissel, Patrick Stüber, Benjamin Wagner, Ralf Bruder, Achim Schweikard, Floris Ernst

W.2.3.3 - Method for measuring the heart rate through fingertip using a low-end video camera and its application in self care

Lucian Pestritu, Alexandra Todiruta, Maria Goga, Nicolae Goga

W.2.3.4 **-** A CUDA based digital X-ray image stitching algorithm

Jiaxiang Huang, Xu Xu

W.2.3.5 **-** An Asthma Management Framework for the RespDoc Clinical Decision Support System Based on the Combination of the Official Clinical Guidelines

Aikaterini Rigopoulou, Dimitrios Lymberopoulos

W.2.3.6 **-** Smart Cards in Healthcare Information Systems: Benefits and Limitations

Anastasis Keliris, Vassileios Kolias, Konstantina Nikita

Session W.2.4 – Imperial: 11:30-13:00

Biomedical Signal Processing

Chair: *Ilias Maglogiannis*

W.2.4.1 **-** Influence on Skin Temperature and Blood Flow of Thermal and Massage Stimuli

Hirotaka Inoue, Hiroshi Hagiwara

W.2.4.2 **-** Efficient C Level Hardware Design for Floating Point Biomedical DSP Applications

Christoforos Economakos, Harry Sidiropoulos, George Economakos

W.2.4.3 **-** Classification of Atrio-Ventricular Reentrant Tachycardia using Intracardiac Signals

Wajeeha Nafees, Bushra Riaz, Nauman Razzaq, Wardah Iftikhar, Tahir Zaidi

W.2.4.4 **-** Estimation of ECG Parameters using Photoplethysmography

Rohan Banerjee, Aniruddha Sinha, Arpan Pal, Anurag Kumar

W.2.4.5 **-** Performance Analysis of Multi-frequency SSVEP-BCI Using Clear and Frosted Colour LED Stimuli

Surej Mouli, Ramaswamy Palaniappan, Ian P Sillitoe, John Q Gan

W.2.4.6 **-** Does Music affect HRV impulse? -A time domain study

Anilesh Dey, Sayan Mukherjee, Sanjay Kumar Palit, D. K. Bhattacharya, D.N. Tibarewala

Imperial Lobby **13:00-13:30**	Light Lunch 

Session W.3.1 – Imperial 1 room: 13:30-15:00

Engineering Models in Bio-Medicine

Chair: *Dimitrios Lymberopoulos*

W.3.1.1 **-** An in-silico Model for Solid Tumor Growth based on the Concept of Glycolysis

Michail Kounelakis, Maria Papadogiorgaki, Michail Zervakis

W.3.1.2 **-** Personalized Glucose-Insulin Metabolism Model based on Self-Organizing Maps for Patients with Type 1 Diabetes Mellitus

Konstantia Zarkogianni, Eleni Litsa, Konstantina Nikita

W.3.1.3 - Unsupervised Clustering of Patient-Centric Models to Cluster-Centric Models for Ubiquitous Healthcare Environment

Maria-Anna Fengou, Iosif Mporas, Dimitrios Lymberopoulos

W.3.1.4 - Biomedical Magnetic Induction Tomography Using Two-Arm Archimedean Spiral Coil: A Feasibility Study

Ziyi Zhang, Peiguo Liu, Dongming Zhou, Hengdong Lei

Session W.3.2 – Imperial 2 room: 13:30-15:00

NeuorEngineering, Neuromuscular Systems and Rehabilitation Engineering

Co-Chairs: *Wei Chen, Panagiotis Bamidis*

W.3.2.1 - A new Multiple ANFIS model for classification of hemiplegic gait

Ahmet Yardimci

W.3.2.2 - Ultra-fast Epileptic Seizure Detection Using EMD based on Multichannel Electroencephalogram

Wei Chen, Yan-Yu Lam, Chia-Ping Shen, Hsian-Ya Sung, Jeng-Wei Lin, Ming-Jang Chiu, Feipei Lai

W.3.2.3 - Handgrip estimation based on total variation denoising filtering for control applications

Julio Reategui, Gonzalo Cucho, Paul Rodrigues, Rocio Callupe, Ericka Madrid

W.3.2.4 - Speech Perception: Single Trial Analysis of the N1/P2 Complex of Unimodal and Audiovisual Evoked Responses

George Zouridakis, Martijn Baart, Jeroen Stekelenburg, Jean Vroomen

W.3.2.5 - Model free predictive control of human heart rate and blood pressure

Amirehsan Sarabadani Tafreshi, Stefania Bernasconi, Verena Klamroth-Marganska, Silvio Nussbaumer, Robert Riener

W.3.2.6 - Enabling e-services based on affective exergaming, social media and the semantic web: a multitude of projects serving the citizen-centric vision for ICT in support of pHealth

Panagiotis Bamidis

Session W.3.3 – Imperial 3 room: 13:30-15:00

Biomedical Data Engineering

Chair: *Huseyin Seker*

W.3.3.1 -SNOMED CT Normal Form and HL7 RIM binding to normalize clinical data from cancer trials

Antonio Rico-Diez, Santiago Aso-Lete, David Perez-Del-Rey, Raul Alonso-Calvo, Anca Bucur, Brecht Claerhout, Victor Maojo

W.3.3.2 - Recommending medical documents by user profile

Kleanthi Lakiotaki, Angelos Hliaoutakis, Serafim Koutsos, Euripides Petrakis

W.3.3.3 - Med-Tree: A User Knowledge Graph Framework for Medical Applications

Maunendra Sankar Desarkar, Sandip Bhaumik, Sailesh Kumar Sathish, Satnam Singh, Rangavittal Narayanan

W.3.3.4 **-** Querying Phenotype-Genotype Associations across Multiple Knowledge Bases using Semantic Web Technologies

Oya Deniz Beyan, Aftab Iqbal, Yasar Khan, Athos Antoniades, John Keane, Panagiotis Hasapis, Christos Georgousopoulos, Myrto Ioannidi, Stefan Decker, Ratnesh Sahay

W.3.3.5 **-** A RF Sensor for in vivo Measurements of the Dielectric Properties of Anisotropic Tissue

Liang Zhang, Dongming Zhou, Peiguo Liu, Xiuzhen Dong

W.3.3.6 **-** Automated prediction procedure for Charcot-Marie-Tooth disease

Athanasios Alexiou, Maria Psiha, Georgia Theocharopoulou, Panayiotis Vlamos

Imperial room **15:00-15:30**	Closing remarks – Student Paper Competition Awards

Book of Abstracts

Session M.1.1 - Imperial 1 room: 08:30-10:00

Special Session #2 - Porting Bio and Health Informatics to the Cloud

Chair: *Christoph Thuemmler*

M.1.1.1 - A Profile-based Trust Management Scheme for Ubiquitous Healthcare Environment

Georgia Athanasiou, Georgios Mantas, Maria-Anna Fengou, Dimitrios Lymberopoulos

Ubiquitous Healthcare environment materializes the patient-centric paradigm providing healthcare services without spatial and temporal limitations. However, the nature of Ubiquitous Healthcare services requiring exchange of sensitive personal data raises trust issues. In this paper, we propose a profile-based Trust Management scheme that enables the patient to select the most trustworthy Healthcare Provider in a Ubiquitous Healthcare environment. Furthermore, we propose an extended User Profile structure integrating trust-related information in order to enhance the functionality of the proposed Trust Management scheme.

M.1.1.2 - Creating dynamic and customized fetal growth curves using cloud computing

Mario Bochicchio, Antonella Longo, Lucia Vaira, Antonio Malvasi, Andrea Tinelli

The modern cloud-based solutions are gaining the upper hand in the most common industrial areas. In the healthcare sector, cloud computing is starting to set foot on, and the major applications are about the possibility to collect and share medical data. One of the hot topics argued in the obstetrics and gynecologist community, is related to the fetal growth and, in particular, to the necessity to have updated standards, since the current references lack information like ethnicity and maternal biometric parameters (essential to evaluate the correct growing parameters). We believe that cloud computing could help the development of such a kind of dynamic and customized fetal growth curves, which in turn could improve the possible detection of anomalies and pathological states during the whole pregnancy period. The paper presents a proposal for resolving the problem of the fetal biometric data obsolescence and the inability to use them in a custom or adapted fashion giving the opportunity to manage clinical data which are dispensed “as a service” on a global scale. The objective of the study is to create and validate a database collecting several fetal growth curves (obtained by means of the available results beginning from 1963 until 2013).

M.1.1.3 - CloudStudy: A Cloud-Based System for Supporting Multi-Centre Studies

Amalia Tsafara, Christos Tryfonopoulos, Spiros Skiadopoulos

Among the basic research tools for (bio)medical science are epidemiological studies that typically involve a number of hospitals, clinics, and research centres scattered around the world, and are often referred to as multi-centre studies. Clearly, the effectiveness and importance of a multi-centre study increases with the number of participating centres and enrolled patients, but at the same time this natural distribution in the production of research data requires sophisticated data management infrastructures to support the participating units. This kind of infrastructure is not only expensive to build and maintain, but also cannot be reused as it is often tailored to a specific study. In this work, we present a cloud-based system, coined CloudStudy, that allows users without any computer science background to design, deploy, and administer platforms aimed for managing, sharing, and analysing clinical data from multi-centre studies. The CloudStudy system provides a zero-administration, zero-cost online tool for creating multi-centre studies that (i) enhances re-usability by introducing study templates, (ii) supports (bio)medical needs through specialised data types, and (iii) emphasises data filtering/export through an expressive yet simple graphical query engine.

M.1.1.4 - An architecture for designing Future Internet (FI) applications in sensitive domains: Expressing the Software to data paradigm by utilizing hybrid cloud technology

Stelios Sotiriadis, Euripides Petrakis, Stefan Covaci, Paolo Zampognaro, Eleni Georga, Christoph Thuemmler

The emergency of cloud computing and Generic Enablers (GEs) as the building blocks of Future Internet (FI) applications highlights new requirements in the area of cloud services. Though, due to the current restrictions of various certification standards related with privacy and safety of health related data, the utilization of cloud computing in such area has been in many instances unlawful. Here, we focus on demonstrating a “software to data” provisioning solution to propose a mapping of FI application use case requirements to software specifications (using GEs). The aim is to establish a provider to consumer cloud setting wherein no sensitive data will be exchanged but it will reside at the back-end site. We propose a prototype architecture that covers the cloud management layer and the operational features that manage data and Internet of Things devices. To show a real life scenario, we present the use case of the diabetes care and a FI application that includes various GEs.

Session M.1.2 – Imperial 2 room: 08:30-10:00

NeuorEngineering, Neuromuscular Systems and Rehabilitation Engineering

Chair: *Athanasios Bibas*

M.1.2.1 - Controlling Variability of Air-Pulses to Determine the Thresholds of Laryngeal-Pharyngeal Reflexes by a Novel Device

Luis F Giraldo, Mauricio Agudelo, Mario Arbulu, Felipe Ortiz, Javier Burguete, Secundino Fernandez

Factors determining the variability of air-pulse pressure to determine the thresholds of laryngeal-pharyngeal reflexes, related to swallowing and airway protection, were explored and a novel device, minimizing variability, was designed. Potential factors affecting reproducibility of air-pulses were experimentally evaluated and included in a multiple linear regression model. A device controlling these factors was designed, its reproducibility was assessed by the coefficient of variation (CV) of pressures and duration of air-pulses, and its validity was assessed comparing obtained with desired pressures and durations. Differences in the pressures of air-pulses categories were assessed by one-way ANOVA of repeated measures, Tukey test and Whisker and box plot. The distance and angle between the exit of the tube conducting the pulses and the surface to be impacted, the diameter of the tube, the feeding pressure of the system, and the duration of air-pulses, significantly affected the accuracy of air-pulses. The novel device incorporated electronic valves and a telemeter to be used during the fiberoptic endoscopic evaluation of swallowing. The differences between the desired and obtained pressures and durations were below 3%. The CV of air-pulse pressures of the novel device was 0.02. The CV of air-pulse duration was 0.05. The Anova, Tukey Tests and Box and whisker plot showed that the outlet pressures of air-pulse categories had statistically significant differences between them, without overlapping between categories, helping to obtain an accurate threshold.

M.1.2.2 - Quering Functional Brain Connectomics to Discover Consistent Subgraph Patterns

Nantia Iakovidou, Stavros Dimitriadis, Nikos Laskaris, Kostas Tsichlas

Dynamic recordings of functional activity maps can naturally and efficiently be represented in the form of functional/effective connectivity networks. New methods for mapping synaptic connections and recording neural signals generate rich and complex data about the structure and dynamics of brain networks. To study the most complex network in nature, the brain, there is need to integrate a huge amount of brain networks collected from laboratories over the world in large databases. Human Brain Project (Europe and USA) aims to explore brain functionality in various ways. Brain networks are central to achieving the goals of this ambitious plan. However, the immense amount of thousands of brain networks, prevent an easy way to utilizable knowledge. In this paper, we demonstrate a data-driven approach that discovers consistent patterns from a collection of brain networks via a querying approach: formulating a query of “finding an increasing or a decreasing consistent subgraph over an amount of subjects” after taking the difference between two sets of graphs referred as two conditions (an active and a baseline). Experiments demonstrated that our data-driven approach allows identifying frequency-dependent selective spatial pattern changes of the EEG functional connectivity network during a mental task. This is the first time that a method fully exploits the connectivity weights of a brain network to discover consistent subgraph patterns.

M.1.2.3 - Design and Simulation of Wheel-chaired Elliptical Stepping Exercise for Stroke Rehabilitation

Saiful Zaimy Yahaya, Zakaria Hussain, Rozan Boudville

Stroke disease is one of the major killer diseases worldwide and most of the survivors will end with certain level of impairment. They commonly are wheelchair bounded and require scheduled rehabilitation exercise to regain their walking capability or mobility. This paper presents the design of elliptical stepping exercise ergometer for functional electrical stimulation (FES) assisted exercise. The concept of wheelchaired cycling and elliptical stepping had been adapted in producing the ergometer design. The dynamic simulation has been performed on Visual Nastran 4D and Matlab Simulink to evaluate the performance of the exercise that includes the exercise ergometer, humanoid model and quadriceps muscle model. In the simulation work, the paretic leg (left side) is moved via FES assisted while the non-paretic leg (right side) is moved via able body control. The result shows that the FES assisted elliptical stepping exercise with able body supports contribute better cadence speed control. Further improvement on the controller design is required to make sure suitable FES pattern can be delivered and better cadence speed control can be achieved.

M.1.2.4 - A system for optically controlling neural circuits with very high spatial and temporal resolution

Chethan Pandarinath, Eric Carlson, Sheila Nirenberg

Optogenetics offers a powerful new approach for controlling neural circuits. It has a vast array of applications in both basic and clinical science. For basic science, it opens the door to unraveling circuit operations, since one can perturb specific circuit components with high spatial (single cell) and high temporal (millisecond) resolution. For clinical applications, it allows new kinds of selective treatments, because it provides a method to inactivate or activate specific components in a malfunctioning circuit and bring it back into a normal operating range [1-3]. To harness the power of optogenetics, though, one needs stimulating tools that work with the same high spatial and temporal resolution as the molecules themselves, the channelrhodopsins. To date, most stimulating tools require a tradeoff between spatial and temporal precision and are prohibitively expensive to integrate into a stimulating/recording setup in a laboratory or a device in a clinical setting [4, 5]. Here we describe a Digital Light Processing (DLP)-based system capable of extremely high temporal resolution (sub-millisecond), without sacrificing spatial resolution. Furthermore, it is constructed using off-the-shelf components, making it feasible for a broad range of biology and bioengineering labs. Using transgenic mice that express channelrhodopsin-2 (ChR2), we demonstrate the system's capability for stimulating channelrhodopsin-expressing neurons in tissue with single cell and sub-millisecond precision.

M.1.2.5 - Towards an Overall 3-D Vector Field Reconstruction via Discretization and a Linear Equations System

Chrysa Papadaniil, Leontios Hadjileontiadis

A tomographic method that efficiently reconstructs three-dimensional fields, despite the ill-posedness of recovering a vector field from line integrals, is presented in this paper. The analysis takes into consideration the methodology set forth in [1] for 2-D reconstruction and demonstrates that with the analogous discretization of the 3-D space and scanning lines, data redundancy is achieved and the solution is obtained from a linear equations system solution, using only information from finite boundary measurements. The adequacy of the method is illustrated by means of simulations on electrostatic fields. The motivation behind this work lies in its potential to bring forward an alternative brain mapping model from EEG recordings.

Session M.1.3- Imperial 3 room: 08:30-10:00

Workshop – ISMSR-13

Healthcare Monitoring Technologies and Methods

Chair: *Nikolaos Bourbakis*

M.1.3.1 -TeleCare of Mental Disorders by Applying Semantic Web Technology

Chryssa Thermolia, Ekaterini Bei, Euripides Petrakis

We present the design of a decision support system aiming to provide specific telecare capabilities between health experts and patients suffering from Bipolar Disorder (BD). Bipolar Disorder is a severe and recurrent mental illness related with high morbidity and evolves constantly in time. We focus on Breakthrough Depressive Episode, a scenario that develops when a patient shows depressive symptoms during pharmaceutical treatment. Using Semantic Web Technologies we developed SybillaTUC, a prototype Clinical Decision Support System, able to predict the evolution of the disease for each patient, alerting the clinician on the possibility of a crucial incident suggesting optimal treatment.

M.1.3.2 - Microstate analysis of the EEG using Local Global graphs

Kostas Michalopoulos, Nikolaos Bourbakis

The topography of the electrical field as reflected in the EEG electrodes does not vary randomly with time but rather displays short periods of stable topographical configurations or spatial patterns, known as microstates. The search of such patterns takes place in the high dimensional electrode space with all the problems that come with it. In this paper, we present a technique for the extraction, detection and representation of EEG microstates based on the Local Global graph (LG graph) technique. We use the Local Global graph to represent the spatial configuration of the topographic map and use a LG graph matching approach to determine the different microstates. We applied the methodology to the average, over trials recording and we were able to retrieve the dominant microstates using our methodology.

M.1.3.3 - A Low-Cost Embedded Real-Time 3D Stereo Matching System for Surveillance Applications

Georgia Rematska, Kyprianos Papadimitriou, Apostolos Dollas

The implementation of low-cost 3D Stereo Vision systems entails the implementation of stereo matching algorithms in real time. Various efforts have been reported in literature, however, these systems require substantial hardware resources. The contribution of the present work is on the low-cost real-time implementation of such a system, which was fully implemented on a small Xilinx FPGA. The system presented in this work extends previous results of the authors through design space exploration, architecture improvements and careful problem sizing.

M.1.3.4 - The MobiFall Dataset: An Initial Evaluation of Fall Detection Algorithms Using Smartphones

George Vavoulas, Matthew Pediaditis, Emmanouil Spanakis, Manolis Tsiknakis

Numerous fall detection systems exist to date that use accelerometers and/ or gyroscopes attached on a person's body as primary signal sources. These systems use either discrete sensors as part of a product engineered specifically for this task or sensors that are embedded in mobile phones or smartphones. The latter approach has the advantage of offering well tested and widely available communication services for calling emergency etc. Although fall detection has been studied intensively and many commercial products are available, it still receives significant attention e.g. in the field of preventive healthcare, especially for the elderly. The aim of this article is to introduce a dataset that will be helpful in testing new methods, as well as performing objective comparisons between different algorithms for fall detection and activity recognition, based on inertialsensor data from smartphones. The dataset contains signals recorded from the accelerometer and gyroscope sensors of a latest technology smartphone for four different falls and nine different activities of daily living. Finally the results of an initial evaluation of three fall detection algorithms using this dataset are presented.

M.1.3.5 - A wearable Ultrasound multi-transducer array system for Abdominal Organs Monitoring

Michael Tsakallakis, Nikolaos Bourbakis

Ultrasound imaging (USI) or Medical Sonography (MS) as it is formally called is widely used in biomedical applications over the last decades. Form the Intensive Care Unit (ICU) minimally invasive monitoring to the recent point of care testing besides the patient's bed. US imaging outcomes can provide clinicians with a thorough view of the internal parts of the human body at a very low expense. In this paper, we insinuate an alternative approach compared to already existing ones of capturing US images. We propose a wearable ultrasound system composed of an array of ultrasound circular 2D transducers, integrated in a belt, for point of care monitoring of the abdominal region and particularly the liver for critical ill subjects. The configuration of the array and the type of the transducers will entail a system capable of providing clinicians with high resolution 2D imaging of the region of interest (ROI) as well as 3D representation of whole organs without theirs assistance.

M.1.3.6 - A Single Chip Solution for Pulse Transmit Time Measurement

Sasa Knezevic, Radovan Stojanovic

This paper proposes a methodology for Pulse Transmit Time measurement for purposes of cuff-less monitoring of Blood Pressure. The ECG and PPG signals are simultaneously acquired and Pulse Transmit Time is determined as a time between R peak in ECG and maximal slope in PPG. To distinguish characteristics points Discrete Wavelet Transform, Derivative Filtering, Modulus Maxima and additional functions are employed and translated in VHDL code and then embedded in a single chip from FPGA technology. The system works on-line, achieving accuracy of 97.53% and 97.09% for R peak and slope detection respectively. The emphasis is given to the description of signal processing approach, system architecture and working principles of fundamental components. Also, the preliminary testing results are presented.

Session M.2.1 – Imperial 1 room: 10:30-12:00

Computer Assisted Intervention Systems

Chair: *Christos Schizas*

M.2.1.1 - Electronic Health Record: Facilitating the Coding Process

Harris Soteriades, Kleanthis Neokleous, George Tsouloupas, Antonis Jossif, Schizas Christos

In this paper, we introduce an intelligent medical assistant tool that offers the ability to suggest appropriate medical diagnostic coding during the examination process through a friendly user interface. Furthermore the tool offers the capability to match medical coding definitions from one standard to another such as ICD 10 and SNOMED CT. The tool has three main functions: a) Easy Search, b) Coding Suggestion and c) Coding Interoperability.

M.2.1.2 - Towards Efficient and Secure in-Home Wearable Insomnia Monitoring and Diagnosis System

Sana Tmar-Ben Hamida, Elyes Ben Hamida, Beena Ahmed, Adnan Abu-Dayya

Sleep disorders, such as insomnia can seriously affect a patient's quality of life. Sleep measurements based on polysomnographic (PSG) signals and patients' questionnaires are necessary for an accurate evaluation of insomnia. Due to recent innovations in technology, it is now possible to continuously monitor a patient's sleep at home and have their sleep data sent to a remote clinical back-end system for collection and assessment. Most of the research on sleep reported in the literature mainly looks into how to automate the analysis of the sleep data and does not address the problem of the efficient and secure transmission of the collected health data. This paper provides an experimental evaluation of communication and security protocols that can be used in in-home sleep monitoring and health care and highlights the most suitable protocol in terms of security and overhead. Design guidelines are then derived for the deployment of effective in-home patients monitoring systems.

M.2.1.3 - Guided Physical Exercise of Cardiac Patients during Rehabilitation: Adherence and Changes in Physiological Variables

Hilkka Runtti, Dimitris Filos, Mark van Gils, Ioanna Chouvarda, Anita Honka, Juha Pärkkä

A system to provide cardiac patients with the possibility to perform safe and beneficial exercise during their rehabilitation was developed within the EU project Heartcycle. Within the system, algorithms use physiological signals from a wearable device (embedded in a shirt) to guide the patient through the exercise. After having been technically validated, the system was deployed for clinical evaluation with 63 patients in Germany (21), Great Britain (25) and Spain (17). The paper describes the first findings of this evaluation study with respect to: technical feasibility, adherence of the patients to the prescribed exercise protocol, and changes in physiological observables as the patients follow their exercise plan. Technically, the system functioned well, and overall the adherence of those patients that actually started using the system was stable, or even improving, in the vast majority of cases. An increase was especially seen in adherence to the protocol set for the warm-up phase of the exercise. This is an important finding for a group of patients that is known to have declining adherence to rehabilitation recommendations in the long term. The recovery analysis showed that specially the recovery of the heart rate as measured in the first minute after the exercise end showed improvement over time.

M.2.1.4 - Ef-Zin: A hybrid framework for ubiquitous management of comorbidity and multimorbidity in chronic diseases.

Foteini Andriopoulou, Konstantinos Birkos, Dimitrios Lymberopoulos

The existence of comorbidity and multimorbidity increases the diagnostic uncertainty and has a variety of negative social and economical impacts. This paper proposes the Ef-Zin framework that aims to manage patients suffering from chronic conditions by means of (a) creating collaborative virtual groups through medical and paramedical professionals and (b) delivering the appropriate therapy to the individual patient. Ef-Zin involves two distinct processing phases for parallel evaluation of patient’s contextual information. For the evaluation it uses rule-based algorithms and Random Forest (RF) machine learning technique for categorizing patients into groups according to the severity levels, making decisions about the services that will be delivered and notifying the appropriate specialized healthcare professionals for patient’s current health status. We have carefully drafted an architecture of the proposed Ef-Zin framework and qualitative evaluation has been conducted in a common use case scenario such as Chronic Obstructive Lung Disease (COPD) and a cardiovascular disease (hypertension) that is the most frequent and significant disease that coexists with COPD.

M.2.1.5 - Detection of occlusal caries based on digital image processing

Georgia Koutsouri, Elias Berdouses, Evanthia Tripoliti, Constantine Oulis, Dimitrios Fotiadis

The aim of this work is to present an automated non supervised method for the detection of occlusal caries based on photographic color images. The proposed method consists of three steps: (a) detection of decalcification areas, (b) detection of occlusal caries areas, and (c) fusion of the results. The detection process includes pre-processing of the images, segmentation and post-processing, where objects not corresponding to areas of interest are eliminated through the utilization of rules expressing the medical knowledge. The pre-processing, segmentation and post-processing are differentiated depending on the areas that have to be detected (decalcification or occlusal areas). The method was evaluated using a set of 60 images where 286 areas of interest were manually segmented by an expert. The obtained sensitivity and precision is 92% and 80%, respectively.

M.2.1.6 - On the Use of Smartphones for Detecting Obstructive Sleep Apnea

Mamoun Al-Mardini, Fadi Aloul, Assim Sagahyroon, Luai Al-Husseini

Obstructive Sleep Apnea (OSA) is a common sleep disorder which is characterized by recurrent blockage of the upper airway, often resulting in oxygen desaturation. Attended overnight polysomnography (PSG) has been recommended as the golden standard for the diagnostic of OSA at hospitals, which requires an expensive attended overnight stay at a hospital with considerable wiring between the PSG device and the human body. In this work, we design a reliable, comfortable, inexpensive, and easily available smartphone system that allows users to apply the OSA test at home without the need for attended overnight tests. The design takes advantage of a smatrphone’s built-in sensors, pervasiveness, computational capabilities, and user-friendly interface to screen OSA. We extract three main physiological signals to diagnose OSA which are (1) oxygen saturation using an external oximeter, (2) respiratory effort using the smartphone's built-in microphone, and (3) body movement using the smartphone's built-in accelerometer. The signals are analyzed solely on the smartphone to screen the OSA. Finally, we examine our system's ability to screen the disease as compared to the golden standard by testing it on 15 subjects. The results showed that 100% of the sick subjects were correctly classified as having OSA, and 85.7% of the healthy subjects were correctly classified as not having OSA. These preliminary results demonstrate the effectiveness of the proposed system when compared to the golden standard and emphasize the important role of smartphones in healthcare.

Session M.2.2 – Imperial 2 room: 10:30-12:00

Special Session #3 - Computational BioEngineering

Chair: *Nenad Filipovic*

M.2.2.1 - Multivariate Discriminant Analysis of Multiparametric Brain MRI to Differentiate High Grade and Low Grade Gliomas - A Computer-Aided Diagnosis Development Study

Füsun Çıtak Er, Zeynep Firat, Ilhami Kovanlikaya, Ugur Ture, Esin Ozturk Isik

The aim of this study is to investigate the predictive capacity of multiparametric magnetic resonance imaging (MRI) findings using multivariate discriminant analysis. Preoperative clinical findings and multiparametric MRI, including diffusion weighted MR imaging, diffusion tensor imaging, perfusion MR imaging and MR spectroscopic imaging are used as predictors to distinguish high grade from the low grade gliomas. This study is a model for a computer aided diagnosis system for glioma grading. Principal component analysis was performed prior to discriminant analysis for dimensional reduction and outlier detection. Linear and quadratic discriminant analysis were performed and compared based on sensitivity and specificity analysis. Quadratic discriminant analysis provided the best diagnostic ability with 100% sensitivity. The specificities of both linear and quadratic discriminant analysis were 71%.

M.2.2.2 - Blind Recovery of Cardiac and Respiratory Sounds Using Non-negative Matrix Factorization & Time-Frequency Masking

Ghafoor Shah, Constantinos Papadias

Auscultation is an effective noninvasive medical procedure for examining the cardiorespiratory system. However, the cardiac and respiratory acoustic sounds interfere in time as well as in spectral contents, which hampers the diagnostibility of the classical stethoscope. We propose a method for smart auscultation by blindly recovering the original cardiac and respiratory sounds from a single observation mixture. We decompose the spectrogram of the mixture into independent, non-redundant components, by employing non-negative matrix factorization (NMF). To group the decomposed components into original sources, a new unsupervised technique is proposed. Time-frequency masking is used to recover the original sources. This smart auscultation method is successfully applied to actual data collected from different subjects in different clinical settings. Our method demonstrates excellent results even in noisy clinical environments.

M.2.2.3 - Graph-theoretic analysis of scalp EEG brain networks in epilepsy - the influence of montage and volume conduction

Manolis Christodoulakis, Avgis Hadjipapas, Eleftherios Papathanasiou, Maria Anastasiadou, Savvas Papacostas, Georgios Mitsis

It is well established that both the choice of recording reference (montage) and volume conduction affect the connectivity measures obtained from scalp EEG. Our purpose in this work is to establish the extent to which they influence the graph theoretic measures of brain networks in epilepsy obtained from scalp EEG. We evaluate and compare two commonly used linear connectivity measures - cross-correlation and coherence - with measures that account for volume conduction, namely corrected cross-correlation, imaginary coherence, phase lag index and weighted phase lag index. We show that the graphs constructed with cross-correlation and coherence are the most affected by volume conduction and montage; however, they demonstrate the same trend - decreasing connectivity at seizure onset, which continues decreasing in the ictal and early post-ictal period, increasing again several minutes after the seizure has ended— with all other measures except imaginary coherence. In particular, networks constructed using cross-correlation yield better discrimination between the pre- ictal and ictal periods than the measures less sensitive to volume conduction/ Thus, somewhat paradoxically, although removing effects of volume conduction allows for a more accurate reconstruction of the true underlying networks this may come at the cost of discrimination ability with respect to brain state.

M.2.2.4 - Experimental and Numerical Investigation of Electromagnetic Field at Different Cancer Cell Lines

Nenad Filipovic, Tijana Djukic, Milos Radovic, Danijela Cvetkovic, Snezana Markovic, Branislav Jeremic

There is a strong interest of investigation of Extremely Low Frequency (ELF) ElectroMagnetic (EM) fields in the clinic. In this study we investigated experimentally in-vitro and in-sillico with computer simulation influence of 50 Hz EM field at three different cancer cell lines: breast cancer MDA-MB-231 and colon cancer SW-480 and HCT-116. Computer reaction-diffusion model with the net rate of cell proliferation and effect of electromagnetic field in time was developed. The fitting procedure for estimation of the computer model parameters was implemented. Experimental and computer model data have shown good comparison. These findings can open a new avenue for better controlling the growth of cancer cells at specific frequencies without affecting normal tissues, which may have a great influence in clinical oncology.

M.2.2.5 - Application of Data Mining Algorithms for Mammogram Classification

Milos Radovic, Marina Djokovic, Aleksandar Peulic

One of the leading causes of cancer death among women is breast cancer. In our work we aim at proposing a prototype of a medical expert system (based on data mining techniques) that could significantly aid medical experts to detect breast cancer. This paper presents the CAD (computer aided diagnosis) system for the detection of normal and abnormal pattern in the breast. The proposed system consists of four major steps: the image preprocessing, the feature extraction, the feature selection and the classification process that classifies mammogram into normal (without tumor) and abnormal (with tumor) pattern. After removing noise from mammogram using the Discrete Wavelet Transformation (DWT), first is selected the region of interest (ROI). By identifying the boundary of the breast, it is possible to remove any artifact present outside the breast area, such as patient markings. Then, a total of 20 GLCM features are extracted from the ROI, which were used as inputs for classification algorithms. In order to compare the classification results, we used seven different classifiers. Normal breast images and breast image with masses (total 150 images) used as input images in this study are taken from the mini-MIAS database.

M.2.2.6 - Estimation of Blood Pressure Levels from Reflective Photoplethysmograph using Smart Phones

Aishwarya Visvanathan, Aniruddha Sinha, Arpan Pal

As part of preventive healthcare, there is a need to regularly monitor blood pressure (BP) of cardiac patients and elderly people. Mobile Healthcare, measuring human vitals like heart rate, Spo2 and blood pressure with smart phones using the Photoplethysmography technique is becoming widely popular. But, for estimating the BP, multiple smart phone sensors or additional hardware is required, which causes uneasiness for patients to use it, individually. In this paper, we present a methodology to estimate the systolic and diastolic BP levels by only using PPG signals captured with smart phones, which adds to the affordability, usability and portability of the system. Initially, a training model (Linear Regression Model or SVM Model) for various known levels of BP is created using a set of PPG features. Later, the model is used to estimate the BP levels from the features of the newly captured PPG signals. Experiments are performed on benchmark hospital dataset and data captured from smart phones in our lab. Results indicate that by additionally adding information of height, weight and age play a vital role in increasing the accuracy of the estimation of BP levels.

Session M.2.3 – Imperial 3 room: 10:30-12:00

Workshop-ISMSR-13

Computational Oncology: From mathematical models to clinical practice

Chair: *Michalis Zervakis*

M.2.3.1 - Towards in-vivo Validation of Computational (in silico) Models of Tumor Growth

V. Sakkalis

M.2.3.2 - Computational Development Models in the Micro-Environment of Cancer

M. Papadogiorgaki

M.2.3.3 - Improving Personalized Therapy Assessment in Cancer Patients based on MRI Image Analysis

K. Marias

M.2.3.4 - Stochastic Approaches for Personalized Modeling of Cancer

G. Mitsis

M.2.3.5 - On the use of Computational Models in Clinical Practice
P. Koliou

Open Discussion

Session M.3.1 – Imperial 1 room: 13:30 -15:30

Bio-Ontology and Data Mining

Chair: *Dimitrios Lymberopoulos*

M.3.1.1 -OnTheFly 2.0: A service to automatically annotate files and extract biological information

Evangelos Pafilis, Georgios A. Pavlopoulos, Venkata P. Satagopam, Nikolas Papanikolaou, Heiko Horn, Christos Arvanitidis, Lars Juhl Jensen, Reinhard Schneider, Ioannis Iliopoulos

Retrieving all of the necessary information from databases about bioentities mentioned in an article is not a trivial or an easy task. Following the daily literature about a specific biological topic and collecting all the necessary information about the bioentities mentioned in the literature manually is tedious and time consuming. OnTheFly 2.0 is a web application mainly designed for non-computer experts which aims to automate data collection and knowledge extraction from biological literature in a user friendly and efficient way. OnTheFly 2.0 is able to extract bioentities from individual articles such as text, Microsoft Word, Excel and PDF files. With a simple drag-and-drop motion, the text of a document is extensively parsed for bioentities such as protein/gene names and chemical compound names. Utilizing high quality data integration platforms, OnTheFly allows the generation of informative summaries, interaction networks and at-a-glance popup windows containing knowledge related to the bioentities found in documents. OnTheFly 2.0 provides a concise application to automate the extraction of bioentities hidden in various documents and is offered as a web based application. It can be found at: http://onthefly.embl.de.

M.3.1.2 - Enhanced Probabilistic Latent Semantic Analysis with Weighting Schemes to Predict Genomic Annotations

Pietro Pinoli, Davide Chicco, Marco Masseroli

Genomic annotations with functional controlled terms, such as the Gene Ontology (GO) ones, are paramount in modern biology. Yet, they are known to be incomplete, since the current biological knowledge is far to be definitive. In this scenario, computational methods that are able to support and quicken the curation of these annotations can be very useful. In a previous work, we discussed the benefits of using the Probabilistic Latent Semantic Analysis algorithm in order to predict novel GO annotations, compared to some Singular Value Decomposition (SVD) based approaches. In this paper, we propose a further enhancement of that method, which aims at weighting the available associations between genes and functional terms before using them as input to the predictive system. The tests that we performed on the annotations of human genes to GO functional terms showed the efficacy of our approach.

M.3.1.3 - Modified Free Energy Model to improve RNA secondary structure prediction with pseudoknots

Kwok-Kit Tong, Kwan-Yau Cheung, Kin-Hong Lee, Kwong-Sak Leung

The free energy (evaluation) models used in RNA secondary structure prediction are one of the most important reasons that makes the prediction a challenging computational problem in Bioinformatics. These models are the key factor determining the accuracy of the prediction algorithms. Previously we have developed a method called GAknot that has obtained good performance on predicting RNA secondary structures with pseudoknots. In this paper, we propose a new free energy model. We first select a number of RNA sequences from a database which contains known RNA secondary structures as a training dataset for learning this new model. From the training dataset, we then extract base pairs patterns in subsequences of pairs of k-mers from the stems of each sequence in the training data and use the patterns to formulate penalty factors. We modify the energy model by adding these penalty factors. Combined with the new modified energy model, the prediction performance of GAknot has been improved significantly. GAknot with the new modified energy model is shown to be the best method in comparison with two state-of-the-art algorithms using a commonly used testing dataset. The penalty factors of the new energy model and dataset can be downloaded at http://appsrv.cse.cuhk.edu.hk/~kktong/NewModel.

M.3.1.4 - Classification of RNAs with Pseudoknots using k-mer Occurrences Count as Attributes

Kwan-Yau Cheung, Kwok-Kit Tong, Kin-Hong Lee, Kwong-Sak Leung

RNAs are functionally important in many biological processes. Predicting secondary structures of RNAs can help understanding 3D structures and functions of RNAs. However, RNA secondary structure prediction with pseudoknots is NP-complete. Predicting whether the RNAs contain pseudoknots in advance can save computation time as secondary structure prediction without pseudoknots is much faster. In this paper, we use k-mer occurrences as attributes to predict whether the RNAs have pseudoknots in the secondary structure. The results show two classifiers can predict 90% of the instance correctly.

M.3.1.5 - Integrative Warehousing of Biomolecular Information to Support Complex Multi-Topic Queries for Biomedical Knowledge Discovery

Arif Canakoglu, Marco Masseroli, Stefano Ceri, Luca Tettamanti, Giorgio Ghisalberti, Alessandro Campi

Biomedical questions are often complex and address multiple topics simultaneously. Answering them requires the comprehensive evaluation of several different types of data. They are often available, but in distributed and heterogeneous data sources; this hampers their global evaluation. We developed a software architecture to create and maintain updated a Genomic and Proteomic Data Warehouse (GPDW), which integrates several of the main of such dispersed data. It uses a modular and multi-level global data schema based on abstraction and generalization of integrated data features. Such a schema eases integration of data sources evolving in data content, structure and number, and assures provenance tracking of all the integrated data. Thanks to the developed software architecture and adopted data schema, the GPDW has been kept updated easily and progressively extended with additional data types and sources; it is publicly usable at http://www.bioinformatics.dei.polimi.it/GPKB/.

Session M.3.2 – Imperial 2 room: 13:30 -15:30

Special Session #3 - Computational BioEngineering

Chair: *Nenad Filipovic*

M.3.2.1 - SIFEM Project: Semantic Infostructure interlinking an open source Finite Element tool and libraries with a model repository for the multi-scale Modelling of the inner-ear

Christos Bellos, Athanasios Bibas, Dimitrios Kikidis, Steve Elliott, Stefan Stenfelt, Ratnesh Sahay, Konstantina Nikita, Dimitrios Koutsouris, Dimitrios Fotiadis

The SIFEM project targets the development of an infrastructure in order to semantically link open source tools and libraries with existing data as well as new knowledge towards the multi-scale finite element modelling of the inner-ear. The SIFEM system is designed based on an open architecture schema that consists of a set of tools and subsystems in order to develop robust multi-scale models. The project mainly delivers: (i) tools for finite elements modelling, (ii) cochlea reconstruction tool and (iii) 3D inner ear models visualization tool. The main scientific results contribute to the knowledge of alterations associated to diverse cochlear disorders and could lead, in long-term, to personalized healthcare. The overview of the SIFEM platform and its architecture is presented in this paper.

M.3.2.2 - SIFEM Project: Finite Element Modeling of the Cochlea

Velibor Isailovic, Milica Obradovic, Dalibor Nikolic, Igor Saveljic, Nenad Filipovic

The cochlea is very interesting part of the body. There are several investigations of experiments on the real cochlea and mathematical models. The cochlea works on the basis of a vibrating system. SIFEM project focuses on the development the multi-scale modelling of the inner-ear with regard to the sensorineural hearing loss. In this study we focused of the finite element model of the cochlea. The first approximation is straight box model where both domain basilar membrane and surrounding fluid are modeled. Fluid-structure interaction problem was implemented. The basilar membrane was modeled as structural plate with 3D brick finite element and fluid domain around the basilar membrane was modeled as full 3D Navier-Stokes equations. ALE formulation was employed for fluid domain and mesh moving algorithm for motion of the membrane and fluid mesh. The results for different frequencies for 3D box and spiral model are presented. It can be observed that viscous fluid allow a sharper response of the membrane, because the viscous fluid would quickly damp out the vibratory motion.

M.3.2.3 - Modeling of Abdominal Aorta Aneurism Rupture by using Experimental Bubble Inflation Test

Igor Koncar, Dalibor Nikolic, Suzana Pantovic, Mirko Rosic, Nikola Mijailovic, Nikola Ilic, Marko Dragas, Zivan Maksimovic, Lazar Davidovic, Nenad Filipovic

Aneurysm rupture is a biomechanical phenomenon that occurs when the mechanical stress acting on the inner wall exceeds the failure strength of the diseased aortic tissue. Besides numerous advantages in surgical and anaesthesiological management, emergency procedure leads to fatal outcome in 20-50% of those who reach hospital. Prediction of influence of dynamic blood flow on natural history of aneurysmatic disease and outcome of therapeutic procedures could contribute to treatment strategy and results. In this study we presented experimental design for estimation of the material property of real human aorta tissue from bubble inflation test. Then we investigated fluid-structure interaction of pulsatile blood flow in the specific patient three-dimensional model of abdominal aortic aneurysms (AAAs). Numerical predictions of blood flow patterns and nonlinear wall stresses in AAAs are performed in compliant wall anisotropic model using the finite element method. These computational procedures together with experimental determination of the nonlinear material property could provide us more accurate assessment of aneurysm rupture risk.

M.3.2.4 - Multi-process Dynamic Modeling of Tumor-specific Evolution

Achilleas Achilleos, Charalambos Loizidis, Marios Hadjiandreou, Triantafyllos Stylianopoulos, Georgios D. Mitsis

We suggest a multi-process dynamic model and a sequential bayesian forecasting method of tumor-specific growth. The mixture model uses prior information obtained from the general population and becomes more individualized as more observations from the tumor are sequentially taken into account. In this study we propose utilizing all available tumor-specific information up to date to approximate the unknown multi-scale process of tumor growth over time, in a stochastic context. The validation of our approach was performed with experimental data from mice and the results show that after few observations from a tumor are obtained and included in the model, the latter becomes more individualized, in the sense that its parameters are adjusted in order to reflect the growth of each individual tumor, yielding more precise estimates of its size.

M.3.2.5 - Towards a Semantic Representation for Multi-Scale Finite Element Biosimulation Experiments

Andre Freitas, Margaret Jones, Kartik Asooja, Christos Bellos, Steve Elliott, Stefan Stenfelt, Panagiotis Hasapis, Christos Georgousopoulos, Torsten Marquardt, Stefan Decker, Ratnesh Sahay

Biosimulation researchers use a variety of models and languages capturing and processing different aspects of biological processes. However, current modeling methods do not capture the underlying semantics of the biosimulation models sufficiently to support building, merging, and reusing multi-scale biosimulation models originating from diverse experiments. In this paper, we propose an ontology based biosimulation model and knowledge services facilitating researchers to share and collaborate their knowledge bases at Web scale. In particular, we study the multi-scale finite element modelling of the inner-ear. The proposed ontology based biosimulation model and knowledge services will provide homogenized and standardized access to the shared, harmonized datasets (histological data, micro-CT images of the cochlea, pathological data) and inner ear models required to execute the simulations. The work presented in this paper is analyzed and designed as part of the SIFEM EU project.

M.3.2.6 - Modeling Atherosclerotic Plaque Growth: A Case Report Based on a 3D Geometry of Left Coronary Arterial Tree from Computed Tomography

Antonis I. Sakellarios, Panagiotis Siogkas, Lambros Athanasiou, Themis Exarchos, Michail

Papafaklis, Christos Bourantas, Katerina Naka, Lampros Michalis, Nenad Filipovic, Oberdan Parodi, Dimitrios Fotiadis

In this study, we present an innovative model for plaque growth utilizing a 3-Dimensional (3D) left coronary arterial tree reconstructed from computed tomographic (CT) data. The proposed model takes into consideration not only the effect of the local hemodynamic factors but also major biological processes such as the low density lipoprotein (LDL) and high density lipoprotein (HDL) transport, the macrophages recruitment and the foam cells formation. The endothelial membrane is considered semi-permeable and endothelial shear stress dependent, while its permeability is modeled using the Kedem-Katscalsky equations. Patient specific biological data are used for the accurate modeling of plaque formation process. The finite element method (FEM) is employed for the solution of the system of partial differential equations. The results of the simulation are compared to the plaque progression in a follow-up CT examination performed three years after the initial investigation. The results show that the proposed model can be used to predict regions prone for plaque development of progression.

Session M.3.3 – Imperial 3 room: 13:30 -15:30

Biomedical Signal Processing

Chair: *Nizamedin Aydin*

M.3.3.1 - A new approach to adaptive noise cancellation in synthetic auditory evoked potentials

Nurettin Acir, Engin Cemal Mengus

This paper presents a new approach for enhancing Auditory Evoked Potentials (AEP). In this study, we first generated synthetic single trial AEP data at some specified noise levels by using gamma-tone function technique and then applied the proposed Lyapunov theory based filter to the noisy AEP synthetic data. Simulation results have been demonstrated that enhanced AEP with LST based adaptive filter can effectively be used to cancel out background EEG noise for a better measurement.

M.3.3.2 - Denoising Simulated EEG Signals: A Comparative Study of EMD, Wavelet Transform and Kalman Filter

Christos Salis, Anastasios Malissovas, Paschalis Bizopoulos, Alexandros Tzallas, Panagiotis Angelidis, Dimitrios Tsalikakis

Electrooculographic (EOG) artefact is one of the most common contaminations of Electroencephalographic (EEG) recordings. The corruption of EEG characteristics from Blinking Artefacts (BAs) affects the results of EEG signal processing methods and also impairs the visual analysis of EEGs. In this paper, our scope was a comparative analysis of the performance of three standard denoising methods like continuous Empirical Mode Decomposition (EMD), Discrete Wavelet Transform (DWT) and Kalman Filter (KF). In order to evaluate the performance of EMD, DWT and KF of noise reduction and to express the quality of the denoised EEG, we calculate several indexes such as the Signal-to-Noise Ratio (SNR). All the results obtained from noise simulated EEG data show that WT achieved the greatest SNR difference and also the mode mixing issue of EMD affected this method’s performance.

M.3.3.3 - TRS-TMS: an EEGLAB plugin for the reconstruction of onsets in EEG-TMS datasets

Sara Petrichella, Luca Vollero, Florinda Ferreri, Giulio Iannello

EEG evoked potentials analysis strongly relies on the correct alignment of different segments of the EEG activity. This alignment is needed in order to extract low event related waves from background signals. Usually the information on onsets, which allows the correct alignment of segments, is provided by the acquisition system. However, wrong configuration of the system or human errors during the acquisition or storage of data may make this information unavailable. Usually these errors are discovered when the dataset is analyzed and this can take place even several months after the start of the dataset’s acquisition. Changes on patients status and the expensiveness of EEG registrations makes unfeasible the repetition of the acquisitions. In this paper we present, describe and evaluate two mechanisms that we included in an EEGLAB plugin for the automatic reconstruction of onsets in EEG-TMS acquisitions. The methods of the TMS Triggers Reconstruction Software (TRS-TMS)plugin are discussed and evaluated obtaining guidelines for their correct configuration in the routine usage.

M.3.3.4 - Unsupervised Approach for Measurement of Cognitive Load using EEG Signals

Diptesh Das, Debatri Chatterjee, Aniruddha Sinha

Individuals exhibit different levels of cognitive load for a given mental task. Measurement of cognitive load can enable real-time personalized content generation for distant learning, usability testing of applications on mobile devices and other areas related to human interactions. Electroencephalogram (EEG) signals can be used to analyze the brain-signals and measure the cognitive load. We have used a low cost and commercially available neuro-headset as the EEG device. A universal model, generated by supervised learning algorithms, for different levels of cognitive load cannot work for all individuals due to the issue of normalization. In this paper, we propose an unsupervised approach for measuring the level of cognitive load on an individual for a given stimulus. Results indicate that the unsupervised approach is comparable and sometimes better than supervised (e.g. support vector machine) method. Further, in the unsupervised domain, the Component based Fuzzy c-Means (CFCM) outperforms the traditional Fuzzy c-Means (FCM) in terms of the measurement accuracy of the cognitive load.

M.3.3.5 - EEG Epileptic Seizure Detection using k-Means Clustering and Marginal Spectrum based on Ensemble Empirical Mode Decomposition

Paschalis Bizopoulos, Dimitrios Tsalikakis, Alexandros Tzallas, Dimitrios Koutsouris, Dimitrios Fotiadis

The detection of epileptic seizures is of primary interest for the diagnosis of patients with epilepsy. Epileptic seizure is a phenomenon of rhythmicity discharge for either a focal area or the entire brain and this individual behavior usually lasts from seconds to minutes. The unpredictable and rare occurrences of epileptic seizures make the automated detection of them highly recommended especially in long term EEG recordings. The present work proposes an automated method to detect the epileptic seizures by using an unsupervised method based on k-means clustering end Ensemble Empirical Decomposition (EEMD). EEG segments are obtained from a publicly available dataset and are classified in two categories “seizure” and “non-seizure”. Using EEMD the Marginal Spectrum (MS) of each one of the EEG segments is calculated. The MS is then divided into equal intervals and the averages of these intervals are used as input features for k-Means clustering. The evaluation results are very promising indicating overall accuracy 98% and are comparable with other related studies. An advantage of this method is that no training data are used due to the unsupervised nature of k-Means clustering.

M.3.3.6 - Synchronization coupling investigation using ICA cluster analysis in resting MEG signals in Reading Difficulties

Marios Antonakakis, Giorgos Giannakakis, Manolis Tsiknakis, Sifis Micheloyannis, Michalis Zervakis

The understanding of the mechanisms of human brain is a demanding issue for neuroscience research. Physiological studies acknowledge the usefulness of synchronization coupling in the study of dysfunctions associated with reading difficulties. Magnetoencephalogram (MEG) is a useful tool towards this direction having been assessed for its superior accuracy over other modalities. In this paper we consider synchronization features for identifying brain operations. Independent Component Analysis (ICA) is applied on MEG surface signals in controls and children with reading difficulties and are clustered to representative components. Then, coupling measures of mutual information and partial directed coherence are estimated in order to reveal dysfunction of cerebral networks and its related coordination.

Session M.4.1 – Imperial 1 room: 15:00-16:30

Bio-Imaging

Chair: *Dimitris Maroulis*

M.4.1.1 - EEG Identification of a localized 1-D neuronal excitation

George Dassios, Konstantia Satrazemi

Albaneze and Monk have demonstrated that it is impossible to identify the three-dimensional support of any primary current living within a conducting medium, from electromagnetic measurements outside the conductor. However, this is not true if the primary current is supported in a subset of dimensionality less than three. In the present report, we demonstrate the truth of this statement by constructing an analytic algorithm that identifies the location, the orientation, and the size of a localized linear distribution of current dipoles within the brain, from a complete knowledge of the electric potential recorded by an electroencephalographer on the surface of the head.

M.4.1.2 - Analysis of errors and bounds in Electroencephalography

George Dassios, Michael Doschoris, Fotini Kariotou, Vasiliki Christina Panagiotopoulou

Electroencephalography (EEG) measures potential differences on part of the surface of the head. These measurements are directly connected with activated regions within the brain, modeled as dipoles, and are accurately interpreted if originating from a average ellipsoidal conductor with semi-axes 5.5, 6.5 and 8.5 cm. However, the volume of modern human brains varies significantly depending on sex and age. These variations in volume could introduce a source of error affecting the location of the dipole if not incorporated in existing models. In what follows, an error estimation is established for EEG readings in the case where the average ellipsoidal brain is replaced by an ellipsoid with different volume.

M.4.1.3 - The Influence of Surface Deformations on EEG Recordings

George Dassios, Michael Doschoris, George Fragoyannis

The precise identification of neuronal currents via Electroencephalographic (EEG) recordings is an important aspect in clinical practice and strongly depends on the accuracy of the corresponding forward problem. In addition, the precision of the EEG forward model is closely connected to the existence of a volume conductor model as realistic as possible. In this paper, the impact of geometric variations of the head on the measured electric potential has been studied by means of a homogeneous spherical conductor. In the case where the activated region is situated in the vicinity of the deformation, the calculated potential values show a slight increase. On the other hand, for neuronal currents away from the deformation no influence upon the surface electric measurements is observed.

M.4.1.4 - 2D-GE Spot Detection Combining Multidirectional Texture and Spatial Intensity Cues

Eleni Zacharia, Eirini Kostopoulou, Dimitris Maroulis, Nicholas P. Anagnou, Kalliopi I. Pappa

Spot detection is a challenging task of 2D Gel Electrophoresis image analysis. The available software packages and techniques miss some of the protein spots while they detect a high number of spurious spots. This paper introduces a novel approach for the detection of protein spots on 2D gel images which is based on multidirectional texture and spatial intensity information. The proposed approach is compared with two commercial software packages using real 2D-GE images. The outcome demonstrates that the proposed approach outperforms the two software packages; it detects almost all of real protein spots and a low number of spurious spots.

M.4.1.5 - Local focus-tolerant image descriptors for classification of biological particles

Nefeli Vassiliki Politi-Stergiou, Ilias Theodorakopoulos, George Economou

In this work we present a new approach to the extraction of features robust to focal mismatches, for the classification of biological particles characterized by 3 dimensional structures. We use SIFT descriptors in order to encode local gradient, fused with features derived from an introduced adaptive filterbank of Gabor filters. We have evaluated the proposed technique using a dataset consisting of 174 images of pollen grains from 29 species, acquired with a low-cost optical microscope in arbitrary focal planes. The proposed descriptor efficiently captures discriminative information by encoding the local inner and outer structure of the transparent pollens in a focus-tolerant manner, achieving approximately 74.5% classification accuracy, demonstrating that local scale invariant features can be robust even under challenging conditions.

M.4.1.6 - Improving Image Quality in Dual Energy CT by Edge-Enhancing Diffusion Denoising

Andreas Petropoulos, Georgios Vlachopoulos, Spyros Skiadopoulos, Anna Karahaliou, Lena Costaridou

The aim of this study is to investigate the effect of edge-enhancing diffusion (EED) denoising on the quality of dual energy CT images, derived by varying the weighting of the two spectra (0.1 to 0.9, 0.1 step). The quality of EED denoised weighted images was quantitatively assessed by means of SNR, contrast and CNR measured on ROIs of phantom images corresponding to 14 mg/ml iodine concentration and bone equivalent. The performance of the EED denoising technique was further compared to the performance of median filtering. EED improves significantly the quality of weighted images.

Session M.4.2 – Imperial 2 room: 15:00-16:30

Special Session #5 - Advanced Concepts in Endoscopic Imaging and Engineering

Chair: *Dimitris K. Iakovidis, Anastasios Koulaouzidis*

M.4.2.1 - Towards a Multimodal Wireless Video Capsule for the Early Detection of Cancerous Polyps

Olivier Romain, Aymeric Histace, Juan Silva, Jad Ayoub, Bertrand Granado

Wireless capsule endoscopy (WCE) is commonly used for noninvasive gastrointestinal tract evaluation, including the identification of polyps. In this paper, a new multimodal embeddable method for polyp detection and classification in wireless capsule endoscopic images was developed and tested. The multimodal wireless capsule used both 2D and 3D data to identify possible polyps and to deliver cancerous information of the polyps based on 3D geometric features. Possible polyps within the image (2D) were extracted using simple geometric shape features and, in a second step, the candidate regions of interest (ROI) were evaluated with a boosting-based method using textural features. Once the 2D identification of polyps has been performed, the two-class (“malignant” or “begnin”) classification of the polyps is achieved using the 3D parameters computed from the preselected ROI using an active stereo vision system. At this stage, a Support Vector Machine (SVM) classifier is used to proceed to the final classification and to make possible a pre diagnosis. The new proposed multimodal approach based on 2D - 3D feature extraction improves WCE capabilities to identify and classify polyps: The boosting-based polyp classification demonstrated a sensitivity of 91%, a specificity of 95% and a false detection rate of 4.8% on a database composed of 300 hundred positive examples and 1200 negative ones; Considering the 3D performance, a large scale demonstrator was evaluated and tested to perform in vitro experiments on an ad hoc polyp database. The performance of the 3D approach achieved a correct classification rate (malignant or bening) of approximately 95%.

M.4.2.2 - Capsule Endoscope Localization based on Visual Features

Dimitris Iakovidis, Evaggelos Spyrou, Dimitris Diamantis, Ilias Tsiompanidis

Computational analysis of wireless capsule endoscopy (WCE) videos has already proved its potentials in the discovery or characterization of lesions and in the reduction of the time required by the endoscopists to perform the examination. An open problem that has only partially been addressed is the localization of the capsule endoscope in the gastrointestinal (GI) tract. Previous works have been based mainly on external, wearable, sensors. In this paper we propose a novel approach based solely on visual information extracted from WCE videos. This approach is based on a feature tracking method for visual odometry, which enables the estimation of both the rotation and the displacement of a capsule endoscope from reference anatomical landmarks. Its implementation is based on a novel, open access Java Video Analysis (JVA) framework, which enables quick and standardized development of intelligent video analysis applications. The experimental evaluation presented in this paper, indicates the feasibility of the proposed methodological approach and the efficiency of its implementation.

M.4.2.3 - Efficient Homography-Based Video Visualization for Wireless Capsule Endoscopy

Dimitris Iakovidis, Evaggelos Spyrou, Dimitris Diamantis

Wireless capsule endoscopy (WCE) is performed by a swallowable pill capsule equipped with a camera wirelessly transmitting color video frames to an external receiver. The resulting video consists usually of several thousands of frames and its visual examination requires hours of endoscopists’ undivided attention. In this paper we propose a novel visualization approach for WCE which enables faster examination of the endoscopic video, while providing a broader field of view. This is achieved by an algorithm that iteratively samples clusters of consecutive frames from the original video. The frames of each cluster are geometrically transformed, so as to generate a seamless collage subsequently projected into a new frame without any information loss. The new frames compose a new WCE video with a smaller number of frames. The video frame collage is based on homography matrix estimation from frame correspondences. The experiments show that the length of the WCE video, and therefore the reading times required can be significantly reduced.

M.4.2.4 - Operation of Ingestible Antennas along the Gastrointestinal Tract: Detuning and Performance

Konstantinos Psathas, Anastasis Keliris, Asimina Kiourti, Konstantina Nikita

In this study, we numerically assess detuning issues for an ingestible antenna which is designed to operate in the Medical Device Radiocommunications Service (MedRadio, 401–406 MHz), as it travels along the gastrointestinal (GI) tract. For this purpose, we evaluate the antenna resonance performance within four canonical single-tissue models of the human esophagus, stomach, small and large intestine. The antenna is further placed at different locations within the aforementioned tissue models in order to assess detuning issues related to its relative positioning within each of them. Inherent detuning issues are observed and discussed in the four different simplified tissue models considering three specific locations of the antenna in each model, resulting in twelve different scenarios. The resonance, radiation and safety performance of the ingestible antenna is, finally, evaluated.

M.4.2.5 - A Comparison of Color Correction Algorithms for Endoscopic Cameras

Ioannis Constantinou, Marios Neofytou, Vasilis Tanos, Marios Pattichis, Christodoulos Christodoulou, Constantinos Pattichis

Quantitative color tissue analysis in endoscopy examinations requires color standardization procedures to be applied, so as to enable compatibility among computer aided diagnosis application from different endoscopy labs. The objective of this study was to examine the usefulness of different color correction algorithms (thus facilitating color standardization), evaluated on four different endoscopy cameras. The following five color correction algorithms were investigated: two gamma correction based algorithms (the classical and a modified one), and three (2nd, 3rd, and 4th order) polynomial based correction algorithms. The above algorithms were applied to four different endoscopy cameras: (a) Circon, (b) Karl-Stortz, (c) Olympus, and (d) Snowden-Pencer. The color correction algorithms and the endoscopic cameras evaluation, was carried out using the testing color palette (24 colors of known digital values) provided by the Edmund Industrial Optics Company. In summary, we have that: (a) the modified gamma correction algorithm gave significantly smaller mean square error compared to the other four algorithms, and (b) the smallest mean square error was obtained for the Circon camera. Future work will focus on evaluating the proposed color correction algorithm in different endoscopy clinics and compare their tissue characterization results.

Session M.4.3 – Imperial 3 room: 15:00-16:30

Engineering Models in Bio-Medicine

Chair: *Carmelina Ruggiero*

M.4.3.1 - The Effects of Synthetic Azurocidin Peptide Analogue on Staphylococcus Aureus Bacterium

Jie Hu, Pantea Peidaee, Eltaher Elshagmani, Taghrid Istivan, Elena Pirogova

Antibiotics are commonly used as anti-infection drugs. However, the rising of microbial resistance to antibiotics imposes a major challenge to their widespread applications. Hence, there is a growing need to find alternative drugs to eradicate the microbial resistance arising from the excessive use of antibiotics. Antimicrobial peptides (AMPs) are natural defence molecules found in human body. These AMP are present virtually in all life forms where they act as the first line defence agents against invading pathogens. Published studies [1] [2] suggest the possible use of AMPs as alternative anti-infective drugs. In this study we evaluated the anti-microbial activity of a synthetic Azurocidin peptide analogue and compared its efficacy with the native natural antimicrobial peptide Azurocidin. The Resonant Recognition Model (RRM) was employed here to computationally design a short Azurocidin peptide analogue, Azu-RRM. According to the RRM, this de novo designed peptide analogue will mimic and exhibit the activity of the natural Azurocidin (Azu) protein. Within this study the antimicrobial activity of Azu-RRM was investigated on Staphylococcus aureus (ATCC 25923) bacterium. The results obtained reveal that the synthetic peptide analogue affected the growth of this gram positive bacterium. The findings also showed that the Azu-RRM is exhibiting the antimicrobial effects on the growth of the studied bacteria comparable with the suppressing effects induced by the natural Azu protein.

M.4.3.2 - Identification the Shape of Biconcave Red Blood Cells Using Histogram of Oriented Gradients and Covariance Features

George Apostolopoulos, Stefanos Tsinopoulos, Evaggelos Dermatas

In this paper, a novel methodology for estimating the shape of human biconcave Red Blood Cells (RBCs), using color scattering images, is presented. The information retrieval process includes, image normalization, features extraction using both Histogram of Oriented Gradients (HoG) and region covariance features (RCoV); and features dimensionality reduction using the Independent Component Analysis (ICA). The points of interest (PoIs) are detected using the Harris corner detector in order to extract the image features. A scheme using adjustable algorithms, i.e. support vectors machine (SVM) is adopted in order to fuse the multimodal features. A Radial Basis Function Neural Network (RBF-NN) estimates the RBC geometrical properties. The proposed method is evaluated in both regression and identification tasks by processing images of a simulated device used to acquire scattering phenomena of moving RBCs. The evaluation database includes 23625 scattering images, obtained by means of the Boundary Element Method. The regression and identification accuracy of the actual RBC shape is estimated using three feature sets in the presence of additive white Gaussian noise from 60 to 10 dB SNR, giving a mean error rate less than 1 percent of the actual RBC shape, and more than 99 percent mean identification rate in a set of valid RBCs size.

M.4.3.3 - Feasibility Study on Serviced-based Method of Data Acquisition for Human Signal Molecule Profiling Database

Xinyan Zhao, Tao Dong

A service-based model of human signal-molecule-profiling database (HSMPD) was proposed to prompt the data acquisition of medical information from blood tests in traditional healthcare systems and to make the data be naturally converted into Health IT (HIT) services through the translational bioinformatics (TBI) community. A self-motivated mechanism to minimize the project investment was designed. The low-cost tool, called 'SMP chip', was employed in blood tests inside hospitals, which results will be decoded and stored in HSMPD automatically. Successively, the HIT services derived from HSMPD will provide a stable income to support the data acquisition processes. To explore the feasibility of the model, a small-scale survey study was performed in a common Chinese hospital. The positive results indicated that the cooperation of IT, engineering, healthcare systems and TBI community could provide a self-motivated solution to build the HSMPD platform.

M.4.3.4 - 3D Printing: Basic concepts Mathematics and Technologies

Athanasios Anastasiou, Charalampos Tsirmpas, Alexandros Rompas, Kostas Giokas, Dimitris Koutsouris

3D printing is the process of being able to print any object layer by layer. But if we question this proposition, can we find any three dimensional objects that can't be printed layer by layer? To banish any disbeliefs we walked together through the mathematics that prove 3d printing is feasible for any real life object. 3d printers create three dimensional objects by building them up layer by layer. The current generation of 3d printers typically requires input from a CAD program in the form of an STL file, which defines a shape by a list of triangle vertices. The vast majority of 3d printers use two techniques, FDM (Fused Deposition Modelling) and PBP (Powder Binder Printing). One advanced form of 3d printing that has been an area of increasing scientific interest the recent years is bioprinting. Cell printers utilizing techniques similar to FDM were developed for bioprinting. These printers give us the ability to place cells in positions that mimic their respective positions in organs. Finally through series of case studies we show that 3d printers in medicine have made a massive breakthrough lately.

M.4.3.5 - Polyelectrolyte Multilayer Coatings for Implant Osseointegration

Massimo Giulianelli, Roberta Ferretti, Laura Pastorino, Carmelina Ruggiero

The number of arthroplasties is rapidly increasing, however most materials used for such applications lack in osseointegration. The improvement of the bone/implant interface has received great attention for many years, with special reference to titanium-based implants. The interface between bone and implant has been considered both by physical approaches focused on surface topography and by chemical/biochemical surface modification by incorporation of organic molecules. The work described here is focused on the fabrication of implant coatings by layer by layer self-assembly of Collagen I (COL) and Hyaluronic acid (HA). The multilayer structure has been characterized by SEM and AFM, and the Titanium substrates coated with these multilayers have been tested with 3T3 cells seeded on Titanium supports. The results show that these coatings are promising for the improvement of implant osseointegration. This fabrication method is easily reproducible, versatile and economic.

Session M.5.1 – Imperial 1 room: 19:00-20:30

Drug Discovery

Chair: *Dimitrios Koutsouris*

M.5.1.1 - An Isometry-Invariant Spectral Approach for Protein-Protein Docking

Dela De Youngster, Eric Paquet, Herna Lydia Viktor, Emil Petriu

The protein docking problem refers to the task of predicting the appropriate matching of one protein molecule (the receptor) to another (the ligand), when attempting to bind them to form a stable complex. Research shows that matching the three-dimensional geometric structures of proteins plays a key role in determining a so-called docking pair. However, the active sites which are responsible for the binding do not always present a rigid-body shape matching problem. Rather, they may undergo deformation when docking occurs, which complicates the process. To address this issue, we present an isometry-invariant and topologically robust partial shape descriptor method for finding complementary protein sites. Our method employs Heat Kernel Signature shape descriptors which are based on the diffusion of heat on surfaces. Our experimental results against the Protein-Protein Benchmark 4.0, demonstrate the viability of our approach.

M.5.1.2 - Drug Screening with Elastic-Net Multiple Kernel Learning

Kitsuchart Pasupa, Zakria Hussain, John Shawe-Taylor, Peter Willett

We apply Elastic-net Multiple Kernel Learning (MKL) to the MDL Drug Data Report (MDDR) database for the problem of drug screening. We show that combining a set of kernels constructed from fingerprint descriptors, can significantly improve the accuracy of prediction, against a Support Vector Machine trained on each kernel separately. To the best of our knowledge, this is the first application of MKL to the MDDR database for drug screening.

M.5.1.3 - A Fast Point Pattern Matching Algorithm for Robust Spatially Addressable Bead Encoding

Abhik Datta, Adams Wai-Kin Kong, Soumita Ghosh, Dieter Trau

Bead encoding is a key problem central to all bead based microarrays. Recently a spatially addressable bead encoding technique has been developed ([1], [2]) that alleviates the need for costly hardware while still allowing high-throughput analysis. This paper proposes a pattern matching based scheme that extends this bead encoding technique's usability to uncontrolled environments. A novel affine invariant point pattern matching algorithm is developed to achieve this. The proposed algorithm uses local features to overcome the combinatorial explosion problem encountered in matching corrupted point patterns. The use of efficient data structures is emphasized to make the algorithm fast and scalable. The proposed scheme can decode bead identities in assays involving thousands of beads in a few seconds. Evaluation results using both real and simulated data are presented.

M.5.1.4 - Implementation of Reversible Multiplier Circuit Using Deoxyribonucleic Acid

Ankur Sarker, Mohd. Istiaq Sharif, Tanvir Ahmed, Md. Atiqur Rahman, S. M. Mahbubur Rashid, Hafiz Md. Hasan Babu

In this paper, we realize the reversible multiplier circuit using Deoxyribonucleic Acid (DNA). Due to reversible logic's emerging characteristics, it has drawn great attention in recent years. As multiplication operation consists of several shift and addition operations, we use shifter and adder circuits as building blocks to construct multiplication circuit. We also present an algorithm for depicting overall procedures of multiplication operation using an example. The proposed circuit is faster, required less space and power due to parallelism, replication properties, compactness and formation of DNA strands, respectively. Additionally, the run time complexity of our proposed system is O(m) instead of O(m(ln2n)2) in existing DNA-based system where m and n are the bit length of multiplier and multiplicand. Also, proposed system needs u+3.2n DNA signals while the existing system needs u.2n where u is the extra tag.

Session M.5.2 – Imperial 2 room: 19:00-20:30

Algorithms, Modeling and Simulation of Bio-Sets

Chair: *Dimitrios Fotiadis*

M.5.2.1 - Biologically Inspired Near Extinct System Reconstruction

Athanasios Bibas, George Spanoudakis, Christos Bellos, Dimitrios Fotiadis, Dimitrios Koutsouris

Recovery software system operations from a state of extensive damage without human intervention is a challenging problem as it may need to be based on a different infrastructure from the one that the system was originally designed for and deployed on (i.e., computational and communication devices) and significant reorganization of system functionalities. In this paper, we introduce a bio-inspired approach for reconstructing nearly extinct complex software systems. Our approach is based on encoding a computational DNA (co-DNA) of a system and computational analogues of biological processes to enable the transmission of co-DNA over computational devices and, through it, the transformation of these devices into system cells that can realise chunks of the system functionality, and spread further its reconstruction process.

M.5.2.2 - A Discrete Optimization Approach for SVD Best Truncation Choice based on ROC Curves

Davide Chicco, Marco Masseroli

Truncated Singular Value Decomposition (SVD) has always been a key algorithm in modern machine learning. Scientists and researchers use this applied mathematics method in many fields. Despite a long history and prevalence, the issue of how to choose the best truncation level still remains an open challenge. In this paper, we describe a new algorithm, akin a the discrete optimization method, that relies on the Receiver Operating Characteristics (ROC) Areas Under the Curve (AUCs) computation. We explore a concrete application of the algorithm to a bioinformatics problem, i.e. the prediction of biomolecular annotations. We applied the algorithm to nine different datasets and the obtained results demostrate the effectiveness of our technique.

M.5.2.3 - Studying the correlation between the extracellular environment geometry and the diffusion processes

Pantelis Ampatzoglou, Maria Hadjinicolaou

The tumor behavior is understood as a complex dynamical system encountering many different scales. Following the principles of Jiang et.al, we also employ a multiscale model, where the environment of a tumor, at the extracellular level is described by reaction diffusion, while at the cellular level an agent based model is applied. We further extend this model by employing a health function, which describes at every time step the health state of any tumor cell. This health function takes into account the biological and biochemical micro environment. A stochastic function is applied to model the mitosis process of proliferating tumor cells.

M.5.2.4 - Identification and correction of substitution errors in Moleculo long reads

Jared Price, Judson Ward, Joshua Udall, Quinn Snell, Mark Clement

Moleculo DNA sequencing technology provides extremely accurate, phased, reads having an average length of over 4,000 bp. Very little is yet known about the precise characteristics of these reads. We estimate a lower bound for the single nucleotide substitution error rate of these reads, and provide probabilities for each type of substitution. We also present preliminary work on the development of an error correction algorithm for these reads which in its current implementation corrects 74,030 single nucleotide errors in a Moleculo data set obtained from Rubus idaeus 'Heritage'. We also demonstrate that the pattern of substitution errors shows no significant bias with respect to the position of an error along the body of a read.

M.5.2.5 - Short-term vs. Long-term Analysis of Diabetes Data: Application of Machine Learning and Data Mining Techniques

Eleni Georga, Vasilios Protopappas, Stavroula Mougiakakou, Dimitrios Fotiadis

Chronic care of diabetes comes with large amounts of data concerning the self- and clinical management of the disease. In this paper, we propose to treat that information from two different perspectives. Firstly, a predictive model of short-term glucose homeostasis relying on machine learning is presented with the aim of preventing hypoglycemic events and prolonged hyperglycemia on a daily basis. Second, data mining approaches are proposed as a tool for explaining and predicting the long-term glucose control and the incidence of diabetic complications.

Session M.5.3– Imperial 3 room: 19:00-20:30

Bio-Imaging

Chair: *George Spyrou*

M.5.3.1 - Segmentation of Enhanced Depth Imaging Optical Coherence Tomography Images Using Wavelet Based Graph Cut Algorithm

Hajar Danesh, Raheleh Kafieh, Hossein Rabbani

Limited numbers of non-invasive imaging techniques are available for assessing the choroid, a structure that may be affected by a variety of retinal disorders or become primarily involved in conditions such as polypoidal choroidal vasculopathy and choroidal tumors. The introduction of enhanced depth imaging optical coherence tomography (EDI-OCT) has provided the advantage of in vivo cross-sectional imaging of the choroid, similar to the retina, with standard commercially available spectral domain OCT machines. A texture-based algorithm is introduced in this paper for fully automatic segmentation of choroidal images obtained from a 1060 nm optical coherence tomography (OCT) system. Dynamic programming is utilized to determine the location of the retinal pigment epithelium (RPE). The Bruch's membrane (BM) is the blood-retina barrier that separates the RPE cells of the retina from the choroid and can be segmented by searching for the pixels with the biggest gradient value below the RPE. A novel method is proposed to segment the choroid–sclera interface (CSI), which employs the wavelet based features to construct a Gaussian mixture model (GMM). The model is then used in a s-t cut graph for segmentation of the choroidal boundary. The proposed algorithm is compared with the manual segmentation and the results show an unsigned error of 1.71±0.91 pixels for BM extraction and 7.65±3.96 pixels for choroid detection.

M.5.3.2 - A Level Set Based Method for Lung Segmentation in CT Images

Shiva Azimi, Hossein Rabbani

In this paper an automatic computer-aided (CAD) method is utilized for lung segmentation using computed tomography (CT) images. We segmented lung regions - based on the CT data- with nodules attached to the chest wall by using level set modeling. This method is made up of 3 steps: In the first step, an adaptive fuzzy thresholding operation is used to binarize the CT images; in the second step, the lung with non-isolated nodules is segmented applying both level set modeling and convex hull algorithm. In the third step, by using the shape features of lung lobe, the lung is segmented. The experimental results show an accuracy of 98% by our method with out performance other exiting methods.

M.5.3.3 - The Use of Real-Time MRI Techniques for Imaging an Extended Field of View in Magnetic Resonance Angiography

Stephen Riederer, Casey Johnson, Paul Weavers

Accurate, fast, sensitive, and safe imaging of the cardiovascular system has major societal benefits owing to the high prevalence of cardiovascular disease. This is particularly challenging in imaging the peripheral vasculature, defined as extending from the renal artery origins to the ankles, because of the long (>120 cm) superior-inferior (S/I) field of view. Contrast-enhanced MR angiography provides major advantages compared to other imaging methods because it uses no ionizing radiation, provides 3D images, and requires only a relatively benign intravenous injection of contrast material. However, such imaging has major technical challenges in that the speed of passage of the contrast-enhanced blood through the vasculature is highly variable from patient to patient and the potentially rapid enhancement of veins can interfere with the radiological interpretation of disease in the companion arteries. The purpose of this work is to describe MRI physics and engineering methods designed to rapidly acquire high spatial resolution images of the peripheral vasculature at individual table positions or "stations," and then to integrate these methods with real-time signal processing to allow interactive control of the MRI patient table, allowing it to advance in synchrony with the advancing contrast on a patient-specific basis. Results are presented with single station techniques to illustrate the potential image performance as well as in the more demanding and desired multi-station application in which the time available for data acquisition is limited at each station.

M.5.3.4 - Modeling of Solitary Pulmonary Nodules in PET/CT images using Monte Carlo Methods

George Tzanoukos, Anastasios Gaitanis Alexandros Georgakopoulos, Achilleas Chatziioannou, Sofia Chatziioannou, George Spyrou

The assessment of solitary pulmonary nodules (SPN) is a very difficult task in PET imaging due to adjacent normal structures. Physicians and computational systems as well, would gain benefit if trained to a large number of SPN cases with controlled topological and morphological characteristics. Our objective was to develop a method for the modeling of the solitary pulmonary nodules in CT and PET images. The modeling of SPN was implemented by Monte Carlo methods taking into consideration morphological characteristics, internal features and Standardized Uptake Value (SUV) activity distribution. For the validation of the model, an observer study from three independent medical experts was performed. The reviewers characterized the lesions as simulated or real and finally they classified them as benign or malignant. According to the results of the human observer study a significant percentage of simulated images could not be differentiated from real ones and the simulated class (benign or malignant) was consistent with the observers' classification.

M.5.3.5 - Comparison of EIT Reconstruction Techniques Applied to IMPETOM

Eduardo Santos, Franco Simini

Electrical Impedance Tomography (EIT) reconstruction can estimate thorax fluid content. Its use in critically ill patients is promising and may prove clinically useful. Boundary voltages (16-electrode frames) were obtained with our 50 kHz-5 mA IMPETOM system. Comparison of the 492-element Newton-Raphson algorithm with EIDORS open source tool (NOSER & GREIT algorithms), applied to a healthy volunteer, suggests that anatomically adjusted 3D models give better results. Nevertheless for phantom imaging an initial uniform image yields more accurate reconstructions.

M.5.3.6 - Evaluation of Modified Median Root Prior on a myocardium study, using realistic PET/MR data

Konstantinos Karaoglanis, Anastasios Gaitanis, Charalampos Tsoumpas

One way of treating the partial volume effect in PET image reconstruction is by using anatomical information from other imaging modalities (MRI or CT). The a priori information of a maximum a posteriori reconstruction algorithm is defined from the anatomical images. In this paper the ordered subsets modified median root prior one step late (OS-MMRP-OSL) algorithm [1], which uses information derived from MR images, is evaluated in a computationally simulated PET FDG myocardium study. The algorithm was implemented in STIR (Software for Tomographic Image Reconstruction) [2], (http://stir.sourceforge.net). Realistic PET data have been used, to compare the standard ordered subsets median root prior one step late (OS-MRP-OSL) algorithm with the OS-MMRP-OSL algorithm using well-aligned segmented and non-segmented MR images. The quantitative results indicate lower bias for OS-MMRP-OSL using segmented MR images and decreased root mean square error (RMSE) in some cases. Moreover, we have improvement in edge preservation.

Session T.1.1 – Imperial 1 room: 08:30-10:00

Special Session #1 - Risk Analysis and Prediction in Cardiovascular Applications

Co-Chairs: *Renata Guarneri, Claudio Silvestro*

T.1.1.1 - The RT3S Project – An Introduction

Gabriele Dubini, Maria Renata Guarneri, Gordon Clapworthy, Nassos Katsaounis, Patricia Lawford, Euripides Petrakis, Michel Rochette, Claudio Silvestro, Debora Testi

RT3S is an EU-funded project in an area of ehealth – ICT for Patient Safety. Specifically, RT3S is developing a patient-centred, probabilistic model for peripheral stent fatigue-fracture, integrated within a real-time, computeraided surgery planning application. RT3S will provide advice on fracture risk for individual combinations of patient anatomy and stent design. Alongside the pre-operational software tool, which is addressed mainly to interventional radiologists, RT3S has also developed a training application that will be of benefit to trainee vascular interventionists and engineers in medical device companies. This paper provides an overview of the work performed during nearly three years of project activities and also addresses the motivation leading to RT3S and the expected impact.

T.1.1.2 - Real Time Prediction of the Fatigue Behavior of Peripheral Stents

Francesco Migliavacca, Michel Rochette, Florent Petiot, Christelle Biochon, Elena Dordoni, Gabriele Dubini, Giancarlo Pennati, Lorenza Petrini

Fatigue resistance of Nitinol peripheral stents implanted into atheroscelorotic femoro-popliteal arteries is a critical issue due to the particular biomechanical environment of this district. Hip and knee joint movements associated with patient' daily activities expose the superficial femoral artery, and therefore the implanted stents, to large and cyclic deformations. These loadings may cause fatigue fracture of stents and may lead to re-occlusion of the artery (in-stent restenosis). In this paper we present a numerical/experimental approach aiming to compare the fatigue performance of different stents taking into account patient-specific factors in real time (i.e. during the planning of the endovascular intervention).

T.1.1.3 - Reconstruction method of a stented coronary bifurcation model for fluid dynamic numerical analyses from optical coherence tomography images

Claudio Chiastra, Eros Montin, Francesco Burzotta, Luca Mainardi, Francesco Migliavacca

The presence of stents within coronary arteries alters the hemodynamic condition. Computational fluid dynamics (CFD) simulations offer the possibility to study local hemodynamics of a stented artery to identify the stimuli of in-stent restenosis, i.e. the local reduction of lumen size after stent deployment. The results of CFD simulations are more accurate when the analyses are performed with a model reproducing real in vivo conditions. For this purpose, optical coherence tomography (OCT) is a promising tool to reconstruct 3D geometries of stented coronary arteries, due to its higher resolution compared to the other imaging techniques. In the present work a reconstruction method of stented coronary bifurcation geometrical models starting from OCT images was developed. An OCT exam performed in a stented coronary bifurcation silicone sample was considered. The vessel and the stent were reconstructed separately, and then they were merged together. Vessel reconstruction was performed with a semi-automatic process: the main branch was reconstructed by fitting the lumen boundary with ellipses and subsequently by creating a mesh of the vessel; the side branch was created like an ideal cylinder. Stent struts were identified with an automatic algorithm; then, the stent was reconstructed in a manual way. After the creation of the 3D geometry of the bifurcation, a transient fluid dynamic simulation was carried out. CFD results showed that the highest risk of restenosis is located in the region near the bifurcation.

T.1.1.4 - AimaSimul: a software tool to plan stent positioning in peripheral arteries and evaluate the associated fatigue fracture risk

Debora Testi, Nigel J. B. McFarlane, Hui Wei, Youbing Zhao, Gordon J. Clapworthy, Desmond M. Ryan, Patricia Lawford

Vascular stent deployment in peripheral arteries is a medical intervention in which a wire mesh tube is inserted into the artery to provide internal support. However, stents positioned in locations such as the femoral artery are subject to cyclic bending, and are therefore at risk of fatigue fracture. A software tool chain, called AimaSimul, is being implemented to support stent modeling, surgical simulation and risk calculation for surgical planning. In particular, the AimaSimul pre-operative planning tool allows clinicians, starting from patient-specific medical images, to interactively assess different stent models and deployment options for the risk of breakage. This paper describes the main functionalities of AimaSimul and, in particular, the stent deployment and deformation.

T.1.1.5 - Crafting Vascular Medicine Training Scenarios: The RT3S Authoring Tool

Evanthia Tripoliti, Ioannis Pappas, Euripides Petrakis, Josep Maria Sans

The RT3S E-learning environment enables experts in vascular medicine to prepare educational training content for their trainees (i.e., future endovascular surgeons). Influenced by the Learning Design (LD) information model and building-upon LAMS, the learning process is realized by means of training scenarios (i.e., as an interactive sequence of learning steps). In RT3S, creating learning scenarios does not require that the editors of the scenarios are familiar with the underlying LAMS environment. The RT3S authoring environment is easy to use and customized (i.e., it can be adapted to the needs of the tutor and of the scenario) and enables tutors (e.g., expert surgeons) to easily prepare new educational content. Students (future surgeons) are trained on the assessment of real (and realistic) patient data and on decision-making processes for the management and treatment of patients.

T.1.1.6 - Application of Decisional Models to the Health-Economic Assessment of New Interactive Clinical Software

Claudio Silvestro, Jonathan Michaels, Spiridoula Dimou, Evanthia Tripoliti, Euripides Petrakis

RT3S (Real Time Simulations for Safer vascular Stenting) is a partially EU-funded research project aiming to develop a software tool for supporting physicians during the preplanning of endovascular stenting procedures. The project is expected to improve the way limb-saving, minimally-invasive stenting procedures are currently performed, with positive clinical and economic impact. A hypothetical cohort of patients was modeled and used to simulate the patient's progression through the treatment of Peripheral Artery Disease (PAD). A Markov health state-based model was implemented based on clinical and economic parameters derived from the literature and clinicians' feedback. The health-economic analysis allowed quantitative estimation of the economic and clinical advantages related to the implementation of the clinical software. A quantitative estimation of the potential health-economic impact was achieved. The model proved to accord well with observed predictions from endovascular experts in the field. It represents an important reference for future assessment of IT-related innovations in the healthcare sector.

Session T.1.2 – Imperial 2 room: 08:30-10:00

Gene Expression Analysis & Bioinformatics Engineering

Chair: *Michalis Zervakis*

T.1.2.1 - A Generic Framework for the Elicitation of Stable and Reliable Gene Expression Signatures

Nick Chlis, Stelios Sfakianakis, Ekaterini Bei, Michalis Zervakis

In the recent years microarray technologies have gained a lot of popularity for their ability to quickly measure the expression of thousands of genes and provide valuable information for linking complex diseases such as cancer to their genetic underpinnings. Nevertheless the large number of parameters to be estimated in relation to the small number of available samples gives rise to an "ill posed" problem where the possible solution is not stable under slight changes either in the dataset or the initial conditions and starting points. In this work we present a generic classification framework that works in an iterative manner and converges to a stable solution that combines good accuracy with biologically meaningful feature selection. The methodology is orthogonal to the specific classification algorithm used. We compare some of the most widely used classifiers based on their average discrimination power and the size of the derived gene signature. According to our proposed model named Stable Bootstrap Validation (SBV), a unified '77 common-gene signature' was selected, which is closely associated with several aspects of breast tumorigenesis and progression, as well as patient-specific molecular and clinical characteristics.

T.1.2.2 -QLZCClust: Quaternary Lempel-Ziv Complexity based Clustering of the RNA-seq Read Block Segments

Ashis Kumer Biswas, Jean X. Gao

The Next Generation Sequencing platform, RNA-seq provides quantitative expression data that exhibit distinctive sequence patterns in the segments of the short-reads level and are found useful in clustering of those segments. However, the result does not reflect the functional chemistry of the non-coding RNAs (ncRNAs). The functions of the ncRNAs are deeply related to their secondary structures. Thus by exploring the clustering in terms of structural profiles of the read block segments rather than their sequence patterns would be essential and useful. We proposed the QLZCClust (Quaternary Lempel-Ziv complexity based Clustering) method which is an extension to the popular Lempel-Ziv algorithm to compute pairwise secondary structure distance. We applied QLZCClust on the short-read segments obtained from the RNA-seq experient and found that it can separate most miRNAs and the tRNAs. Moreover, it can be used to detect structural similarities among different classes of ncRNAs. We compared our algorithm with the clustering of two other structural distance measures -- SimTree edit distance and RNAz based distance, and found that our method performs superior.

T.1.2.3 - Reconstructing Phylogenetic Network with ReTF algorithm (Rearranging Transcriptional Factor)

Shamita Malik, Dolly Sharma

The term Phylogentics is the study of evolutionary relationship between different species, organisms or genes. These relationships are depicted as branched, tree like diagrams that provides insight into the events that occurred during the evolution process. These trees may also have a root which known as the common ancestor. Building the "Tree of Life" had been the objective of many researchers; until it was proved that the tree of life cannot be represented by a tree. Many evolutionary events cannot be shown with the help of a simple tree. Thus, phylogenetic networks came into the picture. Phylogenetic networks can be classified into different categories. In this paper, an algorithm (ReTF) has been proposed which would improve the results of the current phylogenetic networks reconstruction algorithms. The idea behind ReTF is rearranging input sequences in a way that the new arrangement gives a better tree; since the order of input sequences affects the phylogenetic network.

T.1.2.4 - Inference of a robust diagnostic signature in the case of Melanoma: Gene Selection by Information Gain and Gene Ontology Tree Exploration

Ioannis Valavanis, Konstantinos Moutselos, Ilias Maglogiannis, Aristotelis Chatziioannou

Integrated datasets originating from multi-modal data can be used towards the identification of causal biological actions that through a systems level process trigger the development of a disease. We use, here, an integrated dataset related to cutaneous melanoma that comes from two separate sets (microarray and imaging) and the application of data imputation methods. Our goal is to select a subset of genes that comprise candidate biomarkers and compare these to imaging features, that characterize disease at a macroscopic level. Using information gain ratio measurements and exploration of Gene Ontology (GO) tree, we identified a set of 33 genes both highly correlated to the disease status and with a central role in regulatory mechanisms. Selected genes were used to train various classifiers that could generalize well when discriminating malignant from benign melanoma samples. Results showed that classifiers performed better when selected genes were used as input, rather than imaging features selected by information gain measurements. Thus, genes in the backstage of low-level biological processes showed to carry higher information content than the macroscopic imaging features.

T.1.2.5 - Feature Identification and Reduction for Improved Generalization Accuracy in Secondary-Structure Prediction

Seeley Matt, Mark Clement, Quinn Snell

Secondary structure prediction is an important step in understanding gene function. Several algorithms have been proposed for applying machine learning techniques to this problem. This research examines these algorithms and constructs a framework that is effective in providing accurate predictions.

Session T.1.3 – Imperial 3 room: 08:30-10:00

Sequence Search and Alignment & Systems Biology

Chair: *Aristotelis Chatziioannou*

T.1.3.1 - Some Results on Topological Colored Motifs in Metabolic Networks

Elói Araújo, Marco Aurélio Stefanes

In this work, we address the topological colored motif search problem in metabolic networks. This problem is a concern in biology, which seeks to describe the functions and the evolution of metabolism. Recently, several variations of this problem have been studied. Here, we present some hardness results for finding motifs. Furthermore, we describe the first polynomial algorithm for the case in which the motif is a colorful tree. We also detail a data structure that allows finding all of these types of motifs in a metabolic network.

T.1.3.2 - Prediction of Enzymatic Activity of Proteins Based on Structural and Functional Domains

Theodoros Koutsandreas, Eleftherios Pilalis, Aristotelis Chatziioannou

The prediction of the putative enzymatic function of uncharacterized proteins is a major problem in the field of metagenomic research, where large amounts of sequences can be rapidly determined. In this work a machine-learning approach was developed, that attempts the prediction of enzymatic activity based on three protein domain databases, PFAM, CATH and SCOP, which contain functional and structural information of proteins as Hidden Markov Models. Separate and combined classifiers were trained by well-annotated data and their performance was assessed in order to compare the predictive power of different attribute sets corresponding to the three protein domain databases. All classifiers performed well, with an average accuracy of ~96% and an average AUC score of 0.84. As a conclusion, the classification procedure can be integrated to more extended metagenomic analysis workflows.

T.1.3.3 - Fast search of locally repetitive elements based on auto-correlation property in genome

Kyung-Seop Shin, Byung-Chang Chung, Woo-Chan Kim, Dong-Ho Cho

Since the beginning of a human genome project, 12 years have passed. There are many studies regarding the meaning of human genome sequences and the effort to identify the whole genome of other species. Although genes significantly affect phenotype, the importance of other factors has been increased. In this paper, we propose an autocorrelation based method to arrange the repetitive elements which demonstrate a major part of the genomic sequences. The search for the entire genome based on a simple mathematical analysis will be given. The performance of our proposed self autocorrelation based method will be compared with that of conventional scheme for the human chromosome sequence. Fast scanning of the genome sequence based on our proposed scheme can give a clue to analyze the complex function of the genomic sequences.

T.1.3.4 - A Comparison of Community Identication Algorithms for Regulatory Network Motifs

Douglas Oliveira, Marco Carvalho

In the recent years high throughput data about biological processes has become available and thus opened a wide range of possibilities of research in multi-disciplinary areas, like network science. An idea that has been widely accepted is the fact that no life can exist without complex systems formed by interacting macromolecules. Rather than a single gene being responsible for a single phenotype (central dogma), it has been shown that the interaction between several genes is responsible for a given phenotype, a concept called System Biology. Identifying patterns of interactions (motifs) in these complex networks has attracted the attention in the scientific community, given that these networks are often very dense and dynamic. In this work we focus in a particular kind of biological network, a regulatory network where each node is a transcription factor and two nodes are connected if one of them encodes a transcription factor to another one that is regulated by this transcription factor. We focus in a specific kind of motif, a dense overlapping region (DOR) that claims that a set of genes regulated by different transcription factor are more overlapping than expected at a random network. We use different community identification algorithms in order to identify which algorithm best suits to the identification of this particular motif.

T.1.3.5 - A Synthetic Biology Approach to the Realization of Embedded Feedback Controllers for Chemical Reaction Networks

Carlo Cosentino, Mariaconcetta Bilotta, Alessio Merola, Francesco Amato

Chemical Reaction Network (CRN) models based on the mass-action law play an important role in the life sciences, since they can be used to describe dynamical processes of interest in many fields of chemistry and biology. A fundamental challenge related to this kind of systems, is currently represented by the lack, within the framework of Systems and Synthetic Biology, of a general methodology to design control systems for CRNs. The main issue addressed by this work is the development of a technique for designing \emph{embedded} feedback control schemes for an assigned CRN, i.e. controllers that are themselves realizable through a CRN. In particular, we illustrate a general methodology to design and realize a proportional feedback controller assembled from suitable CRNs. The problem is tackled by assembling and interconnecting in a suitable way two subsystems, in the form of CRNs, which implement the subtraction and amplification blocks of a classical feedback control scheme. The effectiveness of the proposed approach is tested by applying it to control a well-known biochemical system.

Session T.1.4 – Imperial room: 08:30-10:00

Biomedical Image Processing, Analysis and Visualization

Chair: *Ilias Maglogiannis*

T.1.4.1 - Segmentation and Recognition of Multi-Food Meal Images for Carbohydrate Counting

Marios Anthimopoulos, Joachim Dehais, Peter Diem, Stavroula Mougiakakou

In this paper, we propose novel methodologies for the automatic segmentation and recognition of multi-food images. The proposed methods implement the first modules of a carbohydrate counting and insulin advisory system for type 1 diabetic patients. Initially the plate is segmented using pyramidal mean-shift filtering and a region growing algorithm. Then each of the resulted segments is described by both color and texture features and classified by a support vector machine into one of six different major food classes. Finally, a modified version of the Huang and Dom evaluation index was proposed, addressing the particular needs of the food segmentation problem. The experimental results prove the effectiveness of the proposed method achieving a segmentation accuracy of 88.5% and recognition rate equal to 87%.

T.1.4.2 - Human Segmentation and Pose Recognition in Fish-eye Video for Assistive Environments

Kostas Delibasis, Theodosios Goudas, Vassilios Plagianakos, Ilias Maglogiannis

In this work, we present a system, which uses computer vision techniques for human silhouette segmentation from video in indoor environments and a parametric 3D human model, in order to recognize the posture of the monitored person. The video data are acquired indoors from a fixed fish-eye camera in the living environment. The implemented 3D human model collaborates with a fish-eye camera model, allowing the calculation of the real human position in the 3D-space and consequently recognizing the posture of the monitored person. The paper discusses briefly the details of the human segmentation, the camera modeling and the posture recognition methodology. Initial results are also presented for a small number of video sequences.

T.1.4.3 - HEp-2 Cells Classification Using Locally Aggregated Features Mapped in the Dissimilarity Space

Dimitrios Kastaniotis, Ilias Theodorakopoulos, George Economou, Spiros Fotopoulos

Indirect Immunofluorescence (IIF) followed by manual evaluation of the acquired slides from specialized personnel is the preferred laboratory technique used for the detection of Antinucleolar Antibodies (ANAs) in patient serum. In this procedure, several limitations appear and thus several automatic techniques have been proposed for the task of ANA detection. In this paper we propose a system for automatic classification of HEp-2 staining patterns, inspired by a recently proposed method for aggregating local image (SIFT) features into a compact and fixed length representation. More specifically we present a novel framework in which aggregated features are mapped into feature vectors in the dissimilarity space where the dimensionality of the descriptors is “naturally reduced”. The final descriptor is low dimensional, while evaluation on a recently published dataset yields state of the art results.

T.1.4.4 - A Scheme for X-ray Medical Image Denoising using Sparse Representations

Evmorfia Adamidi, Evangelos Vlachos, Aris Dermitzakis, Kostas Berberidis, Nicolas Pallikarakis

This paper addresses the problem of noise removal in X-ray medical images. A novel scheme for image denoising is proposed, by leveraging recent advances in sparse and redundant representations. The noisy X-ray image is decomposed, with respect to an overcomplete dictionary which is either fixed or trained on the noisy image, and it is reconstructed using greedy techniques. The new scheme has been tested with both artificial and real X-ray images and it turns out that it may offer superior denoising results as compared to other existing methods.

T.1.4.5 - A Comparison of Ultrasound Intima Media Thickness Measurements of the Left and Right Common Carotid Artery

Christos Loizou, Constantinos Pattichis, Niki Georghiou, Maura Griffin, Andrew Nicolaides

The intima–media thickness (IMT) of the common carotid artery (CCA) is an established indicator of cardiovascular disease (CVD). There have been reports about the difference between the left and the right sides of the CCA IMT and its importance when evaluated with various risk factors as well as their association with the risk of stroke. In this study, we use an automated system based on snakes, for segmenting the CCA and perform measurements of the IMT of the carotid artery and provide their differences between the left and right sides. The study was performed on 205 longitudinal-section ultrasound images acquired from 87 men and 118 women at a mean±SD age of 63±10.47 years, out of which 51 had cardiovascular symptoms. A cardiovascular expert manually measured the IMT on the left CCA side (mean±standard deviation = 0.79±0.21 mm) and the right CCA side (0.76±0.33 mm). The left and right IMT automated measurements were 0.70±0.15 mm and 0.66±0.15 mm, respectively. We found no statistical significant differences: 1) between the left and right IMT measurements, for both the manual and automated measurements, and 2) between the manual and automated measurements for both sides. These findings suggest that the measurement of the CCA IMT on one side only is enough (and this is in agreement with other studies), as well as automated measurements can be used.

T.1.4.6 - Image registration of follow-up examinations in digital dermoscopy

Christos Nikolaos E. Anagnostopoulos, Dimitrios Vergados, Panagiotis Mintzias

Automated assessment tools for dermoscopy images play an important assistive role mainly due to inter- and intra-observer variations in human interpretation. Prior to classification, a robust registration module is necessary. In this paper we propose a fully automatic method for successful registration (matching) of melanocytic nevi images acquired from digital dermoscope to ensure reliable quantitative comparison of the image later. A modified SIFT algorithm (called ROI-SIFT), followed by RANSAC to identify outliers, is used to localize and match correspondence interest points, that will be used to compute affine transformations for the registration of a dermatological image with the respective follow-up examination image. Experimental evaluations of the registration method are reported for image pairs acquired during follow-up examinations. Finally, a short discussion of scheduled future work is proposed.

Session T.2.1 – Imperial 1 room: 11:00-12:30

Special Session #4 - The Digital Patient concept: Vision and Early Demonstrations

Co-Chairs: *Feng Dong, Manolis Tsiknakis*

T.2.1.1- "Digital Patients and their impact on Healthcare"

Roderick Tooher

T.2.1.2 - Exploitation of patient avatars towards stratified medicine through the development of in silico clinical trials approaches

Marios Spanakis, Efrosini Papadaki, Apostolos Karantanas, Thomas G. Maris, Dimitris Kafetzopoulos, Vaggelis Sakkalis, Konstantinos Marias

The generation of “virtual twins” of patients (Avatars) through integration of multiscale data gained from both the clinical profile of the patient and –omics tools, could create an appropriate environment for stratification of patients in fitting cohorts of “virtual populations”. Physiologically based pharmacokinetic & pharmacodynamic (PB/PK/PD) models as in silico clinical trial tools can estimate the PK/PD profiles in specific populations. In this work we discuss examples of how patient Avatars could be exploited in the context of in silico clinical trials and help in identifying novel biomarkers for personalized diagnosis. The PB/PK/PD models, neuroimaging and –omics data, may be fused together to further advance current decision making processes in clinical practice.

T.2.1.3 - Designing a digital patient avatar in the context of the MyHealthAvatar project initiative

Evaggelia Maniadi, Haridimos Kondylakis, Emmanouil G. Spanakis, Marios Spanakis, Manolis Tsiknakis, Kostas Marias, Feng Dong

The digital avatar is a vision for the digital representation of personal health status in body centric views. It is designed as an integrated facility that allows collection of, access to and sharing to life-long and consistent data. A number of Virtual Physiological Human (VPH) communities have started the movement to this direction by creating a digital patient road-map and by supporting data sharing infrastructures. As an innovative concept, the impact of digital patient and avatar to personalized medicine and treatment is yet to be clear. This requires a focused and concerted effort in addressing various questions regarding user perspective, use cases and scenarios. This paper presents use cases and future scenarios realizing the vision for the digital avatar as well as architectural consideration for the envisaged platform.

T.2.1.4 - A Virtual Individual's Model Based on Facial Expression Analysis: a Non-Intrusive Approach for Wellbeing Monitoring and Self-Management

Franco Chiarugi, Eirini Christinaki, Sara Colantonio, Giuseppe Coppini, Paolo Marraccini, Matthew Pediaditis, Ovidio Salvetti, Manolis Tsiknakis

Facial expressions are visible signs of the affective and psychological state of a person which is strictly correlated with the pathogenesis of clinically relevant diseases and more in general with an individual's wellbeing. The main idea highlighted in this paper is the exploitation of the facial expression analysis for wellbeing monitoring and self-management. This will occur by an innovative multisensory device that will be able to collect images and signals, extract quantitative features of facial expression related to stress, anxiety and fatigue and map them to computational descriptors of an individual's wellbeing. The latter phase will be based on a virtual individual's model conceived to allow the computation and tracing of the daily evolution of an individual's wellness. Personalized advices and coaching messages will support the user in keeping a healthy lifestyle and counteract potentially harmful behaviours. The work is part of the FP7 STREP SEMEOTICONS project whose application field will be the prevention of cardio-metabolic risk, for which healthcare systems are registering an exponential growth of social costs.

T.2.1.5 - A Scalable Data Repository for Recording Self-Managed Longitudinal Health Data of Digital Patients

Xia Zhao, Youbing Zhao, Nikolaos Ersotelos, Dina Fan, Enjie Liu, Gordon Clapworthy, Feng Dong

This paper presents the proof-of-concept design of the data repository for 4D digital avatars in the EU MyHealthAvatar project. Taking account of the privacy and legal issues of patient health information, the research generates a set of synthetic data based on the public available survey data. At the prototype stage, these synthetic data are used in the scenarios of data storage and management. The paper discusses the early proof-of-concept design of the technical stack which enables the storage and query of large scale patients' health data and empowers the future data mining and analysis for health care support. It provides the first stage implementation and the use of it for data analytics.

T.2.1.6 - A Cross-platform Approach for Treatment of Amblyopia

Hui Wei, Youbing Zhao, George Saleh, Feng Dong, Gordon Clapworthy, Xujiong Ye

In this paper, we introduced a binocular way of diagnose and treatment for amblyopia through a game form , which is popular around children who aged 3 to 7. Our method is more emphasis on cooperation between two eyes, to achieve a good binocular outcome, further on recovery depth perception. Our method is not limited on a particular device or plat-form, and even not limited on a form of game. We have developed several prototype games including 2D games and 3D games. We introduced our work in following aspect: Recent works in this area, the medicine principle, the requirement of treatment, how to design 2D and 3D games in this purpose.

Session T.2.2 – Imperial 2 room: 11:00-12:30

Identification and Classification of Genes

Chair: *Michalis Zervakis*

T.2.2.1 - Candidate Biomarkers for Response to Tamoxifen in Breast Cancer metastatic patients

Claudia Cava, Gloria Bertoli, Italo Zoppis, Giancarlo Mauri, Maria Carla Gilardi, Isabella Castiglioni

Tamoxifen is currently used for the treatment of breast cancer. Response to tamoxifen in metastatic conditions is a primary issue in cancer development. To find insight on the genetic mechanism of metastasis development, and looking for possible therapeutic effect of tamoxifen in metastatic conditions, we used a cohort of breast cancer patients, treated or not with tamoxifen, and combined these data with the gene signature of metastatic samples. The analysis revealed a group of 21 genes common both to the set of up regulated genes in metastatic BC patients and to the set of down regulated genes in tamoxifen treated patients. These genes could be used as biomarkers for tamoxifen-sensitivity in order to optimize BC treatment.

T.2.2.2 - Automated Selection of Differentially Methylated Regions in Microarray Data

Pavlos Antoniou, Spiros Michalakopoulos, Elisavet Papageorgiou, Philippos Patsalis, Carolina Sismani

Differentially methylated regions (DMRs) are segments or islands of consecutive sequence positions, showing methylation enrichment or depletion compared to each other in different samples or tissues. The identification of DMRs is a crucial first step in the discovery of biomarkers for non-invasive prenatal diagnosis of aneuploidies such as Trisomy 21. In this paper we describe an algorithm to automatically identify the manifestation of DMRs on arrays. Our approach, methylation status mask AND (MS-AND), influenced by the SHIFT-AND methodology, uses bit operations and masking and can be applied to any microarray dataset in General Feature Format (GFF). We show the effectiveness and utilization of our algorithm using data from Methylated DNA Immunoprecipitation arrays for the identification of DMRs in chromosomes 13, 18 and 21. The algorithm runs on Linux and on Windows systems and an implementation is available at sourceforge (http://sourceforge.net/projects/ms-and).

T.2.2.3 - Towards an Integrated Framework for Clinico-Biological Data Management and Analysis: the Case of Chronic Lymphocytic Leukemia

Evangelia Minga, Athanasios Gkoufas, Anna Vardi, Evangelia Stalika, Anastasia Hadzidimitriou, Kostas Stamatopoulos, Nicos Maglaveras, Ioanna Chouvarda

This paper addresses the challenges of gathering, analyzing and employing clinically meaningful biological information, for the advancement of translational medicine. In this respect we propose an approach for the integrated management and analysis of large quantities of clinico-biological data, including high-throughput sequencing data. The proposed concepts are applied in the case of Chronic Lymphocytic Leukemia, a paradigmatic age-related hematologic cancer, and the steps for data integration and information analysis are illustrated via the CLL-BIND framework.

T.2.2.4 - Identifying Gender Independent Biomarkers Responsible for Human Muscle Aging Using Microarray Data

Emmanouil Sifakis, Ioannis Valavanis, Olga Papadodima, Aristotelis Chatziioannou

The scope of this study is the identification of gender-independent muscle transcriptional differences between younger and older subjects using skeletal muscle gene expression profiles. Towards this end, a combination of statistical methods, functional analyses, and machine learning techniques were exploited, and applied on an integrative dataset of publicly available microarray data obtained from healthy males and females. Through the proposed framework, a set of 46 reliable genes was identified that comprise a candidate gender-independent aging signature in human skeletal muscle. The identification was based on differential expression, information gain content, and significance regarding their central regulatory role in the underlying active molecular networks in the GO. The resulted gene subset was also tested for its generalization potency regarding the classification task, through the use of a series of classifiers, and results show that high classification accuracies could be obtained. Therefore, the selected genes comprise a promising group of biomarkers of ageing in human skeletal muscle to be evaluated in future studies.

T.2.2.5 - Hierarchical Multi-Label Gene Function Prediction using Adaptive Mutation in Crowding Niching

Mina Moradi Kordmahalleh, Abdollah Homaifar, Dukka KC

Computational prediction of protein function is an important field in functional genomics. Gene function prediction is a Hierarchical Multi Label Classification (HMC) problem where each gene can belong to more than one functional class simultaneously, while classes are structured in the form of hierarchy. HMC is becoming a necessity in many domains of applications as well. Crowding niching-Adaptive mutation (CAM) is a new proposed method for solving Hierarchical multi-label gene function prediction problem. The classification in CAM-HMC is structured in three different phases. In the first two phases, a sequential procedure is performed. In the first phase, a full cyclic evolutionary crowding algorithm based on new definition of distance between two individuals, and adaptive mutation is applied in order to find classification rules. In the second phase, all the examples that are covered by these rules are removed from the training data. This sequential procedure is repeated until most of the training examples are covered by CAM-HMC rules. In the third phase, consequent generation is determined to show the probability of coverage of each rule for each hierarchical class. Finally, this ratio is applied to classify testing data. Efficiency of this algorithm is displayed by comparing this algorithm with HMC-GA using Precision-Recall curves for three numerical datasets related to protein functions of the Saccharomyces Cerevisiae organism.

Session T.2.3 – Imperial 3 room: 11:00-12:30

Biological Systems and Models

Chair: *Konstantina Nikita*

T.2.3.1 - A Model-Based Retrospective Analysis of the Fixed-Ratio Oscillometric Blood Pressure Measurement

Rein Raamat, Kersti Jagomagi, Jaak Talts, Jana Kivastik

Noninvasive systolic and diastolic blood pressures (Psyst and Pdiast, respectively) are often measured by applying the fixed-ratio oscillometric method, which determines blood pressures using empirically estimated fractions of the oscillometric amplitude envelope. These fractions are known as characteristic ratios (ksyst and kdiast, respectively). A review of studies over a more than 20-years time course shows a noticeable variation of characteristic ratios estimated by different researchers. We compared the literature-based data with data obtained by modeling of the fixed-ratio oscillometric measurement. The results suggest that if the between-study variation of characteristic ratios is described as a change in the difference kdiast - ksyst, then the observed variation can be explained by differences in the symmetry of the arterial wall pressure/volume relationship of the studied groups, and also by differences in cuff handling. In contrast, if a parallel shift of kdiast and ksyst up or down exists, this refers to the different pulse pressure and/or different steepness of the pressure/volume relationship of the studied groups.

T.2.3.2 - Accelerated MR Physics Simulations on multi-GPU systems

Christos Xanthis, Ioannis Venetis, Anthony Aletras

A multi-GPU approach of MRISIMUL, a recently developed step-by-step comprehensive MR physics simulator of the Bloch equation, is presented in this study. The specific aim was to apply MRISIMUL on multi-GPU systems so as to achieve even shorter execution times. We hypothesized that such a simulation platform could achieve a scalable performance with the increasing number of available GPU cards on single node, multi-GPU computer systems. A parallelization strategy was employed using the MATLAB single-program-multiple-data (spmd) statement and an almost linear speedup was observed with the increasing number of available GPU cards on two separate systems: a single computer of 2 quad-core processors and two Tesla C2070 GPU cards and a single computer of 2 hexa-core processors and four Tesla C2075 GPU cards.

T.2.3.3- A Lumped Parameter Model for the Analysis of the Motion of the Muscles of the Lower Limbs under Whole-Body Vibration

Francesco Amato, Paolo Bifulco, Mario Cesarelli, Domenico Colacino, Carlo Cosentino, Antonio Fratini, Alessio Merola, Maria Romano

Through a lumped parameter modelling approach, a dynamical model, which can reproduce the motion of the muscles of a human body standing in different postures during Whole Body Vibrations (WBVs) treatment, has been developed. The key parameters, associated to the dynamics of the motion of the muscles of the lower limbs, have been identified starting from accelerometer measurements. The developed model can be usefully applied to the optimization of WBVs treatments which can effectively enhance muscle activation.

T.2.3.4 - A Mathematical Model for Secondary Structure in Proteins

Alexey Nikolaev, Saad Mneimneh

We propose a new mathematical model for secondary structure in proteins. Our model is inspired by percolation theory on binary strings. What sets us apart from similar work on the subject is our attempt to deviate from a data mining approach (which is mostly the trend is science these days). Therefore, in predicting secondary structures, we make it our challenge to adhere to sequence information alone, in a non ad-hoc way, with only minimal information extracted from databases of known structures. Initial results show that our model captures some essential aspects of structure formation, notably a de novo discovery of hydrophobicity from an optimization perspective. A comparison of our prediction algorithm to similar methods shows improved performance. In addition, some evolutionary algorithms using our model exhibit convergences that are consistent with information obtained from structural biology.

T.2.3.5 - Support vector-based fuzzy system for the prediction of mouse class I MHC peptide binding affinity

Volkan Uslan, Huseyin Seker

The performance of predictive models is crucial in order to accurately determine peptide binding affinity for major histocompatibility complex (MHC) alleles. Data sets extracted to model the relationship between the peptides and their binding affinities are often high-dimensional, complex and non-linear, which require highly sophisticated computational predictive models. Support Vector Machine (SVM)-based predictive methods have been used for this predictive problem, which have been shown to deal with such high dimensional data, however failed to take into account of uncertainty that naturally exists in this type of data. In order to address to the uncertainty issue, Fuzzy System (FS) has generally been utilised in various applications. Therefore, a hybrid method that combines FS and SVM is proposed in this study for the prediction of binding affinity of peptides in mouse class I MHC alleles. The hybrid system is successfully applied to two benchmark data sets of class I MHC peptides, each of which contains over 5000 peptide features. The assessments yield as much as 17% improvement over the previous studies that also include SVM-based experiments. The results also suggest positive impact of the concept of fuzziness on SVM-based predictive methods when combined and that the hybrid model can be generalised for similar non-linear system modelling problems.

T.2.3.6 - A bioinformatics approach for investigating the determinants of Drosha processing

Nestoras Karathanasis, Ioannis Tsamardinos, Panayiota Poirazi

We use a bioinformatics approach to search for the biological features that determine the cleavage site of the Microprocessor complex (or Drosha) within known miRNA hairpins. Towards this goal, we employ a previously developed methodology, termed DuplexSVM, which can accurately identify the four ends of a miRNA:miRNA* duplex. Here we use DuplexSVM to study how the Drosha determines its cleavage site. We perform in silico mutagenesis experiments on 142 hairpins by changing the distance of the Drosha site from the loop tip or the stem – single stranded tails junction by adding or removing matching nucleotides. Our results suggest that the Drosha cleavage site is mainly determined by its distance from the terminal loop tip.

Session T.3.1 – Imperial 1 room: 14:00-15:30

Biomedical Image Processing, Analysis and Visualization

Chair: *Huseyin Seker*

T.3.1.1 - Gradient cumulative filtering to detect MRI thermometry artifacts

Juha Kortelainen, Juha Koikkalainen, Julius Koskela, Gösta Ehnholm

Magnetic resonance imaging (MRI) thermometry is applied for guiding thermal therapy of tumorous tissues using high-intensity focused ultrasound (HIFU). Fast imaging sequences are needed for the on-line MRI operation, and strong artifacts on the temperature map can be found especially for image regions having poor signal-to-noise (S/N) ratio. Detection and masking of the regions with unreliable temperature measurement would be important to avoid unnecessary notification of the HIFU operator or even cancelation of the sonication procedure. This paper presents a specific image processing procedure to improve detection of typical MRI thermometry artifacts. First a region for well behaving temperature map is selected. Then, the remaining region of distorted temperature surface is processed with a novel method using oriented filter on the surface gradient. The result gives a more stable surface over the artifact regions, which can be used further to improve consistency in detection and masking of the temperature errors. Evaluation data is from N=7 patients having thermal therapy for uterine fibroid, including about 300 different sonications and 30,000 MRI thermometry images. The results show that the suggested method decreases variance of the temperature difference between consequent image frames in comparison with a conventional method using 2D phase unwrapping.

T.3.1.2 - Resting state and task related fMRI in small cell lung cancer patients

Konstantinos Bromis, Irene Karanasiou, George Matsopoulos, Errikos Ventouras, Nikolaos Uzunoglu, Georgios Mitsis, Eustratios Karavasilis, Matilda Papathanasiou, Nikolaos Kelekis, Vasileios Kouloulias

Prophylactic cranial irradiation (PCI) is a standard treatment technique for small cell lung cancer patients. However, there is evidence that this technique may contribute to neurocognitive deficits. Therefore the study of anatomical and functional connectivity in patients undergoing PCI as well as their neurocognitive functionality, depending on the type of disease and the phase of treatment and time of clinical examination, is of considerable interest. In this context, we investigate whether there are any differentiations in brain function during resting state and task-related functional magnetic resonance imaging (fMRI) in patients with cancer before PCI compared to healthy subjects. During a finger tapping task, the brain regions that were activated bilaterally for both groups are consistent with previous studies. During rest, the Default Mode Network (DMN) was identified in both groups. The preliminary results presented herein are subject to further investigation with larger patient and control group.

T.3.1.3 - Variations on breast density and subtlety of the findings require different computational intelligence pipelines for the diagnosis of clustered microcalcifications

Ioannis Andreadis, George Spyrou, Panos Ligomenides, Konstantina Nikita

Computer Aided Diagnosis (CADx) systems for mammography have been introduced in order to interpret in an objective way the mammographic findings and assist the radiologists in the diagnostic process. The purpose of our work is to study the factors that influence the efficacy of a proposed CADx framework for the diagnosis of clustered microcalcifications (MCs). We worked on two main axes. Firstly, we applied the CADx framework in a large dataset of mammograms containing cases of varying breast density and findings' subtlety. The reported results indicate that the proposed framework performs towards the right direction as it appears high classification performance for specific subsets of cases, while outperforming at the same time the performance of the radiologists who evaluated the same cases. In a second step, we investigated the effect of the initial enhancement of mammograms in the CADx pipeline. We applied three different image enhancement techniques in order to investigate whether the pre-enhancement of images may provide better classification results. We observed that for cases of dense mammograms, the wavelet-based enhancement algorithm outperformed the rest and provided superior classification performance.

T.3.1.4 - Generation of clustered microcalcifications' atlases for benign and malignant cases

Ioannis Andreadis, George Spyrou, Panos Ligomenides, Konstantina Nikita

Breast microcalcifications are one of the most important mammographic findings related to the existence of the breast cancer. Radiologists usually characterize microcalcifications based on their morphologies, the distribution within the cluster they form, the shape of the cluster and its relative location inside the breast. In this study, we focus on the latter factor and we study its effect on the probability of malignancy. The main purpose of our study is to generate probabilistic breast cancer atlases for clusters of microcalcifications in order to visualize the influence of cluster location on cancer probability. We propose a framework for the generation of such atlases, including segmentation of important breast landmarks and projection of different clusters of microcalcifications on a reference breast shape. The generation of the atlases is implemented using mammograms from the Digital Database of Screening Mammography. The obtained probabilistic atlases reveal specific areas in the breast of higher occurrence of clusters and higher risk of malignancy.

T.3.1.5 - Performance Evaluation of Clustering Algorithms on Microcalcifications as Mammography Findings

Emmanouil Ikonomakis, George Spyrou, Panos Ligomenides, Michael Vrahatis

Breast cancer can be prevented with regular mammography screening. Yet, the incorporation of Computational Intelligence relies on training classifiers on a set of predefined Regions of Interest (ROIs). Data Clustering has been applied to address the problem of ROI detection, yet no extensive research has been carried out on which algorithm to utilize. This contribution focuses on microcalcification clustering as a Data Clustering application, giving insights concerning the performance of three main clustering algorithms.

T.3.1.6 - Investigation of AM-FM Methods for Mammographic Breast Density Classification

Styliani Petroudi, Ioannis Constantinou, Chryso Tziakouri, Marios Pattichis, Constantinos Pattichis

Breasts are composed of a mixture of fibrous and glandular tissue as well as adipose tissue and breast density describes the prevalence of fibroglandular tissue as it appears on a mammogram. Over the past few years, evaluation and reporting of breast density as it appears on mammograms has received a lot of attention because it impacts one's risk of developing breast cancer but also the capability of detecting breast cancer on mammograms. In addition, mammography fails in the identification of breast cancer in almost half of the women with dense breasts. Different image analysis methods have been investigated for automatic breast density classification. The presented method investigates the use of Amplitude-Modulation Frequency-Modulation (AM-FM) multi-scale feature sets for characterization of breast density as the first step in the development of a density specific Computer Aided Detection System. AM-FM decompositions use different scales and bandpass filters to extract the instantaneous frequencies (IF), instantaneous amplitude (IA) and instantaneous phase (IP) components from an image. Normalized histograms of the maximum IA across all frequencies and scales are used to model the different breast density classes. Classification of a new mammogram into one of the breast density classes is achieved using the k-nearest neighbor method with k =5 and the euclidean distance metric. The method is evaluated on the Medical Image Analysis Society (MIAS) mammographic database and the results are presented. The presented method allows breast density classification accuracy reaching over 84%. Future work will involve a new AM-FM methodology approach based on adaptive filterbank design and performance index decision.

Session T.3.2 – Imperial 2 room: 14:00-15:30

Functional Genomics, Proteomics

Co-Chairs: *Costas Papaloukas, Dimitrios Vergados*

T.3.2.1 - Impacts of the Different Spline Orders on the B-spline Association Estimator

Zeyneb Kurt, Nizamedin Aydin, Gökmen Altay

Gene Network Inference (GNI) algorithms enable searching the interactions among the several cell molecules. Many application fields such as computational biology and pharmacology utilize the

GNI algorithms to illustrate the interaction networks of the cell molecules. Association score estimation is the most crucial step of the GNI applications. B-spline is a popular approach, which efficiently estimates the interaction scores between the variable (gene) pairs. In this study inference performance of the B-spline estimator according to the selected spline order is examined. In addition to evaluating B-spline performance according to the spline order, influences of using a frequently used pre-processing operation Copula Transform on the performance of B-spline is also examined. Conservative Causal Core network (C3NET) GNI algorithm is used in the experiments. At the overall analysis, B-spline estimator with the spline order 2 gave the best inference performance among the selected spline orders from 1 to 10.

T.3.2.2 - Identification of signaling pathways related to drug efficacy in hepatocellular carcinoma via integration of phosphoproteomic, genomic and clinical data

Ioannis N Melas, Douglas A Lauffenburger, Leonidas G Alexopoulos

Hepatocellular Carcinoma (HCC) is one of the leading causes of death worldwide, with only a handful of treatments effective in unresectable HCC. Most of the clinical trials for HCC using new generation interventions (drug- targeted therapies) have poor efficacy whereas just a few of them show some promising clinical outcomes [1]. This is amongst the first studies where the mode of action of some of the compounds extensively used in clinical trials is interrogated on the phosphoproteomic level, in an attempt to build predictive models for clinical efficacy. Signaling data are combined with previously published gene expression and clinical data within a consistent framework that identifies drug effects on the phosphoproteomic level and translates them to the gene expression level. The interrogated drugs are then correlated with genes differentially expressed in normal versus tumor tissue, and genes predictive of patient survival. Although the number of clinical trial results considered is small, our approach shows potential for discerning signaling activities that may help predict drug efficacy for HCC.

T.3.2.3 - Novel Biomarkers Discovery for HBV and HCV Monitoring Through Protein Interaction Networks Analysis

Thomas Simos, Costas Papaloukas, George Thyphronitis, Urania Georgopoulou

According to the World Health Organization hepatitis is a global threat to public health. Various statistics reveal that hundreds of millions of people worldwide are infected by chronic hepatitis C (HCV), which accounts for only the 15% of viral hepatitis. Hepatitis B (HBV) is the second chronic type of the virus with even larger numbers that reach up to 350 million carriers. Several research efforts have been focused recently on the underlying mechanisms of the infection and particularly on the assessment of gene/protein expressions. The utilization of protein interaction networks (PINs) is expected to identify novel aspects of the disease concerning both the patients' immune response and preventive treatment regimens. Here we designed several PINs for HCV and HBV and employed topological, modular and functional analysis techniques in order to determine significant network nodes that correspond to prominent candidate biomarkers.

T.3.2.4 - Toll-like Receptor Structural Determinants: Variability Analysis by Digital Signal Processing Methods

Norbert Maggi, Patrizio Arrigo, Carmelina Ruggiero

The design of new drugs delivery systems is strongly dependent on the capability to maximize biocompatibility and reduce immunotoxicity. The minimization of foreign body reactions is one of the critical step, and toll-like receptors play a pivotal role in sensing and activation of response against exogenous elements. The complexity of these molecules brings about the need to identify those local structural elements that preferentially interact with different classes of compounds. We have applied Digital Signal Processing (DSP) methods to identify the regions containing these structural elements. DSP analysis has been carried out on 'wild-type' and several allelic forms of Toll-like receptor 1 cDNA. DSP has enabled the screening of allele specific nucleotide domains that could have an effect on allele-specific response against exogenous compounds.

T.3.2.5 - HRelief: A new algorithm relief hybrid for biological motifs selection

Faouzi Mhamdi, Hanen Mhamdi

Feature selection plays a crucial role in the automatic learning field, since the non relevant and /or redundant ones can influence the strength of discrimination of a learning algorithm. In fact, select a minimum set of informative and relevant features can increase the performance of algorithms and the precision of prediction, minimize the time of data treatment, facilitates their visualization as well as their analysis. In this paper, we present a series of adaptations of algorithms for the motifs selection of Relief filtering algorithm. In the first two adaptation ways (HRelief1 and HRelief2) we transformed Relief in hybrid algorithms by using a classifier to evaluate the subset of the features generated. The third way of adaptation (HRelief3) helps in treating the problem of redundancy of features. Based on the experimentations done so far, these improvements resulted in an interesting outcome that encourages us to go into the depth of this orientation field.

Session T.3.3 – Imperial 3 room: 14:00-15:30

Data Visualization

Chair: *George Spyrou*

T.3.3.1 - Implementing Patient Recruitment on EURECA Semantic Integration Platform through a Groovy Query Engine

Brecht Claerhout, Kristof De Schepper, David Perez-Rey, Raul Alonso-Calvo, Jasper van Leeuwen, Anca Bucur

A substantial amount of clinical trials are subject to failure because they cannot recruit sufficient patients within the foreseen time and budget. Computer assisted evaluation of eligibility criteria is envisaged to improve the recruitment process by increasing coverage (i.e. making sure no eligible patients are ‘missed’) and speeding up the eligibility scanning process; and thus eventually reduce the overall failure rate of clinical trials. In this paper a new recruitment application is presented which assists in evaluating eligibility criteria based on available clinical patient data (e.g. EHR data). The application leverages for the querying of clinical data on a generic semantic integration platform and a new Domain Specific Language (DSL) based on the Groovy programming language.

T.3.3.2 - A user interface design for a patient oriented digital patient

Nikolaos Ersotelos, Xia Zhao, Youbing Zhao, Enjie Liu, Gordon Clapworthy, Feng Dong

MyHealthAvatar is designed to provide a digital representation of patient health status. It aims to become a 'lifetime companion' for individual citizens that will facilitate the collection of, and access to, long term health-status information. This avatar is not only extremely valuable for clinical decision-making, but it will generate data to support clinical investigation, thereby leading to strengthened multidisciplinary research and excellence in supporting innovative medical care across the population. My Health Avatar platform is currently under development. The purpose of this paper is to present the scope, the provided service and the future plans of the platform as well as a detailed description of the visual representation of the MyHealthAvatar platform.

T.3.3.3 - Weighted Committee-Based Structure Learning for Microarray Data

Hasna Njah, Salma Jamoussi

Bayesian networks (BN) are considered to be one of the strongest modeling techniques in bioinformatics thanks to their ability to present features and relations between them in a causal and probabilistic way. Learning the structure of those models needs a large training dataset in order to avoid over-fitting. However, biological data, especially microarray data, suffer from the presence of only few instances. Some recent approaches tried to face this challenge by applying committee based methods. We use this principle in order to suggest a new method supported by a double-weight-assignment technique. We show that our approach has succeeded to learn benchmark structures.

T.3.3.4 -WebGL-based Interactive Rendering of Whole Body Anatomy for Web-oriented Visualisation of Avatar-centered Digital Health Data

Youbing Zhao, Xia Zhao, Nikolaos Ersotelos, Feng Dong, Enjie Liu, Gordon Clapworthy

Whole body anatomy visualisation has a variety of applications in health related visualisation, simulation and analysis. However, traditionally the rendering of complex 3D human anatomy models, can only be fulfilled by standalone applications, and can hardly be achieved via web interface as rendering 3D models, especially large 3D models, is always the weak spot of traditional web browsers. Consequently online access and exploration of 3D human anatomy is almost not possible. With the advent of WebGL and HTML5, high performance OpenGL rendering seamlessly integrated with the web interface is possible, which unfolds the potential of visualising avatar-centered health data via web interface. In this paper a WebGL-based prototype for rendering of whole body anatomy is introduced and the technical details are presented.

Session T.3.4 – Imperial: 14:00-15:30

Biomedical Data Engineering

Chair: *Panagiotis Bamidis*

T.3.4.1 - Clinical Decision Support Framework for Validation of Multiscale Models and Personalization of Treatment in Oncology

Anca Bucur, Jasper van Leeuwen, Traian Cristian Cirstea, Norbert Graf

The implementation of Clinical Decision Support (CDS) solutions is an important prerequisite for reducing the knowledge gap between clinical research and practice, especially in a complex genetic disease such as cancer. However, current CDS solutions are unable to support all the complex decisions required for personalized treatment of cancer patients and become quickly obsolete due to the high rate of change in therapeutic options and knowledge. Our CDS framework enables the development of decision support tools that flexibly integrate a large variety of multiscale models and can leverage the efforts of a large community of modellers. In our implementation, we combine community-developed models described in the literature (e.g. the St. Gallen stratification for early breast cancer) and models derived by mining the comprehensive datasets from clinical trials and care brought together in the p_Medicine collaborative research project. This framework and its underlying solution for models storage, management and execution will also constitute a platform for continuous validation of existing models on new data. Our goal is to enable the reuse of existing models for CDS and for the development of new models, and to support collaboration among modellers, CDS implementers, biomedical researchers and clinicians. We initially develop and deploy our solution in the context of the p-Medicine project in the oncology domain, but we aim to expand our scope and to reach out to a wide community of users in the biomedical area.

T.3.4.2 - Molecular Clustering via Knowledge Mining from Biomedical Scientific Corpora

Panagiotis Hasapis, Dimitrios Ntalaperas, Christos Kannas, Aristos Aristodimou, Dimitrios Alexandrou, Thanassis Bouras, Athos Antoniades, Christos Georgousopoulos, Constantinos Pattichis, Andreas Constantinou

In this paper, an architecture is presented that allows the extraction of argumentation clauses that might exist in publications, in order to perform molecular clustering on referenced molecules. Grammar rules are defined and used to identify sentences corresponding to argumentation being present in publications. The references of those molecules are then compiled as lists that include their structure definition in SMILES format. These lists are given as input to virtual screening tools and then to a molecular clustering tool, with the ultimate goal to classify molecules that are known to be prone to specific diseases, thus leading to the discovery of new drugs.

T.3.4.3 - Decision Tree Induction to Prediction of Prognosis in Severe Traumatic Brain Injury of Brazilian Patients from Florianopolis City

Merisandra Garcia, Ruano Pereira, Evandro Martins, Fernando Azevedo

The data mining consists in identification of characteristics and relationships between data, aiming the transformation of these into useful knowledge. The obtainment of knowledge occurs trough tasks, methods and algorithms that have specific purposes, and that are applied according to the goals of analysis. The analysis showed in this article consists in application of data mining by task of classification by the method of decision tree induction by the C4.5 algorithm for the prediction of prognosis in severe traumatic brain injury. The traumatic brain injury is a public health problem, constituting in one of the main causes of morbidity and mortality. In the development were performed the steps of preprocessing, the application of data mining and the evaluation of generated model, obtaining the accuracy of 87%.

T.3.4.4 -TeleRehabilitation: a novel service oriented platform to support Tele-Supervised rehabilitation programs for ICU patients

Nikolas Stylianides, Andreas Papadopoulos, Ioannis Constantinou, Loizos Loizou, Marios Dikaiakos, Theodoros Kyprianou

This paper introduces a novel service oriented pilot platform developed to support Tele-Supervised rehabilitation programs for patients after hospitalization in Intensive Care Units. The platform is developed under the framework of the TeleRehabilitation project funded by the Cross Border Cooperation Programme Greece Cyprus 2007 – 2013 in order to successfully meet the main technological and clinical objectives of the project. The design and development of the platform is based on composite service architecture (aggregates smaller and fine-grained services such as Web Based applications, Clinical Information Systems and Video Communication Systems). The platform delivers sustainable, maintainable and high quality services and enables multiparty, interregional bidirectional audio/visual communication between clinical practitioners and post-ICU patients, enables patient group-based vital sign real time monitoring, individualized and group-based patient online training and patients clinical record bookkeeping.

T.3.4.5 - In silico study of mechanical stresses at the cellular level during tissue development

Anne Jeannin-Girardon, Pascal Ballet, Vincent Rodin

Mechanical contraints play a key role in tissue morphogenesis. We propose to study these mechanisms at the cellular level, thanks to our virtual biomechanical cell model. This model defines biological cell behaviors, such as cell motility, mitosis and adhesion as well as methods to evaluate cell compression/stretching and shearing. The evaluation of these constraints allows the virtual cells to respond by changing their color during simulation and lead to the observation of emerging patterns in cell differentiation during tissue growth: the main purpose of this evaluation is to give the cells the ability to respond to mechanical constraints by differentiating. This approach allows studying the influence of mechanotransduction during tissue morphogenesis.

T.3.4.6 - "Meleti" Speech and Language Development Support System

Efthyvoulos Kyriacou, Marina Charalambous, Charalambos Theodorou, Christos Iliophotou, George Hadjichristofi, Maria Ioannou

Through this study we are presenting a system that intent to support and monitor speech and language development of children with hearing impairment using hearing aids and/or cochlear implants, or children with language delays. The scope is to support children during their daily life. The system is mainly based on a set of applications for Android devices. These applications can be used anywhere the child and the parents are, they include several tasks presented to the child as a game. The main goal is to support sessions being done by the caregivers like reproducing words, sounds, small phrases etc. The system was created based on the four levels targeted during speech and language support sessions (auditory skills, receptive language, expressive language, speech / articulation). The results from system usage are being recorded from a server where specialists can monitor get results and act accordingly in order to improve the child's performance. Initial design and development steps have been completed. The two first levels of the system have been tested on a small group of user with very encouraging results. Furthermore the development of several other modules related to the levels of language development will continue in order to cover all language development levels.

Session W.1.1 – Imperial 1 room: 09:00-10:30

Gene Expression Analysis & Bioinformatics Engineering

Co-Chairs: *Aristotelis Chatziioannou, Dimitrios Vergados*

W.1.1.1 - Ensemble learning and hierarchical data representation for microarray classification

by Mattia Bosio, Pau Bellot, Philippe Salembier, Albert Oliveras-Vergés

The microarray data classification is an open and active research field. The development of more accurate algorithms is of great interest and many of the developed techniques can be straightforwardly applied in analyzing different kinds of omics data.In this work, an ensemble learning algorithm is applied within a classification framework from [1] that already got good predictive results. Ensemble techniques take individual experts, (i.e. classifiers), to combine them to improve the individual expert results with a voting scheme. In this case, a thinning algorithm is proposed which starts by using all the available experts and removes them one by one focusing on improving the ensemble vote. Two versions of a state of the art ensemble thinning algorithm have been tested and three key elements have been introduced to work with microarray data: the ensemble cohort definition, the nonexpert notion, which defines a set of excluded expert from the thinning process, and a rule to break ties in the thinning process. Experiments have been done on seven public datasets from the Microarray Quality Control study, MAQC [2]. The proposed key elements have shown to be useful for the prediction performance and the studied ensemble technique shown to improve the state of the art results by producing classifiers with better predictions.

W.1.1.2 - Stability of feature selection algorithms for classification in high-throughput genomics datasets

Panagiotis Moulos, Ioannis Kanaris, Gianluca Bontempi

A major goal of the application of Machine Learning techniques to high-throughput genomics data (e.g. DNA microarrays or RNA-Seq), is the identification of “gene signatures”. These signatures can be used to discriminate among healthy or disease states (e.g. normal vs cancerous tissue) or among different biological mechanisms, at the gene expression level. Thus, the literature is plenty of studies, where numerous feature selection techniques are applied, in an effort to reduce the noise and dimensionality of such datasets. However, little attention is given to the stability of these signatures, in cases where the original dataset is perturbed by adding, removing or simply resampling the original observations. In this article, we are assessing the stability of a set of well characterized public cancer microarray datasets, using five popular feature selection algorithms in the field of high-throughput genomics data analysis.

W.1.1.3 - Frequent Weighted Itemset Mining from Gene Expression Data

Elena Baralis, Luca Cagliero, Tania Cerquitelli, Silvia Chiusano, Paolo Garza

Gene Expression Datasets (GEDs) usually consist of the expression values of thousands of genes within hundreds of samples. Frequent itemset and association rule mining algorithms have been applied to discover significant co-expressions among multiple genes from GEDs. To perform these data analyses, gene expression values are commonly discretized into a predefined number of bins. Such an expert-driven and not trivial preprocessing step could bias the quality of the mining result. This paper presents a novel approach to discovering gene correlations from GEDs which does not require data discretization. By representing per-sample gene expression values as item weights, frequent weighted itemsets can be extracted. The discovery of weighted itemsets instead of traditional (not weighted) ones prevents experts from discretizing GEDs before analyzing them and thus improves the effectiveness of the knowledge discovery process. Experiments performed on real GEDs demonstrate the effectiveness of the proposed approach.

W.1.1.4 - A Kernel SVM Algorithm to Detect Mislabeled Microarrays in Human Cancer Samples

Manuel Martín-Merino

DNA Microarrays have been successfully applied to the identification of different cancer types considering the gene expression profiles. However, previous studies have shown that labeling errors are not uncommon in microarray studies. In this case, the training set may contain mislabelled examples that may lead the classifier to poor performance. In this paper we propose a new filtering algorithm based on one-class SVM classification to detect mislabelled samples. To this aim, samples and labels are mapped together to feature space using the kernel of dissimilarities. Next, outliers are detected via one-class classification. Mislabeled samples and outliers in input space can be separated comparing the outliers obtained in input and feature spaces. The algorithm proposed has been tested using several complex cancer microarray datasets in which some samples are mislabelled according to the literature. The experimental results suggest that our algorithm is effective detecting labeling errors and compares favorably with a standard technique such as simple SVM.

W.1.1.5 - Similarity and Dissimilarity of Whole Genomes using Intuitionistic Fuzzy Logic

Subhram Das, D. K. Bhattacharya

Whole genomes in general and poly-nucleotides, in particular, have an interesting representation in twelve dimensional hypercube I12 based on fuzzy set theory, but it has some limitations and drawbacks. With a view to removing such drawbacks of the representation, the present paper derives some new representation of whole genomes and poly-nucleotides based on Intuitionistic Fuzzy set theory and shows that that such a representation is free from any such limitation as mentioned above. Finally it applies the new representation in testing similarity/ dissimilarities of whole genomes and polynucleotides.

Session W.1.2 – Imperial 2 room: 09:00-10:30

Cardiovascular and Respiratory Systems Engineering

Chair: *Francesco Migliavacca*

W.1.2.1 -Multiscale motion analysis of the carotid artery wall from B-mode ultrasound: investigating the optimal wavelet parameterization

Nikolaos Tsiaparas, Aimilia Gastounioti, Spyretta Golemati, Konstantina Nikita

The incorporation of wavelet-based multiscale image decomposition in motion-estimation schemes has been shown to have a favourable impact on accuracy in tracking motion of the carotid artery wall from B-mode ultrasound image sequences. In this work, in an attempt to further enhance accuracy, we investigate the effects of different parameters of multiscale image decomposition. To this end, we optimize multiscale weighted least-squares optical flow (MWLSOF), a previously presented multiscale motion estimator, in terms of (a) the type of wavelet transform (WT) (discrete (DWT) and stationary (SWT) WTs), (b) the WT function and (c) the total number of levels of image decomposition. The optimization is performed in the context of an in silico data framework, consisting of simulated ultrasound image sequences of the carotid artery. We propose SWT, a high-order coiflet function (ex. coif5) and one level of multiscale image decomposition as the optimal parameterization for MWLSOF to achieve maximum accuracy in the particular application. Finally, we demonstrate the usefulness of an accurate motion estimator in real data experiments, by applying the optimized MWLSOF to real image data of patients with carotid atherosclerosis.

W.1.2.2 - Modeling stent deployment in realistic arterial segment geometries: the effect of the plaque composition

Georgia Karanasiou, Antonis Sakellarios, Evanthia Tripoliti, Euripides Petrakis, Michalis Zervakis, Francesco Migliavacca, Gabriele Dubini, Elena Dordoni, Lambros Michalis, Dimitrios Fotiadis

Stents are medical devices used in cardiovascular intervention for unblocking the diseased arteries and restoring blood flow. During stent implantation the deformation of the arterial wall as well as the resulted stresses caused in the arterial morphology are studied. In this paper we study the effect of the composition of the atherosclerotic plaque during the stent deployment procedure, using Finite Element modeling. The stenting procedure is simulated for two different cases; in the first the presence of the plaque is ignored whereas in the second a three dimensional (3D) stiff calcified plaque is located in the stenotic area of the artery. Results indicate that in the second case the von Mises stresses in the arterial wall are higher than the stresses occurred in the first case. In addition, the distribution of the arterial von Mises stress depends on the plaque composition.

W.1.2.3 - Identification of scalp blood flow in NIRS data based on Granger causality

Masako Sugai, Masaharu Adachi

NIRS (Near infra-red spectroscopy) is a spectroscopic device to assess the dynamic changes in the hemoglobin concentration evoked by brain activity non-invasively. It has been said that NIRS data reflects brain activities of cortical surface. Recently, it is reported that NIRS data reflects not only cortex blood flow but also the scalp blood flow. To discuss about this matter, we apply Granger causality for the NIRS data to detect the relationship between scalp and cortex blood flow in motor execution. Five healthy subjects took part in the experiment. We measured scalp blood flow and conventional NIRS data simultaneously using double density probe holder. As a result, in four of five subjects, we detected the Granger causality strongly from the scalp blood flow data to the conventional NIRS data. This method can be useful to quantify the contribution that the scalp blood flow data influences on the conventional NIRS data.

W.1.2.4 - Low-power Hardware Implementation of Noise Tolerant Heart Rate Extractor for a Wearable Monitoring System

Shintaro Izumi, Masanao Nakano, Ken Yamashita, Takahide Fujii, Hiroshi Kawaguchi, Masahiko Yoshimoto

To prevent lifestyle diseases, wearable bio-signal monitoring systems for daily life monitoring have attracted attention. Wearable systems have strict size and weight constraints, which impose significant limitations of the battery capacity and the signal-to-noise ratio of bio-signals. The novelty of this work is the hardware implementation of a noise-tolerant heart rate extraction algorithm that can achieve low-power performance with high reliability. This report describes comparisons of the heart rate extraction algorithm performance and the dedicated hardware implementation of short-term autocorrelation (STAC) method. The proposed heart rate extractor, implemented in 65-nm CMOS process using Verilog-HDL, consumes 1.65 uA at 32.768 kHz operating frequency with 1.1 V supply voltage.

W.1.2.5 - Computational Study of Particle Deposition in Patient Specific Geometries

Marika Pilou, Anastasios Skiadopoulos, Evangelos Makris, Panagiotis Neofytou, Christos Housiadas

The present work focuses on the study of particle deposition in segments of the cardiovascular system. In particular, the geometry of an iliac bifurcation is reconstructed from medical imaging data and the flow fields of both blood and particles are obtained using Computational Fluid Particle Dynamics techniques. Particle convection, diffusion and inertia are taken into account in the simulations. The numerical experiments indicate that diffusion dominates deposition and only 10% of the injected particles deposit in the bifurcation. Both blood flow field and the characteristics of the patient specific geometry influence the particle deposition sites. Overall, the proposed methodology could become a useful tool for the design and optimization of biomedical applications.

Session W.1.3 – Imperial 3 room: 09:00-10:30

Biomedical Signal Processing

Chair: *Konstantina Nikita*

W.1.3.1 - An Information Theoretic Approach to Classify Cognitive States Using fMRI

Itir Onal, Mete Ozay, Orhan Firat, Ilke Oztekin, Fatos T. Yarman Vural

In this study, an information theoretic approach is proposed to model brain connectivity during a cognitive processing task, measured by functional Magnetic Resonance Imaging (fMRI). For this purpose, a local mesh of varying size is formed around each voxel. The arc weights of each mesh are estimated using a linear regression model by minimizing the squared error. Then, the optimal mesh size for each sample, that represents the information distribution in the brain, is estimated by minimizing various information criteria which employ the mean square error of linear regression model. The estimated mesh size shows the degree of locality or degree of connectivity of the voxels for the underlying cognitive process. The samples are generated during an fMRI experiment employing item recognition (IR) and judgment of recency (JOR) tasks. For each sample, estimated arc weights of the local mesh with optimal size are used to classify whether it belongs to IR or JOR tasks. Results indicate that the suggested connectivity model with optimal mesh size for each sample represent the information distribution in the brain better than the state-of –the art methods.

W.1.3.2 - Resting State fMRI Analysis using a Spatial Regression Mixture Model

Vangelis P. Oikonomou, Konstantinos Blekas, Loukas Astrakas

Functional MRI (fMRI) is one of the most important techniques to study the human brain. A relatively new problem to the analysis of fMRI data is the identification of brain networks when the brain is at rest i.e. no external stimulus is applied to the subject.

In this work a method to find the Resting State Networks (RSNs), using fMRI time series, is proposed. To achieve that our method uses the Regression Mixtures Models (RMMs). RMMs are mixture models specifically design to cluster time series. Furthermore, our method takes into account the spatial correlations of fMRI data by using a new functional for the responsibilities of the mixture. Experimental results have showed the usefullness of the proposed approach compared to other methods of the field such as the k - means algorithm.

W.1.3.3 - Developing a Simulator for Multispectral Optoacoustic Tomography

Efthymios Maneas, Stratis Tzoumas, Vasilis Ntziachristos, George Spyrou

The aim of this study was the development of a simulator for Multispectral Optoacoustic Tomography (MSOT). The modelling pathway of the simulator was separated into the optical, the acoustic and the reconstruction part in generating finally a photoacoustic image. In this paper, the presented simulation geometry was based on a recently developed MSOT imaging system, but it can be easily modified to other imaging geometries. Through comparison between experimental and simulated data, a validation of the model as well as its limitations, perspectives and modifications are presented.

W.1.3.4 -Spatio-Spectral Analysis of ECoG Signals during Voice Activity

Vasileios Kanas, Iosif Mporas, Heather Benz, Kyriakos Sgarbas, Nathan Crone, Anastasios Bezerianos

In this paper, we perform spatio-spectral analysis of the human cortex with implanted electrocorticographic (ECoG) electrodes during the voice production process. For this study, the ECoG signals were recorded while the subject performed two-syllable tasks. Additionally, assuming that the speech activity of a subject is expressed as ECoG signal activity disparately distributed over the space of the electrodes, we examined the spectral information in response to the electrode locations. The study was based on spectral features (power spectral density) estimated for each electrode. Quantitative analysis based on the Relief algorithm was followed to estimate the degree of importance of each electrode for describing the voice activity. The experimental results showed that the spectral analysis with resolution of 8Hz offers the highest voice discrimination performance (94.2%) using support vector machines as classifier. Finally, our analysis showed that during voice activity the frequency bands [168,208] Hz are mostly affected.

W.1.3.5 - LBP-Based Ear Recognition

Nazmeen Bibi Boodoo-Jahangeer, Sunilduth Baichoo

The ear, as a biometric, has been given less attention, compared to other biometrics such as fingerprint, face and iris. Since it is a relatively new biometric, no commercial applications involving ear recognition are available. Intensive research in this field is thus required to determine the feasibility of this biometric. In medical field, especially in case of accidents and death, where face of patients cannot be recognized, the use of ear can be helpful. In this work, yet another method of recognizing people through their ears is presented. Local Binary Patterns (LBP) is used as features and the results are compared with that of Principal Components Analysis (PCA).

Session W.2.1 – Imperial 1 room: 11:30-13:00

Gene Expression Analysis & Bioinformatics Engineering

Chair: *Georgios Potamias*

W.2.1.1 - Integrative Transcriptomic Analysis of Two Cell Lines elucidates the Architecture of Endoplasmic Reticulum Stress Signaling in Glioblastoma

Aristotelis Chatziioannou, Olga Papadodima, Nicolas Dejeans, Eric Chevet

The endoplasmic-reticulum (ER) stress response represents a pivotal cellular process, triggered by a variety of stimuli implying incorrect protein folding in the ER. Solid evidence implicates ER stress-induced dysfunction as major contributors in many cancers, among which brain cancers. In this work, an integrative analysis in two transcriptomic datasets scrutinizes the regulatory potency of ER stress mechanisms in glioblastoma. Besides confirming the results of the initial analyses, the integration of both datasets manages to study the effect of cellular stress in conjunction to the dysregulation of the IRE1a branch of the ER stress signaling pathways. Given the respective diversified phenotypic profile of glioblastomas, ranging from increased proliferation to enhanced migration and aggressiveness as a result of the IRE1a molecular switch, this study suggests potential target groups of master regulators of the ER stress pathways, through the application of an established, exhaustive computational framework.

W.2.1.2 - Enhancing the Performance of a Microarray Gridding Algorithm via GPU Computing Techniques

Stamos Katsigiannis, Eleni Zacharia, Dimitris Maroulis

cDNA microarrays are a useful tool for studying the expression levels of genes. Nevertheless, microarray image gridding remains a challenging and complex task. Most of the microarray image analysis tools require human intervention, leading to variations of the gene expression results. Automatic methods have also been proposed, but present high computational complexity. In this work, the performance enhancement via GPU computing techniques of a fully automatic gridding method, previously proposed by the authors' research group, is presented. The NVIDIA CUDA architecture was utilized in order to achieve parallel computation of complex steps of the algorithm. Experimental results showed that the proposed approach provides enhanced performance in terms of computational time, while achieving higher utilization of the available computational resources.

W.2.1.3 -Bonferroni correction hides significant motif combinations

Aika Terada, Jun Sese

Three or more motifs often work together, and the effects are essential in cellular machinery. However, the scanning of the associations of motifs is limited to single motifs or pairs, as the result of scanning for combinations of three or more motifs often includes no significant results. Even if we find a combination with a very small raw P-value in the scan, the combination is not significant because the adjusted P-value by a multiple testing correction, such as the Bonferroni correction, is larger than the given significance level. While it is known that the Bonferroni correction is a very conservative correction, a few biological experiments have used more sensitive random permutation based multiple testing correction such as Westfall-Young procedure (WY procedure). In this paper, we show that the Bonferroni correction and its modified procedure are too conservative to find statistically significant combinations consisting of three or more motifs, while the WY procedure can detect them. These results suggest that the statistically significant epistatic effects have been overlooked and motivate us to reanalyze the publicly available datasets.

W.2.1.4 - Experimental Model Construction and Validation of the ErbB Signaling Pathway

Kalliopi Kalantzaki, Leyteris Koumakis, Ekaterini Bei, Michalis Zervakis, Georgios Potamias, Dimitrios Kafetzopoulos

The importance of ErbB receptor signaling in breast cancer is consistent with its functional role in normal development of mammary gland. The study of the ErbB signaling network and its bidirectional cross-talk with hormonal receptors, such as estrogen receptor (ER) encloses information about the molecular mechanisms on breast cancer evolution, progression and endocrine resistance. With this analysis we attempt to examine the differences in activation/inhibition of intracellular signaling molecules within ErbB signaling cascade on ER+ and ER- breast cancer patients. With the proposed framework we model the genetic interactions in the ErbB signaling pathway as Gaussian approximations and we introduce a robust algorithm for identifying a threshold of activation/inhibition based on expression data. The results indicate a distinct profile of activation/inhibition between the two ER populations and highlight the primary role of PI3K/Akt pathway in breast cancer progression and targeted treatment strategies.

W.2.1.5 - Prioritized Functional Analysis of Biological Experiments Using Resampling and Noise Control Methodologies

Eleftherios Pilalis, Aristotelis Chatziioannou

StRAnGER is a web application for the automated statistical analysis of annotated experiments, exploiting controlled biological vocabularies, like the Gene Ontology or the KEGG pathways terms. In the first version, StRAnGER featured various gene profiling platforms for functional analysis of genomic datasets, starting from a list of significant genes derived from statistical and empirical thresholds. In the current version, various major improvements have been implemented, namely a new ranking algorithm, the expansion of background distributions with protein annotations, the addition of a mode for batch experiments and a noise-control analysis that evaluates the robustness of the prioritized terms through iterative addition of random genes. Overall, StRAnGER enables a systems level functional interpretation through the utilization of bootstrapping techniques and the detection of distribution-independent term enrichments.

Session W.2.2 – Imperial 2 room: 11:30-13:00

Intelligent Therapeutic & Diagnostic Systems

Chair: *Anca Bucur*

W.2.2.1 - Rectangular Patch Antenna on Split-ring Resonators Substrate for THz Brain Imaging: Modeling and Testing

Maria Koutsoupidou, Irene Karanasiou, Nikolaos Uzunoglu

Large biomolecules and proteins associated with brain functions and human diseases, as Alzheimer's disease, exhibit unique fingerprints in the THz spectrum. As a result, THz biomedical imaging with near-field probes is a promising solution for medical diagnosis and brain study. Ultimately, antennas with significantly enhanced performance are required for in-vivo THz biomedical applications. In this work, a THz rectangular patch antenna on a metamaterial substrate operating at 1 THz is presented. The metamaterial substrate based on split-ring resonators improves the antenna's gain and directivity. Finally, measurements at the microwave regime of a scaled version of the proposed antenna have been performed to experimentally verify the theoretically estimated metamaterial effect on the antenna performance.

W.2.2.2 - Towards Generalized Nuclear Segmentation in Histological Images

Abhishek Vahadane, Amit Sethi

Computer aided diagnosis in cancer pathology (computational pathology) using histological images of biopsies is an emerging field. Segmentation of cell nuclei can be an important step in such image processing pipelines. Although seeded watershed segmentation is a simple and computationally efficient segmentation technique, it is prone to errors like oversegmentation when applied to histological images. We report specific enhancements to this technique to improve segmentation of cell nuclei in histological images. Foreground seeds were generated by fast radial symmetry transform (FRST). Otsu thresholding was used on enhanced image to estimate tentative foreground map. Background markers were computed from the tentative foreground map. False detections in the segmented output were removed by logical AND with the tentative foreground map. Using these enhancements nuclear segmentation was significantly improved on histological images (H&E stained breast and intestinal tissue images, Feulgen stained images of prostate tissues).

W.2.2.3 - A New Modality for Quantitative Evaluation of Parkinson's Disease: In-Air Movement

Peter Drotar, Jiri Mekyska, Irena Rektorova, Lucia Masarova, Zdenek Smekal, Marcos Zanuy

Parkinsons disease (PD) is neurodegenerative dis-order with very high prevalence rate occurring mainly among elderly. One of the most typical symptoms of PD is deterioration of handwriting that is usually the first manifestation of Parkinsons disease. In this study, a new modality - in-air trajectory during handwriting - is proposed to efficiently diagnose PD. Experimental results showed that analysis of in-air trajectories is capable of assessing subtle motor abnormalities that are connected with PD. Moreover, conjunction of in-air trajectories with conventional on-surface handwriting allows us to build predictive model with PD classification accuracy over 80%. In total, we compute over 600 handwriting features. Then, we select smaller subset of these features using two feature selection algorithms: Mann-Whitney U-test filter and relief algorithm, and map these feature subsets to binary classification response using support vector machines.

W.2.2.4 - Food Volume Computation for Self Dietary Assessment Applications

Joachim Dehais, Sergey Shevchik, Peter Diem, Stavroula Mougiakakou

There is great demand for easily-accessible, user-friendly dietary self-management applications. Yet accurate, fully-automatic estimation of nutritional intake using computer vision methods remains an open research problem. One key element of this problem is the volume estimation, which can be computed from 3D models obtained using multi-view geometry. The paper presents a computational system for volume estimation based on the processing of two meal images. A 3D model of the served meal is reconstructed using the acquired images and the volume is computed from the shape. The algorithm was tested on food models (dummy foods) with known volume and on real served food. Volume accuracy was in the order of 90 %, while the total execution time was below 15 seconds per image pair. The proposed system combines simple and computational affordable methods for 3D reconstruction, remained stable throughout the experiments, operates in near real time, and places minimum constraints on users.

W.2.2.5 - A Hybrid Genetic Algorithm for the Selection of the Critical Features for Cardiovascular Complications Prognosis in Type 2 Diabetic Patients

Kalliopi Dalakleidi, Konstantia Zarkogianni, Vassilios Karamanos

The purpose of this study is to present a hybrid approach based on the combined use of a genetic algorithm GA) and a nearest neighbours classifier for the selection of the critical clinical features which are strongly related with the incidence of fatal and non fatal Cardiovascular Disease (CVD) in patients with Type 2 Diabetes Mellitus (T2DM). For the development and the evaluation of the proposed algorithm, data from the medical records of 560 patients with T2DM are used. The best subsets of features proposed by the implemented algorithm include the most common risk factors, such as age at diagnosis, duration of diagnosed diabetes, glycosylated haemoglobin (HbA1c), cholesterol concentration, and smoking habit, but also factors related to the presence of other diabetes complications and the use of antihypertensive and diabetes treatment drugs (i.e. proteinuria, calcium antagonists, bblockers, diguanides and insulin). The obtained results demonstrate that the best performance was achieved when the weighted k-nearest neighbours classifier was applied to the CVD dataset with the best subset of features selected by the GA, which resulted in high levels of accuracy (0.96), sensitivity (0.80) and specificity (0.98).

Session W.2.3 – Imperial 3 room: 11:30-13:00

Clinical Engineering

Chair: *Maria Tereza Arredondo*

W.2.3.1 - Guidelines for the economic analysis of a telematic platform for Parkinson's disease monitoring

Jorge Cancela, Maria T Arredondo, Olivia Hurtado

PERFORM (A sophisticated multi-parametric system FOR the continuous effective assessment and monitoring of motor status in Parkinson's disease and other neurodegenerative diseases) is an European project which aim is to provide doctor with a telematic tool for the remote monitoring of Parkinson's disease (PD) patients at their homes. The technical performance of PERFORM has been addressed in previous publications. The aim of this work is to introduce the best well-known methodologies and indicators used in the health economics field, normally linked to the assessment of drugs or devices, and provide a set of guidelines for the use of these methodologies in the assessment of telehealth systems focused on PD patients. PD will also be introduced in economic terms, i.e. burden and cost of PD. This study will be done with special emphasis in European countries.

W.2.3.2 - Preliminary Study on Optical Feature Detection for Head Tracking in Radiation Therapy

Tobias Wissel, Patrick Stüber, Benjamin Wagner, Ralf Bruder, Achim Schweikard, Floris Ernst

Marker-less tracking provides a non-invasive as well as comfortable approach to compensate for head motion in high precision radiotherapy. However, it suffers from a lack of point-to-point correspondences, typically requiring charac-teristic spatial landmarks to match point clouds. In this study, we show that cutaneous and subcutaneous structures can be uncovered using an 850 nm laser setup. For three subjects, we compare features extracted from camera images with MR scans serving as an anatomical ground truth. The results confirm the validity of the optically detected structures. The negative correlation between skin thickness and reflected light energy is likewise predicted by Monte-Carlo simulations and can be used to improve spatial point cloud matching. Tissue thickness and its facial structure can be predicted with sub-millimeter accuracy using a Support Vector regression machine. In addition, the optical measurements reveal the location of vessels that are not immediately visible in the MR scan. These promising findings highly encourage its application for a marker-less tracking system.

W.2.3.3 - Method for measuring the heart rate through fingertip using a low-end video camera and its application in self care

Lucian Pestritu, Alexandra Todiruta, Maria Goga, Nicolae Goga

This article presents a method for monitoring the heart rate using a low-end video camera. The user places the fingertip on the camera lens and the software detects the periodic variations in light intensity caused by the pulsation of blood in the capillary tissue. The measurement technique is based on extracting beat-to-beat intervals by passing the color intensity average through a processing pipeline comprised of six stages. Our tests indicate a measurement error below 3 bpm, when compared to commonly available home care devices. We present a possible application of our method in the area of stress diagnosis and treatment. The application can be used at home to monitor personal health and enable individuals to perform enhanced self care.

W.2.3.4 - A CUDA based digital X-ray image stitching algorithm

Jiaxiang Huang, Xu Xu

To spare the high cost of an extra-large detector for full body length X-ray imaging, this paper presents a digital X-ray image stitching algorithm. This algorithm uses a stitching process to generate a full body length image by merging multiple images captured from a common dimensioned detector. The algorithm can also provide a less distorted outcome with better image quality. Moreover, it tackles the problem of long processing time of other stitching algorithms, to reduce patient waiting time. CUDA is proved to be an effective measure to be used in the imaging algorithm to reduce the processing time for image stitching. A number of clinical tests have been conducted to verify this method and the results show that the digital X-ray image stitching algorithm presented in this paper is accurate, and can markedly improve patients waiting time when a full-body-length image is needed in clinical applications.

W.2.3.5 - An Asthma Management Framework for the RespDoc Clinical Decision Support System Based on the Combination of the Official Clinical Guidelines

Aikaterini Rigopoulou, Dimitrios Lymberopoulos

In this paper we propose a new framework for the in- and out-hospital homogeneous management of childhood asthma through a combination of official clinical guidelines for asthma management. The main indicator used for the assessment of the child's asthma is the measurement and interpretation of Fraction of exhaled Nitric Oxide (FeNO). As a whole, the decision making algorithms that we created are organized as a Clinical Decision Support System (CDSS), termed RespDoc. The performance of the RespDoc has been evaluated by means of data acquired from real world medical cases.

W.2.3.6 - Smart Cards in Healthcare Information Systems: Benefits and Limitations

Anastasis Keliris, Vassileios Kolias, Konstantina Nikita

Smart cards in Health Information Services (HIS) are considered to have great potential to improve the delivery of healthcare services and reduce healthcare costs. On the other hand, HIS smart cards also introduce new challenges and limitations that require further analysis before a full-scale implementation. In this paper, smart cards in HIS are presented, along with current implementations and the benefits and the limitations that arise from their use.

Session W.2.4 – Imperial: 11:30-13:00

Biomedical Signal Processing

Chair: *Ilias Maglogiannis*

W.2.4.1 - Influence on Skin Temperature and Blood Flow of Thermal and Massage Stimuli

Hirotaka Inoue, Hiroshi Hagiwara

Changes in skin temperature are known to be affected by blood flow. The reaction of skin temperature and blood flow when various stimuli are applied to the body has been investigated for many years. However, body reactions when different stimuli are applied concurrently to the body have not been well studied. This study investigated changes in blood flow and skin temperature when massage stimulation and thermal stimulation were applied to the body simultaneously. Skin temperature tended to change quickly when a massage stimulus was present during the task. In addition, MASS values were significantly higher and VELOCITY values tended to be higher during tasks with massage stimulus. Massage stimulation thus appears to significantly affect blood flow and accelerate changes in skin temperature from hot and cool stimulations.

W.2.4.2 - Efficient C Level Hardware Design for Floating Point Biomedical DSP Applications

Christoforos Economakos, Harry Sidiropoulos, George Economakos

Recent advances in embedded system design have increased their interference in different application domains, where software only solutions have prevailed. This new implementation platform require however quality of results in terms of speed, power and computational complexity, along with strict time-to-market schedules. Performance is sought by utilizing modern Field Programmable Gate Array (FPGA) devices, offering hundreds of GFLOPs with maximum power efficiency. Productivity is enforced with High-Level Synthesis (HLS) or Electronic System Level (ESL) or C-based hardware design methodologies, that offer an efficient abstraction level to boost-up early prototyping. However, just like the migration from schematics to Hardware Description Languages (HDLs) required specific coding styles for efficient hardware design, C-based hardware design also requires efficient coding guidelines to be followed. This paper presents a set of such coding guidelines, and evaluates their efficiency for FPGA based scientific, floating point arithmetic calculations. As found through extensive experimentation, the performance and area optimizations offered by efficient coding can improve the ones offered by HLS only, even more than 90%. So, while not every C program can be turned into hardware with the press of a button, efficient coded C programs can offer a profitable productivity boost.

W.2.4.3 - Classification of Atrio-Ventricular Reentrant Tachycardia using Intracardiac Signals

Wajeeha Nafees, Bushra Riaz, Nauman Razzaq, Wardah Iftikhar, Tahir Zaidi

Electrophysiology study (EPS) has been serving as a diagnostic and curative tool for rhythm-related cardiac diseases for more than few decades now. Clinical EPS requires intense knowledge of numerous protocols and run-time analysis of various parameters in order to find the root-cause of the problem. The Intracardiac Electrograms available during EPS are investigated for abnormal activations. The particular sequence of the abnormal activations hints to a specific disease. This crucial diagnosis requires a high level of expertise. In this paper, an automated algorithm to detect AtrioVentricular Reentrant Tachycardia (AVRT), a type of Supraventricular Tachycardia (SVT), has been proposed to assist the beginners and support the decisions of the experts of EPS. After studying the underlying medical mechanisms, exploring the electrograms formed by reentrant circuit and analyzing temporal progression of cardiac activations of AVRT, a novel algorithm exploiting the above relationships is presented. The algorithm detects AVRT with 87.06% sensitivity.

W.2.4.4 - Estimation of ECG Parameters using Photoplethysmography

Rohan Banerjee, Aniruddha Sinha, Arpan Pal, Anurag Kumar

Regular Electrocardiogram (ECG) monitoring is a good practice for cardiac patients as well as elderly people. In this paper we propose a low cost methodology to coarsely estimate the range of some important parameters of ECG using Photoplethysmography (PPG). PPG is easy to measure and strongly related to the human cardio-vascular system like ECG. A set of feature is extracted from PPG signal for analysis. A statistical analysis is performed between each of the ECG parameters and all the PPG features to find the most relevant set of features corresponding to a particular ECG parameter. Training model for different ECG parameters are created based on those selected features. Both artificial neural network and support vector machine based supervised learning approach is used for performance comparison. Experimental results, performed on benchmark dataset shows that good accuracy in the estimation of ECG parameter can be achieved in our proposed methodology. Results also show that the overall performance improves in using feature selection technique rather than using all the PPG features for classification.

W.2.4.5 - Performance Analysis of Multi-frequency SSVEP-BCI Using Clear and Frosted Colour LED Stimuli

Surej Mouli, Ramaswamy Palaniappan, Ian P Sillitoe, John Q Gan

Among the many paradigms used in brain-computer interface (BCI), steady state visual evoked potential (SSVEP) offers the quickest response; however it is disadvantageous from the point of view of visual fatigue, which prevents subjects from prolonged usage of visual stimuli especially when LEDs are used. In this paper, we propose a visual stimulator using readily available RGB LEDs with clear and frosted glass, with the latter being tested for performance and qualitative user comfort using electroencephalogram (EEG) data from four subjects. Furthermore, we also compare frosted and clear stimuli for three colours Red, Green and Blue with frequency values of 7, 8, 9 and 10 Hz. The results using band-pass filtering and Fast Fourier Transform showed that 7 Hz Green clear LED stimuli gave the highest response in general, although all the subjects indicated that they were more comfortable with frosted LED stimuli.

W.2.4.6 - Does Music affect HRV impulse? -A time domain study

Anilesh Dey, Sayan Mukherjee, Sanjay Kumar Palit, D. K. Bhattacharya, D.N. Tibarewala

The 2D Poincare′ plot of HRV signal reflects the effect of different external stimuli on ANS. The classification is generally done by fitting an ‘ellipse’ on the dense region of the constructed Poincare′ plot of HRV signal. However 2D Poincare′ plot sometimes fails to describe the proper behaviour of the system. One such example is 2D Poincare′ plot of HRV signal in pre-music and on-music condition. In fact 2D Poincare′ plots in pre and on-music condition look almost similar for few subjects. So a proper classification tool is sought for. In this article, an improved technique called “3D Poincare′ plot with proper delay” has been applied to properly distinguish the pre-music and onmusic state of some normal healthy subjects. The whole experiment is carried out at School of Bio-Science and Engineering, Jadavpur University, Kolkata, India.

Session W.3.1 – Imperial 1 room: 13:30-15:00

Engineering Models in Bio-Medicine

Chair: *Dimitrios Lymberopoulos*

W.3.1.1 - An in-silico Model for Solid Tumor Growth based on the Concept of Glycolysis

Michail Kounelakis, Maria Papadogiorgaki, Michail Zervakis

Cancer growth is a complex process which depends on several tasks that cancer cells have to perform in order to live and proliferate. Among these tasks, perhaps the most significant one is to reach adequate sources of nutrients, such as oxygen and glucose, from their surrounding environment in order to initiate their respiration process and provide them with the necessary energy in the form of ATP molecules. Cellular respiration is a biological mechanism that consists of two sequential processes, named 'glycolysis' and 'oxidative phosporylation' (OXPHOS). Since 1956, when the biologist Otto Warburg discovered the increase of glycolysis in cancer cell compared to healthy cells, glycolysis has been studied in depth in order to understand its role in cancer genesis and growth. Towards this direction we propose a new in-silico cancer growth model which embeds the glycolytic potential of the cancer cells in the growth process. The experimental observations obtained show that the model fits the cancer data predicting the tumor’s growth, in the proliferative, hypoxic and necrotic zone, quite satisfactory.

W.3.1.2 - Personalized Glucose-Insulin Metabolism Model based on Self-Organizing Maps for Patients with Type 1 Diabetes Mellitus

Konstantia Zarkogianni, Eleni Litsa, Konstantina Nikita

The present paper aims at the design, the development and the evaluation of a personalized glucose-insulin metabolism model for patients with Type 1 Diabetes Mellitus (T1DM). The personalized model is based on the combined use of Compartmental Models (CMs) and a Self Organizing Map (SOM). The model receives information related to previous glucose levels, subcutaneous insulin infusion rates and the time and amount of carbohydrates ingested. Previous glucose measurements along with the outputs of the CMs which simulate the sc insulin kinetics and the glucose absorption from the gut into the blood, respectively, are fed into the SOM which simulates glucose kinetics in order for the latter to provide with future glucose profile. The personalized model is evaluated using data from the medical records of 12 patients with T1DM for the time being on insulin pumps and CGMS. The obtained results demonstrate the ability of the proposed model to capture the metabolic behavior of a patient with T1DM and to handle intra- and inter-patient variability.

W.3.1.3 - Unsupervised Clustering of Patient-Centric Models to Cluster-Centric Models for Ubiquitous Healthcare Environment

Maria-Anna Fengou, Iosif Mporas, Dimitrios Lymberopoulos

In this paper we present an approach based on data-driven clustering of patient-centric models for ubiquitous healthcare environments. The use of clusters of models instead of patient-specific models offers the advance of dynamic reconfiguration of the models according to upcoming healthcare events that appear for members of the cluster. The healthcare events are related to the patient's health condition.

W.3.1.4 - Biomedical Magnetic Induction Tomography Using Two-Arm Archimedean Spiral Coil: A Feasibility Study

Ziyi Zhang, Peiguo Liu, Dongming Zhou, Hengdong Lei

Based on the principle of primary excitation magnetic field counteraction, in this paper a new type of excitation coil named two-arm Archimedean spiral coil (TAASC) is designed and first introduced into biomedical MIT coil system to improve the coil system sensitivity. The primary voltage and the scaled level map of secondary voltage perturbation for the TAASC are calculated through theory and simulation. The coil system sensitivity curves when using the TAASC as excitation coil are tested at different positions, electrical conductivities and frequencies by simulation experiments. As a control, all the theoretical calculations and simulation experiments are conducted again for the circular excitation coil. The results show that the primary excitation magnetic field can be markedly counteracted while the secondary induction magnetic field perturbation is nearly at the same order of magnitude, and the coil system has a bigger sensitivity with an improvement factor of 103 to 104 by using this new type of TAASC as excitation coil, compared with the common circular excitation coil. The simulated results are in good agreement with the theoretical results.

Session W.3.2 – Imperial 2 room: 13:30-15:00

NeuorEngineering, Neuromuscular Systems and Rehabilitation Engineering

Chair: *Wei Chen*

W.3.2.1 - A new Multiple ANFIS model for classification of hemiplegic gait

Ahmet Yardimci

Neuro-fuzzy system is a combination of neural network and fuzzy system in such a way that neural network learning algorithms, is used to determine parameters of the fuzzy system. This paper describes the application of multiple adaptive neuro-fuzzy inference system (MANFIS) model which has hybrid learning algorithm for classification of hemiplegic gait acceleration (HGA) signals. Decision making was performed in two stages: feature extraction using the wavelet transforms (WT) and the ANFIS trained with the backpropagation gradient descent method in combination with the least squares method. The performance of the ANFIS model was evaluated in terms of training performance and classification accuracies and the results confirmed that the proposed ANFIS model has potential in classifying the HGA signals.

W.3.2.2 - Ultra-fast Epileptic Seizure Detection Using EMD based on Multichannel Electroencephalogram

Wei Chen, Yan-Yu Lam, Chia-Ping Shen, Hsian-Ya Sung, Jeng-Wei Lin, Ming-Jang Chiu, Feipei Lai

We present a system to detect seizure and spike in Epilepsy Electroencephalogram (EEG) analysis and characterize different epilepsy EEG types. After extracting features from three EEG types, Normal, Seizure and Spike, with Empirical Mode Decomposition (EMD), we do Analysis of variance (ANOVA) to classify conspicuous features and low-resolution features, and build Gaussian distributions of conspicuous features for probability density function (PDF) to do classification. Using EMD, the recognition rate improved from 70% to 90%. With ANOVA, the recognition rate can reach 99%. The linear model accelerates the system from 2 hours to 90 seconds compare to the previous approach.

W.3.2.3 - Handgrip estimation based on total variation denoising filtering for control applications

Julio Reategui , Gonzalo Cucho, Paul Rodriguez, Rocio Callupe, Ericka Madrid

In many biomechanical studies and control applications, such as ergonomics studies, control of upper limb prosthesis, and sports performance is required handgrip force estimation for both monitoring and control purposes. As it was proven in previous works, features extraction from the extensor carpi radialis longus (ecrl) sEMG had a linear relationship with the gripforce of the hand. However, most of the developed estimations have shown high variation, which are not quite suitable for control applications. Therefore we propose a methodology to estimate the grip force, which models the extrated features as the handgrip force signal with the presence gaussian noise. In order to estimate the force, these features are filtered with a regularized optimization problem based on total variation denoising (TVD). Furthermore, since TVD is not a trivial minimization problem it was used ADMM algorithm as a meant to implement the proposed methodology. The developed methodology yielded promising results ($\rho > 0.94$, NRMSE < 0.07) between 30%-50% MVC.

W.3.2.4 - Speech Perception: Single Trial Analysis of the N1/P2 Complex of Unimodal and Audiovisual Evoked Responses

George Zouridakis, Martijn Baart, Jeroen Stekelenburg, Jean Vroomen

Audiovisual speech integration is reflected in the electrophysiological N1/P2 complex. Here, we analyzed recordings of electroencephalographic brain activity from 28 subjects who were presented with combinations of auditory, visual, and audiovisual stimuli, using single trial analysis based on an independent component analysis procedure. We found that, with respect to the N1/P2 complex, single trials across all subjects and all conditions could be separated into two groups, one with ‘typical’ responses having the same polarity as the average response and another one with ‘aberrant’ responses having opposite polarity. Furthermore, the number of aberrant responses in non-speech interpretation of auditory stimuli was significantly lower compared to speech, which may affect the N1/P2 complex in the ensemble average EP.

W.3.2.5 - Model free predictive control of human heart rate and blood pressure

Amirehsan Sarabadani Tafreshi, Stefania Bernasconi, Verena Klamroth-Marganska, Silvio Nussbaumer, Robert Riener

Prolonged bed rest in severely paralyzed or intensive care patients is associated with adverse secondary effects on cardiopulmonary function. To counteract these effects of immobility in bed-ridden patients, we aim at controlling and stabilizing the cardiovascular system via multiple mechanical input variables. A challenge in this control problem is to provide an accurate model of the plant to be controlled. As humans are time variant systems and show individual physiological reactions to external stimuli the identification of such a model appears to be challenging. The current work presents a model-free predictive controller which takes into account these challenges. In this paper we present data concerning the control of heart rate, systolic and diastolic blood pressures, and mean arterial blood pressure via body tilting and leg mobilization. The controller was validated in a simulation study and feasibility was tested on two healthy subjects. The experimental results with healthy subjects show that the mean value differed in average less than 1 beat per minute (bpm) from the desired heart rate values and less than 1 mm Hg from the desired blood pressure values. The long term goal of this project is to control also breathing via body tilting, stepping and electrical muscle stimulation.

W.3.2.6 - Enabling e-services based on affective exergaming, social media and the semantic web: a multitude of projects serving the citizen-centric vision for ICT in support of pHealth

Panagiotis Bamidis

Recent studies and workshops have stressed the fundamental importance of providing harmonised health and social care services that meet the extended needs of the individual, taking into account diversity in need, preferences, ability and support.

For a real caring society, the notion of "information sharing" becomes clearly crucial when communication and interaction in health care is needed. This paper revisits recent funded projects undertaken by our team, in view of the so-called coordination of planned activities for elderly/disabled care and independent living support. Three development pillars are taken under consideration herein, namely, affective exergaming services for seniors/disabled, social media and the semantic web. Outputs from a multitude of projects are then used to provide evidence of how issues recently encountered under the so-called blue line dimensions are tackled; these are technological interoperability, semantic integration, modern interfaces, people needs/expectations and societal incentives. As the latter synthesize a con-temporary puzzle of personalised health care approach, this paper provides an innovative perspective of interlinking developments and outputs of research in view of improving healthcare.

Session W.3.3 – Imperial 3 room: 13:30-15:00

Biomedical Data Engineering

Chair: *Huseyin Seker*

W.3.3.1 -SNOMED CT Normal Form and HL7 RIM binding to normalize clinical data from cancer trials

Antonio Rico-Diez, Santiago Aso-Lete, David Perez-Del-Rey, Raul Alonso-Calvo, Anca Bucur, Brecht Claerhout, Victor Maojo

Current research in oncology, require the involvement of several institutions participating in clinical trials. Heterogeneities of data formats and models require advanced methods to achieve semantic interoperability and provide sus- tainable solutions. In this field, the EU funded INTEGRATE project aims to develop the basic knowledge to allow data sharing of data from post-genomic clinical trials on breast cancer. In this paper, we describe the procedure implemented in this project and the required binding between relevant terminologies such as SNOMED CT and an HL7 v3 Reference Information Model (RIM)-based data model. After following the HL7 recommendations, we also describe the main issues of this process and the proposed solution, such as concept overlapping and coverage of the domain terminology. Despite the fact that the data from this domain presents a high level of heterogeneity, the methods and solutions introduced in this paper have been successfully applied within the INTEGRATE project context. Results suggest that the level of semantic interoperability required to manage patient data in modern clinical trials on breast cancer can be achieved with the proposed methodology.

W.3.3.2 - Recommending medical documents by user profile

Kleanthi Lakiotaki, Angelos Hliaoutakis, Serafim Koutsos, Euripides Petrakis

The overwhelmed amount of medical information available online, makes the use of automated recommendation methods essential for identifying relevant information according to user profile needs. This paper presents a method to address the problem of medical document classification into documents for medical professionals (experts) and non-professionals (consumers). Documents are represented by terms extracted from AMTEx, a medical document indexing method, specifically designed for the automatic indexing of documents in large medical collections, such as MEDLINE, and then mapped to the UMLS Semantic Network (SN) categories. Multiple Criteria Decision Analysis (MCDA) tools are applied to calculate the membership of each SN category to the document classification. Several factors such as the classification nature of the problem and the incorporation of common readability formulas are also examined.

W.3.3.3 - Med-Tree: A User Knowledge Graph Framework for Medical Applications

Maunendra Sankar Desarkar, Sandip Bhaumik, Sailesh Kumar Sathish, Satnam Singh, Rangavittal Narayanan

The field of Context and Intelligence, as a topic of pervasive computing, has been gaining due momentum. Typically, Context-Aware Intelligence is applied to understand the situation of the users and the users' behavior to provide adaptive services related to their situations. However, we have taken an orthogonal approach wherein we try to model the users' propositional knowledge and belief. This is achieved by building a connected graph model of topics based on the familiarity of the users, or on certain facts on which a fair level of belief is imposed by the user. In this paper, we propose to create person's belief graph, called Med-Tree, and explore its particular application in medical domain. We model a person's propositional knowledge by mining domain specific personal data sources, the domain in the present case being Healthcare, and provisioning an appropriate representation of such knowledge for wide variety of medical applications. Subject to privacy conditions, we open up the so called belief graph for establishing objective based social connections that get contextually bound. The Med-Tree allows personal medical queries enabling ad-hoc networks to be built in-order to service such queries. Leveraging on user's knowledge or belief graph the proposed Med-Tree could be exploited to provide better self-care and management.

W.3.3.4 - Querying Phenotype-Genotype Associations across Multiple Knowledge Bases using Semantic Web Technologies

Oya Deniz Beyan, Aftab Iqbal, Yasar Khan, Athos Antoniades, John Keane, Panagiotis Hasapis, Christos Georgousopoulos, Myrto Ioannidi, Stefan Decker, Ratnesh Sahay

Biomedical and genomic data are inherently heterogeneous and their recent proliferation over the Web has demanded innovative querying methods to help domain experts in their clinical and research studies. In this paper we present the use of Semantic Web technologies in querying diverse phenotype-genotype associations for supporting personalized medicine and potentially helping to discover new associations. Our initial results suggest that Semantic Web technologies has competitive advantages in extracting, consolidating and presenting phenotype-genotype associations that resides in various bioinformatics resources. The developed querying method could support researchers and medical professionals in discovering and utilizing information on published associations relating disease, treatment, adverse events and environmental factors to genetic markers from multiple repositories.

W.3.3.5 - A RF Sensor for in vivo Measurements of the Dielectric Properties of Anisotropic Tissue

Liang Zhang, Dongming Zhou, Peiguo Liu, Xiuzhen Dong

In this paper, a new sensor is referred to for the dielectric properties in vivo measurement of anisotropic tissue in radio frequency band. The simulative studies were performed in a frequency band ranged from 10MHz to 150MHz, which validate the potential ability of this sensor in vivo measurement of dielectric properties of anisotropic tissue. According to the simulative results, several technical expatiations were given, e.g. the influence of energy coupling and the sensor sensitivity to different anisotropy ratios with different probe dimension designs. Equivalent circuit model was proposed to calculate the dielectric properties of anisotropic tissue, results shows that the relative error of measurement can be kept blow 12%. This novel sensor may indicate the dielectric properties of anisotropic tissue conveniently and accurately in radio frequency band.

W.3.3.6 - Automated prediction procedure for Charcot-Marie-Tooth disease

Athanasios Alexiou, Maria Psiha, Georgia Theocharopoulou, Panayiotis Vlamos

The diagnosis of inherited peripheral neuropathies can be a challenging issue in several ways. Current research is focused on a multidisciplinary approach, developing new therapeutic strategies mainly involving online databases and repositories for sharing data and models used in some clinical trials. In this paper authors introduce the general architecture of an automated neural network based model for simulating the prediction procedure of Charcot-Marie-Tooth disease, according to the latest clinical studies.

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