BMIINT Editorial

SCENE. Entering the post-genomics epoch a new challenging mission is posted: to bring innovative biomedical research findings directly to the clinic and the bedside. The mission could be accomplished by *intersecting* the clinical, biological and information sciences. Endeavour is inspired by the needs raised by genomic and personalised medicine; it targets the *in-silico* biology domain; and, it is enabled by the transition to *interdisciplinary* principles and orientation. Transition is guided by the **'-***omics*' revolution as realised by advances in transcriptomics, proteomics, metabolomics, physiomics *and* nanomedicine. The '-omics' levels extends traditional clinical data models and medical decision making in two sides: on the one side to include genotypes, and on the other to include (when appropriate) '-omics' findings - the phenotypes. Yet integration is not easy simply because at both ends (genotype, phenotype) the amount of available data is immense, and complexity of processes is high. At the up-stream (or research) level scientists may be interested in the investigation between genotype-phenotype information to form *associations* and *patterns* of disease and *susceptibility* indices. At the middle-stream (industrial level) technology and service providers are interested in embedding research advances into concrete products and services via intelligent devices. Device impact is further enhanced by advances in the '*nano'* field, as expressed by nanomaterials, nanomedicine and nanoinformatics. At the down-stream (clinical theatre) level healthcare professionals (and patients as well) look forward to apply new technology on the vision of continuously improving social welfare decision making**.**

Actors & **Director.** The primary item in the respective multidisciplinary R&D agenda is *translational research* with *Biomedical Informatics* (BMI) as the driver, and *Artificial Intelligence* (AI) called to provide the needed analytical and decision-making machinery. **BMIINT** liaisons the clinical, biology, core- and Bioinformatics fields, and provides a forum for the presentation of advances at the conjunction of BMI and AI components and procedures. It takes an interdisciplinary perspective and focuses on theory, methods, techniques, tools, systems and services, which support integration, management and intelligent analysis of respective bio-related information and data sources. Emphasis is placed on the *repositioning* of methods and techniques from other domains of application into the BMIINT frontier

Plot(s)**.** BMIINT includes nine papers, which report on R&D work with broad coverage of BMIINT context. Article by Martin-Sanchez and colleagues, reports the organizational aspects and scientific aspects in relation to the COMBIOMED: A Cooperative Thematic Research Network on COMputational BIOMEDicine in Spain. The network focuses on gene-disease associations, pharmainformatics and decision support systems at the point of care. Work reported by Bonsma and Vrijnsen; Exarchos, Goletsis and Fotiadis focus on heterogeneous data integration. Bonsma and Vrijnsen provide an enrichment of the OGSA-DAI web-services framework to access medical images and microarray data; work carried out in the context of Advanced Clinico-Genomic Trials in Cancer (ACGT) project (FP6-IST-2005-026996). Exarchos et al., integrate clinical, imaging and genomic data sources to induce reliable biomarkers for the progression of oral cancer – work relates to the NeoMark project (FP7-ICT-2007-224483). Related to the two aforementioned papers is the work presented by Sfakianakis and colleagues as well by Koumakis and colleagues. Sfakianakis and colleagues endeavour on the

daily work of clinicians and bio-statisticians, develop usability criteria and propose a front-end interface layer for a Grid based architecture able to support huge computational tasks. The work of Koumakis and colleagues takes a step backwards and captures scientific-workflow design and operation specifics with due regard to a clinical scenario that achieves the seamless integration of clinico-genetic heterogeneous data sources, and the discovery of indicative SNP-phenotype associations and predictive models. Both articles draw from the ACGT project experience while Koumakis and colleagues work relates also to the GEN2PHEN project (co-funded via the European Commission, Health theme, project number 200754). Remaining articles focus on more specific BMIINT subjects. Tsiliki and colleagues overview requirements and context of cross-platform integration; the subject has immense interest, given the multitude of microarray platforms. Blachon and colleagues as well as Kanterakis and colleagues bring into BMIINT a systems biology flavor. Blachon and colleagues work is on the Ewing sarcoma; using a comparative genomic hybridization array they present data collection and preprocessing procedures and then move on to a gene influence network to model discovery of links between gene copy number variations and expression level variations – work relates to the SITCON project (from the ANR BIOSYS-2006 program). Kanterakis and colleagues reports on a methodology that couples gene-regulatory networks and microarray gene-expression data to reveal and identify molecular paths that differentiate between different disease phenotypes (with targets to the Wilms tunor domain) – work also relates to the ACGT project. Finally, Vegoudakis and colleagues report on an interface that supports patterns matching over genomic and proteomic sequences on a Grid based system – work relates to the EGEE project, co funded by the European Commission.

Elias Siores, University of Bolton, UK
Srdjan Stankovic, University of Belgrad, YU
Ioannis Tollis, University of Crete & FORTH / Institute of Computer Science (ICS), GR
Oswaldo Trelles, University of Malaga, ES
Ioannis Tsamardinos, University of Crete & FORTH-ICS, GR
Manolis Tsiknakis, FORTH / Institute of Computer Science (ICS), GR
Michael Zervakis, Technical University of Crete, GR

The Chairs of AIAI 2009/BMIINT

Dr. George Potamias, Institute of Computer Science, BMI Lab, FORTH – Heraklion, Greece

Prof. Vassilis Moustakis, Institute of Computer Science, BMI Lab, FORTH & Technical University of Crete, Department of Production Engineering and Management, Management Systems Laboratory, Chania, Greece

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