



# **IWBBIO 2014**

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

**April 7-9  
Granada (Spain)**

# **PROGRAM**



# IWBBIO 2014 Short Program

<b>Monday, April 7, 2014</b>		
8:00-8:30	<b>IWBBIO Registration (Conference Desk)</b>	
8:30-10:15	<b>Session A.1 (SS10):</b> <i>"Effective Soft Computing Methods for Biomedical Signals"</i>	<b>Session B.1 (SS9):</b> <i>"Biomaterials in Biomedicine: Computational approaches"</i>
10:15-10:45	<b>COFFEE BREAK</b>	
10:45-12:00	<b>Session A.2 (SS1):</b> <i>"Multi-biomarker and informatics in cancer diagnosis"</i>	<b>Session B.2 (SS6):</b> <i>"ePathology - Realities and Perspectives"</i>
12:00-13:00	<b>Session A.3 (SS7):</b> <i>"Modelling of cellular pathways and disease"</i>	<b>Session B.3:</b> <i>"Biomedical Data Mining"</i>
13:00-14:30	<b>LUNCH</b>	
14:30-15:45	<b>Session A.4 (SS2 - Part I):</b> <i>"Discovery of non-coding and structured RNAs"</i>	<b>Session B.4 (SS14):</b> <i>"Better Oncology Treatment and Patient Outcomes by Using TRSC/TRSC-C and a Computerized Two-Way Communication System"</i>
15:45-17:00	<b>Session A.5 (SS2 - Part II):</b> <i>"Discovery of non-coding and structured RNAs"</i>	<b>Session B.5:</b> <i>"High Performance Computing for Sequence Analysis"</i>
17:00-18:00	<b>Session A.6-B.6: Poster Session (I)</b>	
20:00	<b>Light dinner at Carmen de los Mártires</b>	

<b>Tuesday, April 8, 2014</b>		
8:30-10:00	<b>Session A.7 (SS11):</b> <i>"Chaperone Therapy for Protein Misfolding Disorders with Brain Dysfunction"</i>	<b>Session B.7 (SS8 - Part I):</b> <i>"Integration of data, methods and tools in biosciences"</i>
10:00-10:30	<b>COFFEE BREAK</b>	
10:30-11:45	<b>Session A.8 (SS4 - Part I):</b> <i>"High Performance Computing in Bioinformatics"</i>	<b>Session B.8 (SS8 - Part II):</b> <i>"Integration of data, methods and tools in biosciences"</i>
11:45-13:00	<b>Session A.9 (SS4 - Part II):</b> <i>"High Performance Computing in Bioinformatics"</i>	<b>Session B.9 (SS3):</b> <i>"Biological Knowledge Visualization"</i>
13:00-14:30	<b>LUNCH</b>	
14:30-15:30	<b>Session A.10 (SS4 - Part III):</b> <i>"High Performance Computing in Bioinformatics"</i>	<b>Session B.10:</b> <i>"Bioinformatics tools and databases"</i>
15:30-16:25	<b>Session A.11 (SS13):</b> <i>"Computational analysis of gene regulatory elements with NGS data"</i>	<b>Session B.11:</b> <i>"Gene Expression and Microarrays"</i>
16:25-16:45		<b>Session B.11S:</b> <i>"Ethical Principles in Biotechnology and Bioengineering"</i>
16:45-17:30	<b>Session A.12-B.12: Poster Session (II)</b>	
20:00	<b>Gala dinner at Palacio de Santa Paula</b>	

Wednesday, April 9, 2014		
8:30-10:00	Session A.13: <i>"Biomedical Engineering and eHealth Applications"</i>	Session B.13 (SS15): <i>"Computational MRI: Theory, Dynamics and Applications"</i>
10:00-10:30	COFFEE BREAK	
10:30-11:45	Session A.14: <i>"Computational Proteomics and Biological Systems"</i>	Session B.14: <i>"High Performance Bioinformatics for Healthcare and Diseases"</i>
11:45-13:00	Session A.15: <i>"miRNA Regulation Networks"</i>	Session B.15: <i>"Computational Approaches for Genomics and NGS"</i>
13:00-14:30	LUNCH	
14:30-15:30	Session A.16 (SS16): <i>"Bioinformatical Approaches to Disordered Proteins"</i>	Session B.16 (SS18): <i>"Stochastic Modelling of Biological Systems"</i>
16:00	Visit to Alhambra	

### NOTE:

- All **Sessions A** will be held in Salón de Grados, Edificio Mecenás (just 20 meters from the Facultad de Ciencias).
- All **Sessions B** will be held in Salón de Grados, Facultad de Ciencias.
- The **Poster Sessions** will be held in the Hall of Facultad de Ciencias.
- The conference desk will be located close to the **Sessions A** room, Salón de Grados, Edificio Mecenás. It will open from Monday, April 7th at 8:00.

# IWBBIO 2014 Conference Venue

**Conference Desk**  
**Edificio Mecenas**

**Salón De Grados.**  
**SESSIONS A**  
**Edificio Mecenas**

**Salón De Grados.**  
**SESSIONS B**  
**Facultad de Ciencias**

**Hall**  
**POSTER SESSIONS**  
**Facultad de Ciencias**

**MAIN**  
**ENTRANCE**



# IWBBIO 2014 FULL PROGRAM

Monday, April 7, 2014

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**Session A.1 (SS10): "Effective Soft Computing Methods for Biomedical Signals"**

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*Chairman: Dr. Bekir Karlik*

Comparison Machine Learning Algorithms for Recognition of Epileptic Seizures in EEG

*Bekir Karlik and Sengul Bayrak Hayta*

A new computational measure for detection of extrapyramidal symptoms

*Jose Ignacio Aznarte, Sergio Iglesias-Parro, Antonio Ibañez-Molina and Maria Felipa Soriano*

The Optimization of Breathing Signals and Ventilatory Control with Nonlinear Respiratory Mechanics under Hypercapnia and Eucapnia

*Shyan-Lung Lin, Yu-Zhe Tsai and Andy Liao*

A Novel Feature Extraction Method for Heart Sounds Classification

*Yucel Koyigit*

Task Related & Spatially Regularized Common Spatial Patterns for Brain Computer Interfaces

*Ayhan Yuksel and Tamer Olmez*

Fuzzy Clustering of ECG Beats Using a New Metaheuristic Approach

*Berat Dogan and Tamer lmez*

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**Session B.1 (SS9): " Biomaterials in Biomedicine: Computational approaches"**

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*Chairmen: Drs Razvan Ghinea, Luis Javier Herrera and Maria del Mar Perez*

Predictive algorithms for determination of quantity of pigments within experimental dental resin composites from reflectance data

*Razvan Ghinea, Oscar E. Pecho, Luis Javier Herrera, Ana Maria Ionescu, Juan De La Cruz Cardona, Maria Purificacion Sanchez Sanchez, Rade D. Paravina and Maria Del Mar Perez Gomez*

Ultrasonic monitoring of artificial tissue mechanical properties in biorreactor

*Guillermo Rus, Nicolas Bochud, Juan Melchor, Laura Peralta, Juan Chiachio, Manuel Chiachio and Antonio Gomez*

FDTD simulations for ultrasound propagation in a 2-D cervical tissue model

*Laura Peralta, Guillermo Rus, Nicolas Bochud, Juan Melchor, Juan Chiachio and Manuel Chiachio*

Model-based probability of detection of pathologies in soft tissue

*Juan Melchor, Guillermo Rus, Nicolas Bochud, Laura Peralta, Juan Chiachio, Manuel Chiachio and Antonio Gomez*

Information-theory approach to model class assessment for tissue-engineered cultures  
consistence evolution

*Juan Chiachio-Ruano, Manuel Chiachio Ruano, Guillermo Rus-Carlborg, Nicolas  
Bochud, Laura Peralta Pereira and Juan Manuel Melchor Rodriguez*

Designing preterm neonatal cyanosis simulation

*Peter Peters, Frank Delbressine and Loe Feijs*

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**Session A.2 (SS1): "Multi-biomarker and informatics in cancer diagnosis"**

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**Chairman: Prof. Yaping Tian**

The mathematical models of serum HE4 and CA125 combined application to improve  
the pelvic tumor differential diagnosis rate

*Yaping Tian, Chuanxin Wang, Liming Cheng, Peng Zhang, Lin Guo, Wanli Liu,  
Zhongying Zhang, Yanchun Huang, Qishui Ou, Xinyu Wen, Yuelei Xing, Guixi  
Zheng, Ziyong Sun, Huijun Li, Aimin Zhang, Ying Chen, Wen Liu, Huiming Ye, Yi  
Xu, Yishan Huo and Jing Chen*

Exploration of ovarian cancer micro array data focus on gene expression patterns  
relevant to survival using artificial neural networks.

*Clare Coveney, Dong Tong, David Boocock, Robert Rees and Graham Ball*

High efficiency for activated KRAS detection from peripheral blood using weighted  
enzymatic gene chip array method

*Tai Feng Hsu, Ming Yii Huang, Hsueh Chiao Liu, Jia Yuan Chang, Jian Jhang  
Huang and Shiu Ru Lin*

HER-2/neu Breast Cancer Diagnosis Procedure, Based on Histopathology Image Analysis

*Martin Tabakov, Marta Tabakov, Halina Kwasnicka, Pawel Kozak and Bartosz Pula*

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**Session B.2 (SS6): "ePathology - Realities and Perspectives"**

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**Chairman: Dr. Thomas Schrader**

Image Quality Assessment in Digital Pathology - The Analysis of Background in Whole  
Slide Images

*Thomas Schrader, Anne Nadolny, Robert Piduch and Peter Hufnagl*

Automatic image quality assessment in digital pathology.

*David Ameisen, Christophe Deroulers, Valerie Perrier, Fatiha Bouhidel, Maxime  
Battistella, Luc Legre's, Anne Janin, Philippe Bertheau and Jean-Baptiste Yuns*

Web-based remote diagnosis system using virtual slide for routine pathology slides,  
analysis of discrepancies between virtual and real microscopic diagnosis.

*Ichiro Mori, Takashi Ozaki, Yasuteru Muragaki and Yoshiyuki Osamura*

Evaluation of cytokeratin-19 in breast cancer tissue samples: a comparison of automatic  
and manual evaluations of scanned tissue microarray cylinders

*Cristina Callau, Marylne Lejeune, Anna Korzynska, Marcial Garcia, Gloria Bueno,  
Ramon Bosch, Joaquin Jaen, Guifre Orero, Teresa Salvad and Carlos Lopez*

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**Session A.3 (SS7): "Modelling of cellular pathways and disease"**


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*Chairmen: Dr. Jean-Marc Schwartz and Dr. Marija Krstic-Demonacos*

In silico prediction of elementary mode fluxes

*Jean-Marc Schwartz and Peter Neal Taylor*

Applications of p53 interactome analysis to personalised drug discovery

*Michelle Hussain, Benjamin Stutchbury, Kun Tian, Rengul Atalay, Jean-Marc Schwartz and Marija Krstic-Demonacos*

Evolutionary and functional studies on the novel Hepatitis C virus core+1/ARF protein

*Ioly Kotta-Loizou*

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**Session B.3: "Biomedical Data Mining"**


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*Chairman: Dr. Vicky Dritsou*

Using Biomedical Terminologies to extract Noun Phrases for managing knowledge evolution

*Adila Merabti, Lina F. Soualmia and Stefan J Darmoni*

Computing Pathways in Bio-Models Derived from Bio-Science Text Sources

*Troels Andreassen, Henrik Bulskov, Jorgen Fischer Nilsson and Per Anker Jensen*

Comparing BioPortal and HeTOP: towards a unique biomedical ontology portal?

*Julien Grosjean, Lina F. Soualmia, Khedidja Bouarech, Clement Jonquet and Stefan J. Darmoni*

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**Session A.4 (SS2 - Part I): "Discovery of non-coding and structured RNAs"**


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*Chairman: Dr. Walter Moss*

In silico discovery of de novo structured RNAs in genomic and transcriptomic sequence

*Søren Mørk and Jan Gorodkin*

Identifying functional SNVs that map to non-coding regions of the genome and alter RNA Structure.

*Alain Laederach*

Comparative Detection of Processed Small RNAs in Archaea

*Christian Hoener Zu Siederdisen, Sarah Berkemer, Fabian Amman, Axel Wintsche, Sebastian Will, Sonja J. Prohaska and Peter Stadler*

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**Session B.4 (SS14): "Better Oncology Treatment and Patient Outcomes by Using TRSC/TRSC-C and a Computerized Two-Way Communication System"**


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*Chairmen: Dr. Arthur R. Williams and Dr. Phoebe D. Williams*

The Development and Application of an Oncology Therapy-Related Symptom Checklist for Adults (TRSC) and Children (TRSC-C)

*Arthur R. Williams, David D. Williams and Phoebe D. Williams*

The TRSC-C and Childhood Leukemia in Thailand and the USA: Symptom Occurrence/Severity and Care Strategies for Symptom Relief

*Phoebe D. Williams, Ubolrat Piamjariyakul and Jenna Degennaro*



The TRSC and Symptom Monitoring, Alleviation, and Self-Care among Mexican-Americans during Outpatient Cancer Treatments

*Phoebe D. Williams, Leticia S. Lantican, Julia O. Bader and Daniela Lerma*

Computers that Show Recognition of Patients' Symptoms

*Farrokh A. Alemi, Hosai Hesham, Arthur R. Williams, Phoebe D. Williams, Blaine Donley and Raya E. Kheirbek*

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**Session A.5 (SS2 - Part II): "Discovery of non-coding and structured RNAs"**

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**Chairman: Dr. Walter Moss**

Transcriptomic analysis of human liver identifies a novel class of regulatory RNAs in chronic viral hepatitis and associated cancer

*Praveen Sethupathy*

New frontiers in the investigation of structural functional RNA domains in viral genomes. Understanding the hepatitis C virus (HCV)

*Alfredo Berzal-Herranz and Cristina Romero-Lopez*

Detection of structural constraints and conformational transitions in the influenza virus RNA genome using structure predictions and mutual information calculations

*Alexander Gultyaev, Rene Olsthoorn, Monique Spronken and Ron Fouchier*

Analyses of non-coding RNAs generated from the Epstein-Barr virus W repeat region.

*Walter Moss*

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**Session B.5: "High Performance Computing for Sequence Analysis"**

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**Chairman: Dr. Andrei S. Alic**

Profiling and Taxonomy of Sequence Alignment Algorithms on Reconfigurable Platforms

*Xin Chang, Fernando A. Escobar, Carlos Valderrama and Vincent Robert*

AutoFlow: an easy way to build workflows

*Pedro Seoane, Rosario Carmona, Rocío Bautista, Dario Guerrero and M. Gonzalo Claros*

Inexact Sequence Mapping Study Cases: Hybrid GPU Computing and Memory Demanding Indexes

*Jose Salavert, Andres Tomas, Ignacio Medina and Ignacio Blanquer*

A Probabilistic Genome-Wide Gene Reading Frame Sequence Model

*Christian Theil Have and Soren Mork*

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**Session A.6-B.6: "Poster Session (I)"**

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Motif discovery in speech: application to monitoring Alzheimer's disease

*Dragana Nikolic, Anna Barney, Vanda Nemes and Peter Garrard*

Computational approach for modeling and testing NF- $\kappa$ B binding sites

*Marcin Pacholczyk, Karolina Smolinska, Marta Iwanaszko and Marek Kimmel*

Dynamic Gap Selector: A Smith Waterman Sequence Alignment Algorithm with Affine Gap Model Optimization

*Gianvito Urgese, Giulia Paciello, Andrea Acquaviva, Elisa Ficarra, Mariagrazia Graziano and Maurizio Zamboni*

Multiple-criteria decision making: application to medical devices

*Vladimir Rogalewicz and Ivana Jurickova*

Barriers to implementation of a clinical information system in an emergency department

*Ivana Jurickova and Pavla Hejmova*

Case study: Mobile X-ray equipment selection for a traumatology department using value engineering and multi-criteria decision methods

*Ivana Jurickova, Ales Kraina and Tereza Brazinova*

Automatically building database from biological ontology

*Zina Nakhla and Kaouther Nouira*

Statika: managing cloud resources, bioinformatics tools and data

*Alexey Alekhin, Evdokim Kovach, Pablo Pareja-Tobes, Marina Manrique, Eduardo Pareja, Raquel Tobes and Eduardo Pareja-Tobes*

Nispero: a cloud-computing based Scala tool specially suited for bioinformatics data processing

*Evdokim Kovach, Alexey Alekhin, Marina Manrique, Pablo Pareja-Tobes, Eduardo Pareja, Raquel Tobes and Eduardo Pareja-Tobes*

Acoustic Study of a Neonatal Intensive Care Unit: Preliminary Results

*Ganna Raboshchuk, Climent Nadeu, Blanca Muñoz Mahamud, Ana Riverola de Veciana and Santiago Navarro Hervas*

Optimal preictal period in seizure prediction

*Mojtaba Bandarabadi, Jalil Rasekhi, Cesar Teixeira and Antonio Dourado*

Revealing Helitron signatures in *Caenorhabditis elegans* by the Complex Morlet Analysis based on the Frequency Chaos Game Signals

*Imen Messaoudi, Afef Elloumi Oueslati and Zied Lachiri*

The impact of the quality filter for RNA-Seq data over differential expression profile

*Pablo C. Gomes de Sa, Siomar de Castro Soares, Adonney A. de Oliveira Veras, Anne C. Pinto, Luis Guimaraes, Vasco Azevedo, Artur Silva and Rommel Ramos*

An Automatic Wavelet Selection Scheme for Heart Sounds Denoising

*Omari Tahar and Bereksi-Reguig Fethi*

DIGITAL HUMAN MODEL AND MOTION CAPTURE TECHNIQUES FOR HOME KINESITHERAPY

*Karolina Grzechnik and Tadeusz Burczynski*

Analysis of ATM signaling pathway as an activator of p53 and NF- $\kappa$ B regulatory modules and the role of PPM1D

*Krzysztof Puszynski, Katarzyna Jonak, Monika Kurpas, Patryk Janus and Katarzyna Szoltysek*

Pervasive System for Searching the Appropriate Road: A Mobile Physician on Road Network Case Study

*Hanen Faiez and Jalel Akaichi*

The experimental model of lysozyme sustained release based on poly(3-hydroxybutyrate)-poly(ethylene glycol)/hydroxyapatite microparticles

*A.L. Zernov, E.V. Ivanova and K.V. Shaitan*

The experimental model of mesenchymal stem cells growth and differentiation based on application of porous scaffold from bacterial origin poly(3-hydroxybutyrate)-poly(ethylene glycol)

*I.I. Zharkova, E.A. Akulina, N.V. Andreeva and K.V. Shaitan*

The Necessity for Improvement of the Algorithms Used for In Silico Allergenicity Assessment of Novel Proteins

*Najaf Allahyari Fard*

Trajectory data warehouse modeling based on a Trajectory UML profile: Medical example

*Wided Oueslati and Jalel Akaichi*

Instrumented 30-s Chair Stand Test: evaluation of an exercise program in frail nonagenarians

*Nora Millor, Marisol Gomez, Pablo Lecumberri, Alicia Martinez-Ramirez and Mikel Izquierdo*

A semantic cache for queries optimization of Health care services communities

*Hela Limam and Jalel Akaichi*

CHEEK FORCE: A device for quantitative evaluation

*Monalise Berbert, Carlos Thomas and Rogerio Marczak*

A performance comparison between conventional SSVEP and Emokey based Emotiv EPOC matrix speller

*S M Abdullah Al Mamun*

Impact of missing genotype imputation on the power of Genome Wide Association Studies

*Lukasz Krol, Ghazi Alsbeih, Christophe Badie and Joanna Polanska*

Automatic Peptides Selection for Targeted Proteomics

*Yassene Mohammed, Dominik Domanski, Angela M. Jackson, Derek S. Smith, Andre M. Deelder, Magnus N. Palmblad and Christoph H. Borchers*

Discriminative Modeling of Cell Signaling as Bayesian Networks

*Ayşe Gul Yaman, Aybar C Acar, Volkan Atalay and Rengul Cetin-Atalay*

Data Recycling of Historical Records and Integration in New Information Systems in Cardiology service

*R. Penafiel, Alberto Guillen and Luis Javier Herrera Maldonado*

Development of Soft-Computing techniques capable of diagnosing Alzheimers Disease in its pre-clinical stage combining MRI and FDG-PET images

*Olga Valenzuela, Belen San-Roman, Francisco Ortuño, Jose Luis Bernier Villamor, Maria Jose Saez, Fernando Rojas and Ignacio Rojas*

Advanced Soft-Computing techniques and Clustering Algorithm for Gene Expression  
Microarray Data Classification.

*Olga Valenzuela, Fernando Rojas, Francisco Ortuño, Jose Luis Bernier, M. Jose  
Saez, Belen San-Roman, Luis Javier Herrera, Alberto Guillen, Ignacio Rojas*

Tuesday, April 8, 2014
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**Session A.7 (SS11): "Chaperone Therapy for Protein Misfolding Disorders with Brain Dysfunction"**

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*Chairman: Dr. Jose M. Garcia Fernandez*

Concept and Development of Chaperone Therapy for Protein Misfolding Diseases

*Yoshiyuki Suzuki*

Design and Synthesis of Bioactive Valienamine-type Chaperones

*Seiichiro Ogawa, Shinichi Kuno, Katsumi Higaki, Atsushi Takahashi and Eiji Nanba*

Pharmacological Chaperones by Design

*Jose M. Garcia Fernandez*

Enzyme Enhancement Therapy through non-competitive pharmacological chaperones

*Juan Aymami, Xavier Barril, Aida Delgado, Marc Reves, Rodolfo Lavilla, Katsumi Higaki, Ana Maria Garcia-Collazo, Laura Rodriguez-Pascau, Elena Cubero, Pilar Pizcueta and Marc Martinell*

Structural basis of pharmacological chaperoning for human  $\beta$ -galactosidase

*Toshiyuki Shimizu*

Identification and characterization of chaperone compounds for human  $\beta$ -galactosidase deficiency

*Eiji Nanba and Katsumi Higaki*

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**"Session B.7 (SS8 - Part I): "Integration of data, methods and tools in biosciences"**

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*Chairman: Dr. Vesna Pajic*

Integration of data in biosciences

*Vesna Pajic, Gordana Pavlovic Lazetic, Dragana Dudic, Dragica Radovanovic and Jelena Kozoderovic*

A Machine Learning Approach to Enhance Scoring Performance in Docking-Based Virtual Screening Experiments: COX-1 as a Case Study

*Candida Silva, Pedro Carreiras, Elsa Henriques, Carlos Simoes and Rui Brito*

Omic Data Modelling for Information Retrieval

*Chloe Cabot, Julien Grosjean, Romain Lelong, Arnaud Lefebvre, Thierry Lecroq, Lina F. Soualmia and Stefan J. Darmoni*

Numerical Simulation of ISFET Structures for BioSensing Devices with TCAD Tools

*Daniele Passeri, Arianna Morozzi, Keida Kanxheri and Andrea Scorzoni*

Mining Associations for Organism Characteristics in Prokaryotes ? an Integrative Approach

*Gordana Pavlovic Lazetic, Vesna Pajic, Nenad Mitic, Jovana Kovacevic and Milos Beljanski*

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**Session A.8 (SS4 - Part I): "High Performance Computing in Bioinformatics"**


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*Chairmen: Drs. Horacio Perez-Sanchez, Jose M. Cecilia and Ivan Merelli*

The role of High Performance Computing in Bioinformatics

*Horacio Perez-Sanchez, Jose M. Cecilia and Ivan Merelli*

Experience with Lamport Clock Ordered Events with Intel Threading Building Blocks in a Glucose-Level Prediction Software

*Tomas Koutny*

Hermite Polynomial Characterization of Heartbeats with Graphics Processing Units

*Alberto Gil, Gabriel Caffarena, David G. Marquez and Abraham Otero*

High-throughput, Scalable, Quantitative, Cellular Phenotyping using X-Ray Tomographic Microscopy

*Kevin Mader, Leah-Rae Donahue, Ralph Müller and Marco Stampanoni*

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**"Session B.8 (SS8 - Part II): "Integration of data, methods and tools in biosciences"**


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*Chairman: Dr. Vesna Pajic*

LPS: a strategy for the generation of longer DNA sequence fragments from short reads

*Francisco Vera Voronisky, Ansel Y. Rodriguez Gonzalez, Ivan Olmos Pineda, Patricia Sanchez Alonso, Candelario Vazquez Cruz and Jesus A. Gonzalez*

In Search of Predictive Models for Inhibitors of 5-alpha Reductase 2 Based on the Integration of Bioactivity and Molecular Descriptors Data

*Joana Sousa, Rui Brito, Jorge Salvador and Cndida Silva*

Assisted prescription for improving treatments in Obstetrics-Gynecology Department

*Mihaela Marcella Crisan-Vida, Oana Lupsa and Lacramioara Stoicu-Tivadar*

Integrating Expression Data from Different Microarray Platforms in Search of Biomarkers of Radiosensitivity

*Anna Papiiez, Paul Finnon, Christophe Badie, Simon Bouffler and Joanna Polanska*

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**Session A.9 (SS4 - Part II): "High Performance Computing in Bioinformatics"**


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*Chairmen: Drs. Horacio Perez-Sanchez, Jose M. Cecilia and Ivan Merelli*

Entropy-based High Performance Computation of Boolean SNP-SNP Interactions Using GPUs

*Carlos Riveros, Manuel Ujaldon and Pablo Moscato*

Evaluating mixed HTC/cloud approaches for parameter sweep applications in systems biology

*Ivan Merelli, Ettore Mosca, Daniele Cesini, Elisabetta Ronchieri and Luciano Milanese*

Design of a Generic Architecture for executing Bioinformatics Workflows on Distributed Infrastructures

*Abel Carrion, Ignacio Blanquer, Miguel Caballer, Cristina Yenyxe Gonzalez and Ignacio Medina*

An Efficient Solvent Accessible Surface Area calculation applied in Ab Initio Protein Structure Prediction

*Daniel Bonetti, Horacio Perez-Sanchez and Alexandre Delbem*

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**Session B.9 (SS3): "Biological Knowledge Visualization"**

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**Chairman: Dr. Rodrigo Santamaria**

Generalized macro level models of amino acid sequences using passive electrical circuits

*Roger Marshall*

Exploratory Visualization of Misclassified GPCRs from their transformed unaligned sequences using manifold learning techniques

*Martha Ivon Cardenas, Alfredo Vellido, Caroline König, Rene Alquezar and Jesus Giraldo*

Mapping regional changes in the glycerophosphocholine second messenger lipidome following brain injury using CIRCOS

*Graeme Taylor, Hongbin Xu, Andrew Syrett and Steffany Bennett*

Multi-dimensional anatomical representation: A volumetric comparison of the C57BL/6 and N3 C57BL/6 x 12- SV mouse brain modeled from serial section using Autodesk Maya

*Stephen Fai, Katie Wurts, Andrew Syrett, Brendan Trickey, Nico Valenzuela and Steffany Bennett*

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**Session A.10 (SS4 - Part III): "High Performance Computing in Bioinformatics"**

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**Chairmen: Drs. Horacio Perez-Sanchez, Jose M. Cecilia and Ivan Merelli**

Parallel Computation of Non-Bonded Interactions in Drug Discovery: Nvidia GPUs vs. Intel Xeon Phi

*Jianbin Fang, Ana Lucia Varbanescu, Baldomero Imbernon, Jose Cecilia and Horacio Perez-Sanchez*

Accelerating Phylogenetic Inference on GPUs: an OpenACC and CUDA comparison

*Lidia Kuan, Joao Neves, Frederico Pratas, Pedro Tomas and Leonel Sousa*

High Performance Computing Studies of RNA Nanotubes

*Shyam Badu, Roderik Melnik, Maxim V. Paliy, Sanjay Prabhakar, Bruce A. Shapiro and Ali Sebetci*

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**Session B.10: "Bioinformatics Tools and Databases"**

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**Chairman: Dr. Jean-Fred Fontaine**

Bio4j: bigger, faster, leaner

*Pablo Pareja-Tobes, Alexey Alekhin, Evdokim Kovach, Marina Manrique, Eduardo Pareja, Raquel Tobes and Eduardo Pareja-Tobes*

Massive Automatic Functional Annotation - MAFA

*Cristian Alejandro Rojas Quintero, Nelson Enrique Vera Parra and Jose Nelson Perez Castillo*

MG7: A fast horizontally scalable tool based on cloud computing and graph databases for microbial community profiling

*Evdokim Kovach, Alexey Alekhin, Marina Manrique, Pablo Pareja-Tobes, Eduardo Pareja, Raquel Tobes and Eduardo Pareja-Tobes*

Advancing Lipidomic Bioinformatic Technologies: Visualization and Phospholipid Identification (VaLID) version 3.0

*Graeme S.V Mcdowell, Alexandre P. Blanchard, Daniel Figeys, Stephen Fai and Steffany A.L. Bennett*

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**Session A.11 (SS13): "Computational analysis of gene regulatory elements with NGS data"**

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*Chairman: Dr. Philipp Bucher*

Principles of ChIP-seq Data Analysis Illustrated with Examples

*Giovanna Ambrosini, Rene Dreos and Philipp Bucher*

Transcription Factor Binding Site Detection Algorithm Using Distance Metrics Based on a Position Frequency Matrix Concept

*Mohammad Al Bataineh, Lun Huang and Guillermo Atkin*

TATA-box binding and nucleosome positioning are alternative pathways for transcription start site selection in eukaryotic promoters

*Rene Dreos, Giovanna Ambrosini and Philipp Bucher*

Changes in heat shock duration influence regulatory schemes of HSF1 activity.

*Marta Iwanaszko, Patryk Janus and Marek Kimmel*

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**Session B.11: "Gene Expression and Microarrays"**

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*Chairman: Dr. Marcin Pacholczyk*

Implications of RBBP6 in various types of cancer

*Firdous Khan, Mushal Allam, Marius Tincho and Ashley Pretorius*

Automatic detection of outlying microarrays using multi-array quality metrics

*Michal Marczyk, Lukasz Krol and Joanna Polanska*

Formal Concept Analysis and Knowledge Integration for Highlighting Statistically Enriched Functions from Microarrays Data.

*Sidahmed Benabderrahmane*

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**Session B.11S: "Ethical Principles in Biotechnology and Bioengineering"**

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Biotechnology, Biomedicine and the Precautionary Principle

*Robin Attfield*



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**Session A.12-B.12: "Poster Session (II)"**

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Shape of a dilution curve as the consequence of stochasticity within microcirculation

*Victor Kislukhin*

Physicochemical properties of the modeled structure of astacin metalloprotease moulting enzyme NAS-36 and Mapping the Druggable Allosteric Space of *Heamonchus contortus*, *Brugia malayi* and *Ceanorhabditis elegans* via Molecular Dynamics Simulation

*Om Prakash Sharma, Sonali Agrawal and M. Suresh Kumar*

Identification of Potent Inhibitors for Resistant Form of Chronic Myelogenous Leukaemia (CML)

*Hemanth Naick B, Om Prakash Sharma, Muthuvel Suresh Kumar and Baskaran Rajasekaran*

Comparison of pregnancy predictive models applied to women who received IVF/ICSI in Valencia (Spain) using ROC curves

*Ana Debon, Patricia Carracedo and Inmaculada Molina*

Applying Stacked and Cascade Generalizations to B-cell Epitope Prediction

*Yuh-Jyh Hu, Shun-Chien Lin and Yu-Lung Lin*

An Interactive X-Ray Image Segmentation Technique for Bone Extraction

*Cristina Stolojescu-Crisan and Stefan Holban*

Sequencing by Ligation with Double-Labeled Fluorescent Probes

*Dan Pu, Jing Chen and Pengfeng Xiao*

Fast Parallel Bayesian Networks Reconstruction with BNFinder

*Alina Frolova and Bartek Wilczynski*

Patient Trajectory Modeling and Analysis

*Jalel Akaichi and Marwa Manaa*

N-body Information Theory (NbIT) Analysis of Rigid-Body Dynamics in Intracellular Loop 2 of the 5-HT<sub>2A</sub> Receptor

*Michael V. Levine, Jose Manuel Perez-Aguilar and Harel Weinstein*

Doctors and researchers: integrating data for bipolar disorder studies

*Patricia Rodriguez Tome, Carla Melis, Raffaella Ardu, Caterina Chillotti, Maria Del Zompo, Alessio Squassina and Giovanni Severino*

Fully Automatic Renal Parenchyma Volumetry in LDA-based Probability Maps Using Variational Outer Cortex Edge Alignment Forces

*Oliver Gloger, Volkmar Liebscher, Klaus Tönnies and Henry Völzke*

Positioning Method Based on Infrared Spectrum Detection of Neurotransmitter for Electrical Nerve Stimulation after Spinal Cord Injury

*Min Nie and Guang Yang*

Specificities of Medical Devices Affecting Health Technology Assessment Methodology

*Vladimir Rogalewicz and Ivana Jurickova*

Supervised Retinal Vessel Segmentation Based on Neural Network Using Broader Aging Dataset

*Mohd Zulfaezal Che Azemin, Fadilah Abd Hamid, Mohd Izzuddin Mohd Tamrin, and Anang Hdaya Muhamad Amin*

Label-free detection of viruses using liquid crystals on a polymeric surface with periodic nanostructures

*Chang-Hyun Jang and Dong Min Kim*

Improving Stability of Feature Selection for Brain Tumour Diagnosis Using 1H-MRS Data

*Albert Vilamala and Lluis A. Belanche*

Stress-strain analyses of the jaws with multiple keratocysts before and after surgery

*Josef Danek, Tatjana Dostalova, Milan Hubacek and Nima Mahdian*

Intelligent System for Premature Babies Healthcare at Home based on Case-based Reasoning

*Beatriz Lopez, Fco. I. Gamero, Jordi Coll, Natlia Mordvaniuk, Abel Lopez-Bermejo and Eva Bargallo*

Quantitative Analysis of Pathological Mitochondrial Morphology in Neuronal Cells in Confocal Laser Scanning Microscopy Images

*Herbert Süße, Wolfgang Ortmann, Janin Lautenschläger, Christian Lautenschläger, Marco Körner, Julian Grosskreutz and Joachim Denzler*

PETRA: Multivariate analyses for neuroimaging data

*Fermin Segovia Roman, Ignacio Alvarez Illan, Diego Salas Gonzalez, Francisco Jesus Martinez Murcia, Christophe Phillips, Carlos Garcia Puntonet, Javier Ramirez Perez de Inestrosa and Juan Manuel Gorriz Saez*

Liposomes in polymer matrix. Stability of liposomes in PEG 400 and PEG 8000 solutions.

*Magdalena Bajgrowicz, Jerzy Detyna and Marek Langner*

Biochemical Reactions as Renewal Processes: the case of mRNA Degradation

*Paolo Paradisi and Davide Chiarugi*

An Effective 3-Dimensional Regional Myocardial Strain Computation Method with Displacement ENcoding with Stimulated Echoes (DENSE) in Dilated Cardiomyopathy Patients and Healthy Subjects

*Julia Kar, Andrew Knutsen, Kevin Kulshrestha, Brian Cupps and Michael Pasque*

A New Algorithm for Fetal QRS Detection in Abdominal Recordings

*Bouabida Zohra, Hadj Slimane Zinne Eddine and Bereksi Reguig Fethi*

Voice controller for Image Guided Surgery and per-sonalized Interactive Visualisation

*Andoni Beristain, Alesssandro De Mauro, Koen Van De Weyer and Dominique Segers*

Infectious disease risk from anti-psychotic drug use: A population-based study

*Usman Iqbal and Yu-Chuan Li*

In-silico approaches to sequence and structure based scrutiny of nonsynonymous SNPs and synteny of ACAA2 for its implicated role in metabolomics.

*Sidrah Anjum*

An Integrative Analysis of ncRNA-mRNA Using Co-expression Network to Discover Potential Contributions of Coding-non-coding RNA Clusters

*Li Guo, Yang Zhao, Sheng Yang, Hui Zhang and Feng Chen*

Multi-point accelerometric detection and principal component analysis of heart sounds

*Simone De Panfilis, Carlo Moroni, Fabrizio Pompili, Giorgio Parisi and Rosario Cassone*

Docking analysis and catalytic site prediction of azoreductase in *E. coli*, with a wide range of industrially important azodyes

*Samrat Adhikari, Samudra Sutradhar, Nangkyntiewbor Jungai, Bikash Thakuria and Gopesh Paul*

Computational docking analysis on selective inhibition and binding affinity of synthetic inhibitors towards Matrix Metalloproteinase (MMPs) isoforms

*Sudandiradoss C and Petrek Martin*

An improved Fuzzy Clustering methodology applied to the study of Protein Conformational Ensembles

*Duhu Man, Isabel Maria Timon-Perez, Jesus Soto-Espinosa, Antonio Flores-Sintas, Jose M. Cecilia and Horacio Perez-Sanchez*

Determination of changes in plasma structure during extracorporeal circulation - studies by ATR-FTIR spectroscopy and machine learning methods

*Sylwia Olsztynska-Janus, Barbara Kmiecik, Bartosz Krawczyk and Malgorzata Komorowska*

Wednesday, April 9, 2014
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**Session A.13: "Biomedical Engineering and eHealth Applications"**


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*Chairman: Dr. Gabriel Caffarena*

Evaluating the effects of signal segmentation on activity recognition

*Oresti Baños, Juan Manuel Galvez, Miguel Damas, Alberto Guillen, Luis Javier Herrera, Hector Pomares and Ignacio Rojas*

A Supervised Cooperative Learning System for Early Detection of Language Disorders

*Maria Luisa Martin Ruiz, Miguel angel Valero Duboy, Ivan Pau de La Cruz, Maria Peñafiel Puerto and Carmen Torcal Loriente*

Improvement in the accuracy of Nuclear Magnetic Resonance spectrum analysis by automatic tuning of phase correction algorithms.

*Franciszek Binczyk, Rafal Tarnawski and Joanna Polanska*

Analysis of Respiratory Flow Signals to Identify Success of Patients on Weaning Trials

*Hernando Gonzalez Acevedo, Carlos Arizmendi and Beatriz Giraldo*

A novel framework to enhance scientific knowledge of cardiovascular MRI biomarkers and their application to pediatric cardiomyopathy classification

*Vanathi Gopalakrishnan, Prahlad Menon and Shobhit Madan*

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**Session B.13 (SS15): "Computational MRI: Theory, Dynamics and Applications"**


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*Chairman: Dr. Omotayo Bamidele Awojoyogbe*

Resolving the enhanced flow parameters for an indepth analysis of the MRI-Neuroimaging

*Moses Emetere, Bamidele Awojoyogbe, Uno Uno, Kasim Isah and Michael M. Dada*

Computational Magnetic Resonance Imaging based on bloch NMR flow equation and bessel functions

*Bamidele Omotayo Awojoyogbe, Michael Oluwaseun Dada and Adewale Omoniyi Adesola*

Multiple Sclerosis lesion segmentation using Active Contours model and adaptive outlier detection method

*Foued Derraz, Antonio Pinti, Laurent Peyrodie, Miloud Boussahla, Hechmi Toumi and Patrick Hautecoeur*

Computational phase contrast magnetic resonance imaging based on legendre polynomials

*Michael Oluwaseun Dada and Omotayo Bamidele Awojoyogbe*

Computational model of NMR molecular dynamics for the analysis blood brain barrier

*Michael Oluwaseun Dada, Omotayo Bamidele Awojoyogbe and Simona Baroni*

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**Session A.14: "Computational Proteomics and Biological Systems"**


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**Chairman: Dr. Peter Tompa**

ProteINSIDE: a web service to computerize a systematic and integrative analysis of protein's biological knowledge

*Nicolas Kaspric, Brigitte Picard, Matthieu Reichstadt, Jeremy Tournayre and Muriel Bonnet*

Protein Fold Classification using Kohonen's Self-Organizing Map

*Ozlem Ozbudak and Zümray Dokur*

A framework for modelling spatially dependent interactions of biological systems in CCP

*Davide Chiarugi, Moreno Falaschi, Diana Hermith and Carlos Olarte*

Rewriting Logic and Symbolic Systems Biology applied to EGF Signaling Pathway

*Gustavo Santos Garcia, Javier De Las Rivas and Carolyn Talcott*

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**Session B.14: "High Performance Bioinformatics for Healthcare and Diseases"**


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**Chairman: Dr. Vanathi Gopalakrishnan**

Blood Vessel Segmentation in Retinal Images based on Local Binary Patterns and Evolutionary Neural Networks

*Antonio Rodriguez-Jimenez and Enrique J. Carmona*

Outlier detection for single particle analysis in Electron Microscopy

*Carlos O.S. Sorzano, Javier Vargas, Jose Miguel de La Rosa-Trevin, Airen Zaldivar-Peraza, Joaquin Oton, Vahid Abrishami, Ignacio Foche, Roberto Marabini, Gabriel Caffarena and Jose M. Caraza*

2D and 3D Alignment for Electron Microscopy via Graphics Processing Units

*Eduardo Garcia de La Cueva, Miguel Mateo de La Puente, Alessandro Deideri, Gabriel Caffarena, Carlos O.S. Sorzano and Ana Iriarte*

Application of parallel blind docking with BINDSURF for the study of platinum derived compounds as anticancer drugs

*Jose P. Ceron Carrasco, Javier Cerezo, Jose Zuñiga, Alberto Requena, Julia Contreras-Garcia, Sonali Chavan, Miguel Manrubia-Cobo, Baldomero Imbernon, Jose M. Cecilia and Horacio Perez-Sanchez*

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**Session A.15: "miRNA Regulation Networks"**


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**Chairman: Dr. Mohammad Al Bataineh (to be confirmed)**

Model-based design of synthetic networks

*Liliana Ironi and Diana X Tran*

miRNAO: An Ontology Unfolding the Domain of microRNAs

*Vicky Dritsou, Pantelis Topalis, Elvira Mitraka, Emmanuel Dialynas and Christos Louis*

Inference of Circadian Regulatory Networks

*Marco Grzegorzczuk, Andrej Aderhold, V. Anne Smith and Dirk Husmeier*

miR-SEA: miRNA Seed Extension based Aligner Pipeline for NGS Expression Level Extraction

*Gianvito Urgese, Giulia Paciello, Claudio Isella, Enzo Medico, Enrico Macii, Elisa Ficarra and Andrea Acquaviva*

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**Session B.15: "Computational Approaches for Genomics and NGS"**

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**Chairman: René Dreos**

An Integrated Approach to Comparative Assembly

*John Healy and Desmond Chambers*

Hkera, a human transcriptome partitioner

*Austin Chiang, Grace Shaw and Ming-Jing Hwang*

Robust Error Correction for De Novo Assembly via Spectral Partitioning and Sequence Alignment

*Andrei Alic, Andres Tomas, Jose Salavert Torres, Ignacio Medina and Ignacio Blanquer*

Using a Random Forest proximity measure for variable importance stratification in genotypic data

*Jose A. Seoane, Ian N.M. Day, Colin Campbell and Tom R. Gaunt*

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**Session A.16 (SS16): "Bioinformatical Approaches to Disordered Proteins"**

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**Chairman: Dr. Istvan Simon**

Predicting functional sites in disordered proteins - implications in disease

*Balint Meszaros, Istvan Simon and Zsuzsanna Dosztanyi*

Dynamic approaches to structural ensembles of intrinsically disordered proteins

*Peter Tompa*

The Roles of Short Linear Motifs in Human Diseases

*Bora Uyar and Toby Gibson*

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**Session B.16 (SS18): "Stochastic Modelling of Biological Systems"**

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**Chairmen: Dr. Davide Chiarugi and Dr. Paolo Paradisi**

Multiscale flexible docking of the fragment of troponin I to a two-domain protein - troponin C

*Jacek Wabik, Mateusz Kurcinski and Andrzej Kolinski*

Incorporating covariates in a flowgraph model for bladder carcinoma

*Gregorio Rubio, Belen Garcia-Mora, Cristina Santamaria and Francisco Santonja*

Analysis of risk factors of hip fracture with causal Bayesian networks

*Alex Aussem, Pascal Caillet, Zara Klemm, Maxime Gasse, Anne-Marie Schott and Michel Ducher*

VIRTUAL PRESENTATIONS
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Hospital bed management support using regression data mining models

*Sergio Oliveira, Filipe Portela and Manuel Filipe Santos*

Introducing the Concept of Second Neighbours to FPNC algorithm for Improving the Functional Modules Detection

*Mohammad Rahman and Nafisa Chowdhury*

The Binding Sites of miR-619-5p, miR-5095, miR-5096 and miR-5585-3p in the Human mRNAs

*Anatoly Ivashchenko, Olga Berillo, Anna Pyrkova, Raigul Niyazova and Shara Atambayeva*

Real-time True-color Stereo Visualization of Multi-channel 3D CLSM Images Based on CUDA

*Yakang Dai, Yunhai Zhang, Zhiyong Zhou, Haomin Yang and Xiaojun Xue*

Computation Based Disease Associations in Disease Inference

*Preeti Kale and Jagannath Aghav*

Impact of Single amino acid Polymorphisms in Protein-Protein interactions in tumorigenic cluster A and cluster B of VHL: Computational molecular dynamics

*George Priya Doss C, Chiranjib Chakraborty, Siddarth R, Nagasundaram N, Magesh R, Udhayakumar S, Priyanka N and Priyadarshini Christy J*

Physiological Data Stream from Monitoring System in Intensive Care Unit

*Fahmi Ben Rejab, Kaouther Nouira and Bilel Amri*

State and Parameter Estimation of a Neural Mass Model from Electrophysiological Signals during Induced Status Epilepticus

*Armando Lopez-Cuevas, Bernardino Castillo-Toledo, Laura Medina-Ceja and Consuelo Ventura-Mejia*

Cardiac Arrhythmia Classification Using a combination of Quadratic Spline Wavelet Transform and Artificial Neural Classification Network.

*Jose Antonio Gutierrez Gnechi, Rodrigo Morfin Magaa, Adriana Del Carmen Tellez Anguiano, Daniel Lorias Espinoza and Enrique Reyes-Archundia*

Electrical Impedance Spectroscopy imaging of the thigh using current excitation frequencies in the mid- $\beta$  frequency dispersion range.

*Jose Antonio Gutierrez Gnechi, Miguel Angel Mendoza Mendoza, Carlos Eduardo Guillen Nepita, Daniel Lorias Espinoza and Adriana Del Carmen Tellez Anguiano*

Global Topology of Codon Usage Equality Networks of Escherichia Coli Essential Genes

*Mohammad-Hadi Foroughmand-Araabi, Sama Goliaei and Bahram Goliaei*

A parallel approach for accelerated parameter identification of Gene Regulatory Networks

*M. Tariq Saeed and Jamil Ahmad*

Enhancing Hotelling's T<sup>2</sup> Statistic using Shrinkage Covariance Matrix for Identifying Differentially Expressed Gene Sets

*Suryaefza Karjanto, Rasimah Aripin, Norazan Mohamed Ramli and Nor Azura Md Ghani*

Hamming Distance based Binary PSO for Feature Selection and Classification from high dimensional Gene Expression Data

*Haider Banka and Suresh Dara*

ERROR-RELATED POTENTIAL -IN BRAIN- ACTUATED WHEELCHAIR

*Mana Taeb, Mohamad.B Shamsollahi, Farnaz Ghassemi and Behnam Asefi*

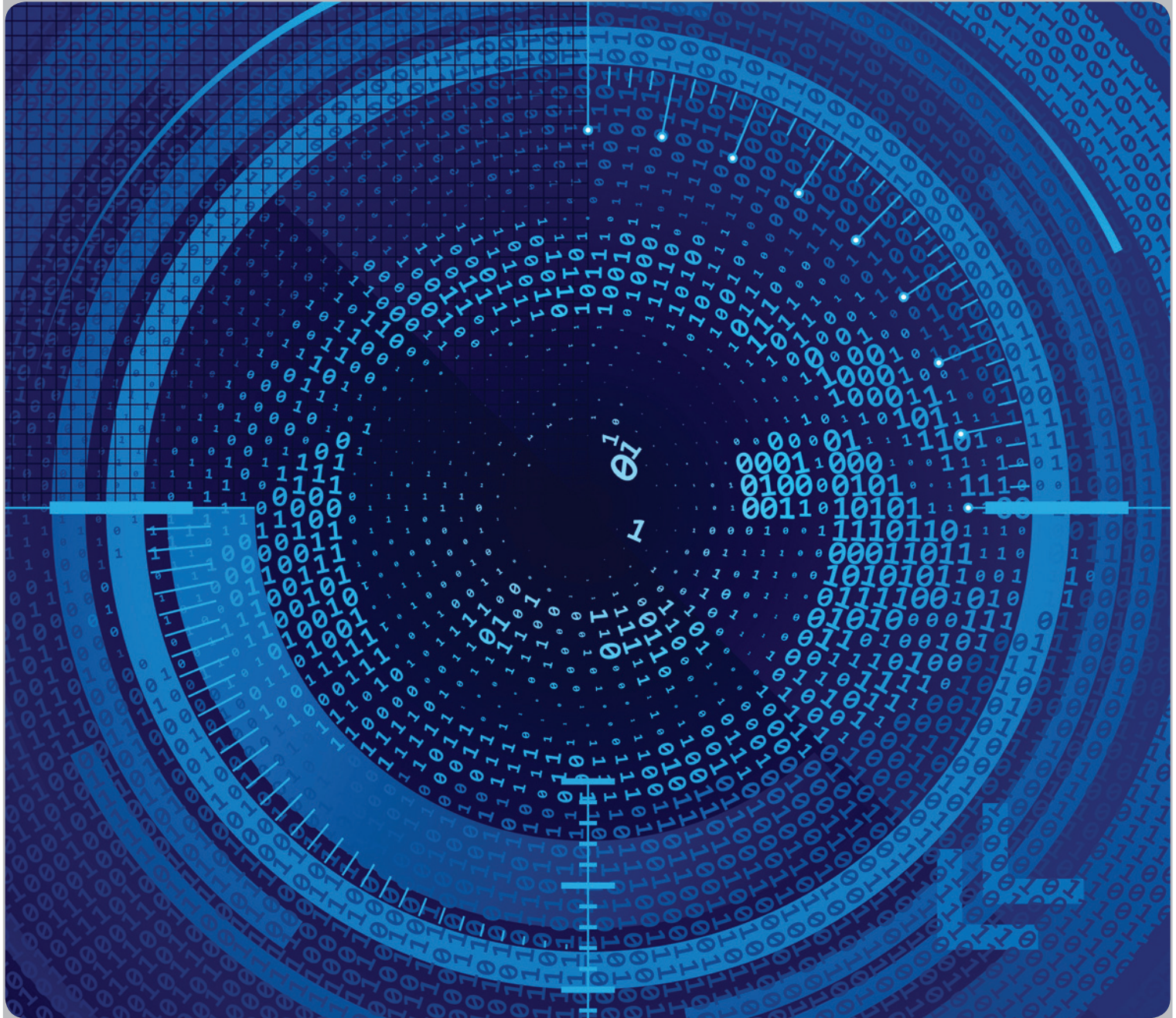
Influence of the Length in Biomimetic Ion Channels Based on Derivatized  $\alpha,\gamma$ -Self Assembled Peptide Nanotubes. A Molecular Dynamics study.

*Rebeca Garcia-Fandino, Juan Outeiral, Saulo Vazquez and Juan R. Granja*



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