



Deliverable No. 3.3

Annual report on the Open Consultation Process and Architectural Refinements

Grant Agreement No.: 270089
Deliverable No.: D3.3
Deliverable Name: Annual report on the Open Consultation Process and Architectural Refinements
Contractual Submission Date: 31/01/2013
Actual Submission Date: 31/01/2013

Dissemination Level		
PU	Public	X
PP	Restricted to other programme participants (including the Commission Services)	
RE	Restricted to a group specified by the consortium (including the Commission Services)	
CO	Confidential, only for members of the consortium (including the Commission Services)	



COVER AND CONTROL PAGE OF DOCUMENT

Project Acronym:	p-medicine
Project Full Name:	From data sharing and integration via VPH models to personalized medicine
Deliverable No.:	D 3.3
Document name:	Annual report on the Open Consultation Process and Architectural Refinements
Nature (R, P, D, O) ¹	R
Dissemination Level (PU, PP, RE, CO) ²	PU
Version:	1.0
Actual Submission Date:	31/01/2013
Editor: Institution: E-Mail:	Stelios Sfakianakis FORTH ssfak@ics.forth.gr

ABSTRACT:

This document reports on the open consultation efforts undertaken in the context of WP3 and presents the results and details of this task.

KEYWORD LIST: standards, open consultation, architecture

The research leading to these results has received funding from the European Community's Seventh Framework Programme (FP7/2007-2013) under grant agreement n° 270089.

The author is solely responsible for its content, it does not represent the opinion of the European Community and the Community is not responsible for any use that might be made of data appearing therein.

¹ R=Report, P=Prototype, D=Demonstrator, O=Other

² PU=Public, PP=Restricted to other programme participants (including the Commission Services), RE=Restricted to a group specified by the consortium (including the Commission Services), CO=Confidential, only for members of the consortium (including the Commission Services)

MODIFICATION CONTROL			
Version	Date	Status	Author
0.5	10/12/2012	First draft	Stelios Sfakianakis
1.0	28/01/2012	Final	Stelios Sfakianakis

List of contributors

- Manolis Tsiknakis, FORTH
- Kostas Marias, FORTH
- George Zacharioudakis, FORTH
- Lefteris Koumakis, FORTH
- Vaggelis Sakkalis, FORTH
- Norbert Graf, USAAR

Contents

EXECUTIVE SUMMARY	5
INTRODUCTION	6
REPORT ON THE ANNUAL OPEN CONSULTATION PROCESS	7
1.1. SEMANTIC INTEROPERABILITY FOR CLINICAL DATA AND VPH MODELS WORKSHOP	7
1.2. TECHNICAL MEETING WITH THE VPH-SHARE PROJECT	9
1.3. CONFERENCES AND SPECIAL SESSIONS	10
1.1.1. <i>Special Session in the 12th IEEE International Conference on BioInformatics and BioEngineering</i>	10
1.1.2. <i>Issue of the IEEE journal on Biomedical and Health Informatics.....</i>	16
1.1.3. <i>Special session proposal in 35th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC'13).....</i>	17
CONCLUSIONS	18

Executive Summary

The *p-medicine* architecture definition process needs to leverage state of the art standards and technologies from international standardization bodies like W3C and Oasis. To this end the open consultation process of Work Package 3 aims to build a communication channel and outreach with user communities, standardization organizations, and similar projects in a bidirectional and cross-pollinating way. This report documents such efforts in the previous year and presents their details and results.

Introduction

The p-medicine project aims to develop an innovative and integrated technological solution to facilitate personalized medicine. This endeavor is based on formulating an open, modular framework of tools and services supporting the efficient and secure sharing and handling of large personalized data sets. It is evident that such an ambitious effort should be based on common, accepted, and best-of-breed methodologies and standards. The use of open standards for interoperability, security, data formats, etc., in particular, is of the utmost importance.

But what is an *open standard*? According to the W3C the characteristic of open standards that sets them apart from the “closed” ones is the process by which the standard was defined³, focusing on the transparency of the process, relevance to the user/market needs, openness in the participation, availability of the standard’s text, etc. In agreement with these policies and the approach towards standardization, the project has dedicated tasks in its technical annex focusing on standards, both as a contributor and as a consumer. The activities involve monitoring of standards development, critical review and assessment of their applicability in the p-medicine framework, refining such standards based on domain-specific requirements. For this purpose annual dedicated scientific workshops are to be held (either internally to the project, or in the context of relevant international scientific events), with the participation of key international experts in respective domains. In parallel an open consultation process is foreseen, as an enabler for significant contributions to European and global standards.

³ Daniel Dardailler (ed.), Definition of Open Standards, <http://www.w3.org/2005/09/dd-osd.html> World Wide Web Consortium, 2007

Report on the Annual Open Consultation process

During the previous year the p-medicine consortium members organized and participated in a number of sessions and workshops that we briefly describe in the following sections. The objectives of these events are threefold:

- To increase the familiarization of the community to the project's objectives and requirements and support its visibility and outreach.
- To gather feedback and experiences of the relevant stakeholders (users, IT developers, clinicians, bioinformaticians, etc)
- To influence and leverage the development and adoption of open standards in related domain areas.

1.1. Semantic interoperability for clinical data and VPH models workshop

The Semantic interoperability workshop, organized as part of the VPH2012 conference⁴ in London, UK, aimed at discussing and promoting interoperability between model resources and databases as well as between the software systems that are in use within the VPH community in order to improve interoperability within the VPH⁵.

In this workshop the RICORDO project⁶ and its approach for addressing semantic interoperability in VPH were presented. The RICORDO approach seems to be highly relevant to the semantic interoperability methodology proposed in the p-medicine architectural blueprint and therefore members of the consortium (FORTH and USAAR) were present in this workshop and had the chance to discuss the RICORDO methods and process. Additionally, during this technical meeting with the representatives of RICORDO we have discussed the p-medicine reference architecture and its semantic requirements. This discussion is ongoing and the possibility of integrating some of the RICORDO infrastructure into the p-medicine architecture is currently investigated.

The official agenda and the details of the presentations in this workshop are as follows:

⁴ <http://www.vph-noe.eu/vph2012/>

⁵ Virtual Physiological Human (VPH) Network of Excellence, <http://www.vph-noe.eu/>

⁶ <http://www.ricordo.eu/>

RICORDO @VPH2012 LONDON

INTEROPERABLE ANATOMY AND PHYSIOLOGY

9:45am - 10:30am (Bernard de Bono)

Introduction To RICORDO

A general introduction to biomedical ontologies, semantic metadata management, knowledge visualization, clinical application examples and RICORDO objectives. Followed by an interactive discussion on annotation and metadata requirements.

10:30am - 12:00pm (Sarala Wimalaratne)

DEMO: RICORDO Infrastructure for Semantic Management

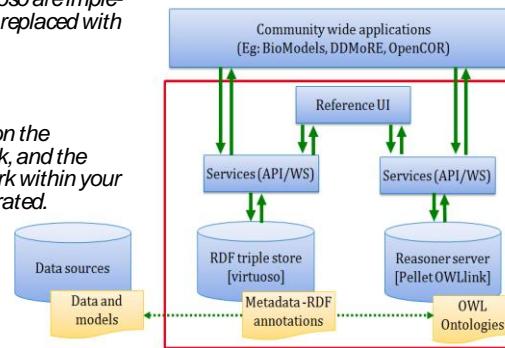
An infrastructure for supporting the semantic interoperability of resources based on the management (i.e. storing and inference-based querying) of their ontology-based annotations (see figure below). The infrastructure consists of:

- (i) a repository to store and query ontology-based annotations;
- (ii) a knowledge base server with an inference engine to support the storage of and reasoning over ontologies used in the annotation of resources;
- (iii) a set of applications and services allowing interaction with the integrated repository and knowledge base.

The framework presents a configurable, deployable infrastructure to allow individual communities to deploy within their environments. Configuration files are provided to configure each module to work within individual communities.

(N.B Pellet OWLlink and Virtuoso are implementation details and can be replaced with other reasoners and rdf-store implementations via Spring configuration files.)

In the second half of the session the functionality of the framework, and the configuration of the framework within your environment will be demonstrated.





12:00pm - 12:50pm (*Daniel L. Cook*)

Semantic integration of biosimulation models across multiple scales and domains

Goal: describe recent progress in rapid prototyping of multiscale/multidomain biosimulation models using semantic methods for the reuse and recomposition of models and model parts.

Description of semi- and fully-automatic methods for leveraging the semantics of available biomedical ontologies to streamline the reuse and recomposition of legacy multiscale, multidomain biosimulation models and model parts. This section covers:

1. *SemGen, an application that semi-automatically derives semantic simulation (SemSim) models from legacy biosimulation code from multiple platforms/languages (SBML, CellML, JSimMML) to decompose, extract, and recompose SemSim models which can be encoded any of the source language as well as MatLab.*
2. *SBML Harvester automatically transforms in-line model annotations in the BioModels database into OWL annotations that are used for retrieval and other analyses of the contents of BioModels. We will then introduce BioSimConnector which identifies potential pathway linkages between biosimulation models by finding pathways that exist within the Reactome knowledge resource, in the CellML model repository, as well as in the BioModels database.*
3. *More recent work whereby SemGen extracts and extends SemSim models to produce PhysioMaps that explicitly represent and interlink the physiological processes and their participants as derived from biosimulation model code. We will show how the Chalkboard displays PhysioMaps as editable diagrams that can be queried by modelers and experimentalists to display qualitative outcomes of physiological “thought experiments.”*

12:50pm - 1:00pm

Plenary discussion and follow up plans

— \$ —

1.2. Technical Meeting with the VPH-Share project

In August 2012 a joint meeting of p-medicine and VPH-Share technical teams took place in Sankt Augustin, Germany. The need for cultivating a synergy between these two IP projects has been recognised early on and after the joint review meeting that took place in Brussels in November 2011 the two consortia organized this technical meeting. The objective of this meeting was to discuss and compare the approaches pursued in the different projects as well as to identify areas of cooperation and synergistic actions. The list of the presenting attendees and the main items of the discussion are shown below.



VPH-Share and p-medicine

31st August 2012
Sankt Augustin

Minutes 1v1



VPH-Share and p-medicine Joint Meeting #15 Sankt Augustin – Friday, 31st August 2012 (09:00-17:00 CEST)

Presenting Attendees

p-medicine

Norbert Graf	Scientific Coordinator	USAAR	NG
Elias Neri	WP3 (IT Architecture)	CUSTODIX	EN
Nikolaus Forgó	WP5 (Legal and Ethical Framework)	Hannover	NF
Benjamin Jefferys	WP7 (Data Warehouse)	UCL	BJ
Juliusz Pukacki	WP7 (Data Warehouse)	PSNC	JP
Holger Stenzhorn	WP7 (Data warehouse)	USAAR	HS
Stefan Kiefer	WP10 (Access to Biobanks)	Fraunhofer	SK
Georgios Stamatakos	WP12 (VPH Modelling)	ICCS	GS
Stelios Sfakianakis	WP12 (VPH Modelling)	FORTH	SS
Corinna Hahn	PMO	USAAR	CH

VPH-Share

Rod Hose	Scientific Coordinator/WP1	USFD	RH
Marian Bubak	WP2 (Cloud)	CYFRONET	MB
Piotr Nowakowski	WP2 (Cloud)	CYFRONET	PN
Dario Ruiz	WP2 (Security) & WP4 (Semantics)	AOSAE	DR
Steven Wood	WP3 (Infrastructure)	STH	SW
Karl Stroetmann	WP7 (Exploitation)	EMPIRICA	KS
Norman Powell	PMO	USFD	NP
Keith McCormack	PMO	USFD	KM

Apologies from those who Prepared Presentations

Tomás Pariente	WP4 (Semantics)	AOSAE	TP
Luigi Carotenuto	WP6 (User Interface)	UPF	LC
Peter Singleton	WP7 (Ethics)	EMPIRICA	PS
Debora Testi	WP8 (Outreach)	SCS	DT

Ref	Summary of Actions	Resp	
PS03-A01	Explore the possibility of sharing p-medicine meta-data through VPH-Share for discovery	01-Mar-13	BJ & SW
PS03-A02	Understand the impact of EUDAT on p-medicine and VPH-Share	01-Mar-13	JS & SW
PS03-A03	Accelerate the timetable of Ethics discussions between the two projects and involve technical representatives	01-Mar-13	NF & PS
PS03-A04	GS and Susheel Varma (SV) to explore the utility of tools and services from VPH-Share Tasks 5.1, 5.2, 5.3 for p-medicine	01-Mar-13	GS & SV
PS03-A05	Projects to share deliverables at and if possible prior to their submission	Open	PMOs

1.3. Conferences and Special Sessions

1.1.1. Special Session in the 12th IEEE International Conference on BioInformatics and BioEngineering

We have organized a special session entitled “*Computational solutions to large-scale data management and analysis in translational, personalized and predictive medicine*” during the recent 12th IEEE International Conference on BioInformatics and BioEngineering⁷ (BIBE).

The description of the session and the final program follows:

⁷ <http://bibe2012.cs.ucy.ac.cy/>



Special Session on: Computational Solutions to Large-scale Data Management and Analysis in Translational and Personalized Medicine

Medicine is undergoing a revolution that is transforming the nature of healthcare from reactive to preventive. The changes are catalyzed by a new systems approach to disease that focuses on integrated diagnosis, treatment and prevention of disease in individuals. This is expected to replace our current mode of medicine over the coming years with a personalized and predictive treatment. While the goal is clear, the path is fraught with challenges.

Our success in addressing these challenges depends on our ability to properly interpret the large-scale, high-dimensional data sets that are generated by modern technologies, manage dimensionality problems and extract meaningful prognosis/ diagnosis biomarkers, since it is becoming increasingly clear that a comprehensive analysis of biological systems requires the integration of all fingerprints of cellular function: genome sequence, maps of gene expression, protein expression, metabolic output, and *in vivo* enzymatic expression (activity). This need for integration is especially clear in the case of complex, multifactorial diseases, such as cancer.

At the same time the Virtual Physiological Human (VPH) framework aims to define models and technologies that once fully established will enable the investigation of the human body as a whole, eventually leading to a better healthcare system that offers personalized care solutions, more holistic approach to medicine and a preventative approach to the treatment of disease. Although consensus exists about what the fundamental tools are (integration of high-throughput data from several biologic scales, high-definition imaging, and computational modeling), no such consensus exists as to what are the most promising scientific approaches in responding to these challenges.

A growing awareness is found that, despite significant technological advances in various domains of relevance, fundamental obstacles separate systems biology from clinical applications. Bridging these gaps will require a focused and concerted effort in addressing various questions, such as:

- What defines systems medicine as a discipline?
- What should it seek to accomplish?
- How to develop optimal frameworks for large-scale data sharing distributed scientific collaboration and collective research efforts?
- How to exploit data from hospital information systems, EHRs and PHRs and how to curate these data?
- How should knowledge from disparate sources be assembled into ontologies relevant to systems medicine?
- How do you develop and evaluate appropriate algorithms for marker selection, diagnosis and prognosis as well as therapeutic agent, identification and evaluation?
- How do you manage the problems of dimensionality?
- How are multiscale data to be synthesized by corresponding multiscale models?
- How should models be represented, stored, managed and shared?
- Health recommender systems: How to deliver personalized health information?
- What is the burden of proof that such models are valid and predictive of clinically relevant outcomes?

Furthermore, because of the necessary multiscale nature of the models bridging embedded levels of organization from molecules, organelles, cells, tissues, organs, and all the way to individuals, environmental factors, populations, and ecosystems, systems medicine aims to discover and select the key factors at each level and integrate them into models of translational relevance, which include measurable readouts and clinical predictions.

The Special Session will build on experiences as well as technological and scientific developments stemming from some flagship projects funded by the EU under the FP7 framework programme aiming to bring together researchers working in the fields of infrastructures and technologies for integrative biomedical research, ICT for predictive and translational medicine and the VPH at large.

In addition the Special Session covers the aspects of Cancer Informatics with a focus on revealing progress, and challenges in some of core domains that support the vision of predictive and personalised medicine in the domain of cancer.

A total of 17 papers will be presented under the following three sessions: i. *Frameworks for Large-scale Data Sharing, Semantics & Related Sociotechnical Issues*, ii. *Algorithms for Marker Selection, Diagnosis, Prognosis & Patient Empowerment*, and iii. *Modeling and Analysis Frameworks*.

Organisers:

Prof Manolis Tsiknakis, *TEI Crete and FORTH, Co-ordinator*
Dr Kostas Marias, *FORTH*
Dr Vangelis Sakkalis, *FORTH*
Prof Norbert Graf, *University of Saarland*
Dr Anca Bucur, *Philips Research, Eindhoven, NL*
Dr Georgios Mitsis, *University of Cyprus*
Prof Constantinos S. Pattichis, *University of Cyprus*
Prof Nikolaus Forgo, *University of Hannover*
Dr Aristotelis A Chatzilooannou, *National Hellenic Research Foundation*
Dr Athos Antoniades, *University of Cyprus*

Projects:

The Special session will draw upon experiences from some flagship EU funded projects such as:

ContraCancrum (<http://www.contracancrum.eu/>)
TUMOR (<http://tumor-project.eu/>)
p-medicine (<http://www.p-medicine.eu/>)
INTEGRATE (<http://www.fp7-integrate.eu/>)
GRANATUM (<http://www.granatum.org/>)
Linked2Safety (<http://www.linked2safety-project.eu/>)
CONTRACT (<http://www.contract-fp7.eu/>)
EnviroGenomarkers (<http://www.envirogenomarkers.net/>)
ΥΠ.ΕΡ.ΘΕ.Ν. (<http://www.yperthen.gr>)

Special issue:

Extended versions of the best papers of the conference will be invited for publication in the IEEE Journal of Biomedical and Health Informatics (J-BHI) (see call for papers for Journal Special Issues).

Tuesday Morning, 13th November

Session: **Special Session 1¹ – Frameworks for large-scale data sharing, semantics and related sociotechnical issues**

Time & Place: **8:30-10:00 - Les Etoiles**

Chairpersons: **Vaggelis Sakkalis, Computer Medicine Laboratory, Institute of Computer Science, FORTH, Heraklion, Crete, Greece**
Athos Antoniades, University of Cyprus, Cyprus

Tue. SS. 13.1 **08:30-08:45**

Data Integration and Feature Selection in High-volume Molecular and Imaging Datasets

Konstantinos Moutselos¹, Ilias Maglogiannis¹ and Aristotelis Chatzioannou²

¹*Konstantinos Moutselos, Ilias Maglogiannis Department of Computer Science and Biomedical Informatics University of Central Greece, Lamia, Greece;* ²*Institute of Biological Research and Biotechnology National Hellenic Research Foundation Athens, Greece*

Tue. SS. 13.2 **08:45-09:00**

Identifying the Semantics of Eligibility Criteria of Clinical Trials based on relevant Medical Ontologies

Anca Bucur¹, Jasper van Leeuwen¹, David Perez Del Rey², Brecht Claerhout³, Kristof de Schepper³ and Raul Alonso Calvo²

¹*Healthcare Information Management Philips Research Europe, Eindhoven, the Netherlands;* ²*Grupo de Informática Biomédica, Department Inteligencia Artificial, Facultad de Informática, Universidad Politécnica de Madrid, Boadilla del Monte, Madrid, Spain;* ³*Custodix NV Kortrijkssteenweg 214b3, Sint-Martens-Latem, Belgium*

Tue. SS. 13.3 **09:00-09:15**

A technical infrastructure to support Personalized Medicine

Stelios Sfakianakis¹, Manolis Tsiknakis¹, Konstantinos Marias¹ and Norbert Graf²

¹*Computer Medicine Laboratory, Institute of Computer Science, FORTH, Heraklion, Crete, Greece;*

²*Department for Ped, Oncology / Hematology University Hospital Homburg, Homburg, Germany*

Tue. 13.4 **09:15-09:30**

Legal and Ethical Issues in Integrating Databases for Translational Medical Research within the EU

Iheanyi Nwankwo, Stefanie Haenold and Nikolaus Forgo

Forgó Institute for Legal Informatics, Leibniz Universität Hannover

Tue. SS. 13.5 **09:30-09:45**

e-Prolipsis: A web based risk estimation platform to support and register breast cancer diagnosis in Greece

Alexandros Dimopoulos, John Lakoumentas, Argyro Antarakis, Antonios Frigas, Emmanouil Ikonomakis, Marinos Sampson, Anastasios Tagaris, Aikaterini Liakou, Emmanouil Athanasiadis, George Spyrou and Panos Ligomenides

Biomedical Research Foundation of the Academy of Athens (BRFAA), Athens, Greece

¹ See Special Session description: *Computational Solutions to Large-scale Data Management and Analysis in Translational and Personalized Medicine*

Tuesday Morning, 13th November

Session: Special Session 2² – Algorithms for Marker Selection, Diagnosis, Prognosis and Patient Empowerment

Time & Place: 12:00-13:15 – Les Etoiles

Chairpersons: Anca Bucur, *Healthcare Information Management Philips Research Europe, Eindhoven, the Netherlands*
Konstantinos Marias, *Computational Medicine Laboratory, FORTH-ICS Heraklion, Crete, Greece*

Tue. SS. 16.1

12:00-12:15

Linked2Safety: A secure linked data medical information space for semantically-interconnecting EHRs advancing patients' safety in medical research

Athos Antoniades¹, Christos Georgousopoulos², Nikolaus Forgo³, Aristos Aristodimou¹, Federica Tozzi⁴, Panagiotis Hasapis², Konstantinos Perakis⁵, Thanasis Bouras⁵, Dimitris Alexandrou⁵, Eleni Kamateri⁶, Eleni Panopoulou⁶, Konstantinos Tarabanis⁶ and Constantinos Pattichis¹

¹University of Cyprus, Nicosia, Cyprus; ²INTRASOFT International, Brussels, Luxembourg; ³Gottfried Wilhelm Leibniz Universität Hannover, Hannover, Germany; ⁴School of Medicine, University of North Carolina, Chapel Hill, NC, USA; ⁵Ubitech Ltd., Athens, Greece; ⁶The Centre for Research and Technology Hellas, Thessaloniki, Greece

Tue. SS. 16.2

12:15-12:30

Influence of Algorithmic Parameters on Marker Selection in Genomic Datasets

Theodora Viggideli¹, Ekaterini Bei¹, Michalis Zervakis¹ and Dimitrios Kafetzopoulos²

¹Department of Electronic and Computer Engineering, Technical University of Crete, Chania, Crete, Greece; ²Institute of Molecular Biology and Biotechnology, Foundation of Research and Technology Hellas (FORTH), Heraklion Crete, Greece

Tue. SS. 16.3

12:30-12:45

Design Rules for Cancer Nanomedicines

Triantafyllos Stylianopoulos¹, Konstantinos Soteriou¹, Dai Fukumura² and Rakesh Jain²

¹Department of Mechanical and Manufacturing Engineering, University of Cyprus, Nicosia, Cyprus; ²Edwin L. Steele laboratory, Department of Radiation Oncology, Massachusetts General Hospital and Harvard Medical School, Boston, USA

Tue. SS. 16.4

12:45-13:00

IEmS: A collaborative Environment for Patient Empowerment

Haridimos Kondylakis¹, Lefteris Koumakis¹, Eirini Genitsaridi¹, Manolis Tsiknakis^{1,2}, Konstantinos Marias¹, Gabriella Pravettoni³, Alessandra Gorini⁴ and Ketti Mazzocco³

¹Computational Medicine Laboratory, FORTH-ICS Heraklio, Crete, Greece; ²Department of Applied Informatics and Multimedia, Technological Educational Institute, Heraklion, Crete; ³Centro Interdipartimentale di Ricerca e Intervento sui, Processi Decisionali (IRIDe) Università degli Studi di Milano; ⁴Department of Decision Sciences, Bocconi University, Milan and eCancer – Cancer Intelligence Limited

Tue. SS. 16.5

13:00-13:15

Security Issues in research projects with patient's medical data

Nikolaus Forgo, Magdalena Goralczyk and Constantin Graf von Rex
Institute for Legal Informatics, LUH Hannover, Germany

Lunch Break

13:30-14:30

² See Special Session description: Computational Solutions to Large-scale Data Management and Analysis in Translational and Personalized Medicine

Tuesday Afternoon, 13th November

Session:	Special Session 3³ – Modeling and Analysis Frameworks
Time & Place:	14:30-16:00 – Les Etoiles
Chairpersons:	Norbert Graf, University of the Saarland, Department of Pediatric Oncology and Hematology, Homburg, Germany Georgios Mitsis, Department of Electrical and Computer Engineering, University of Cyprus, Cyprus

Tue. SS. 19.1 **14:30-14:45****Model-based control of tumor progression**

Marios Hadjia Andreou and Georgios Mitsis

*Department of Electrical and Computer Engineering, University of Cyprus, Nicosia, Cyprus***Tue. SS. 19.2** **14:45-15:00****An innovative mathematical analysis of routine MRI scans in patients with glioblastoma using DoctorEye**Jonathan Zepp¹, Norbert Graf¹, Ioannis Karatzanis², Holger Stenzhorn¹, Georgios Manikis², Vangelis Sakkalis², Wolfgang Reith³, Georgios Stamatakos⁴, Konstantinos Marias²¹*University of the Saarland, Department of Pediatric Oncology and Hematology, D-66421 Homburg, Germany;* ²*Institute of Computer Science at FORTH, Heraklion, Crete, Greece;* ³*University of the Saarland, Department of Neuroradiology, Homburg, Germany;* ⁴*Institute of Communications and Computer Systems, National Technical University of Athens, In Silico Oncology Group, Zografos, Greece***Tue. SS. 19.3** **15:00-15:15****The effects of near optimal growth solutions in genome-scale human cancer metabolic model**

Eleftheria Tzamali, Vangelis Sakkalis and Konstantinos Marias

*Institute of Computer Science, Foundation for Research and Technology-Hellas (FORTH), Heraklion, Crete, Greece***Tue. SS. 19.4** **15:15-15:30****Analysis of DNA Methylation Epidemiological Data through a Generic Composite Statistical Framework**

Ioannis Valavanis, Emmanouil Sifakis, Panagiotis Georgiadis, Sotirios Kyrtopoulos and Aristotelis Chatzioannou

*Institute of Biology, Medicinal Chemistry & Biotechnology, National Hellenic Research Foundation, Athens, Greece***Tue. SS. 19.5** **15:30-15:45****Strengths and Weaknesses of the European Concept of Informed Consent: Theoretical Issues and Practical Examples**

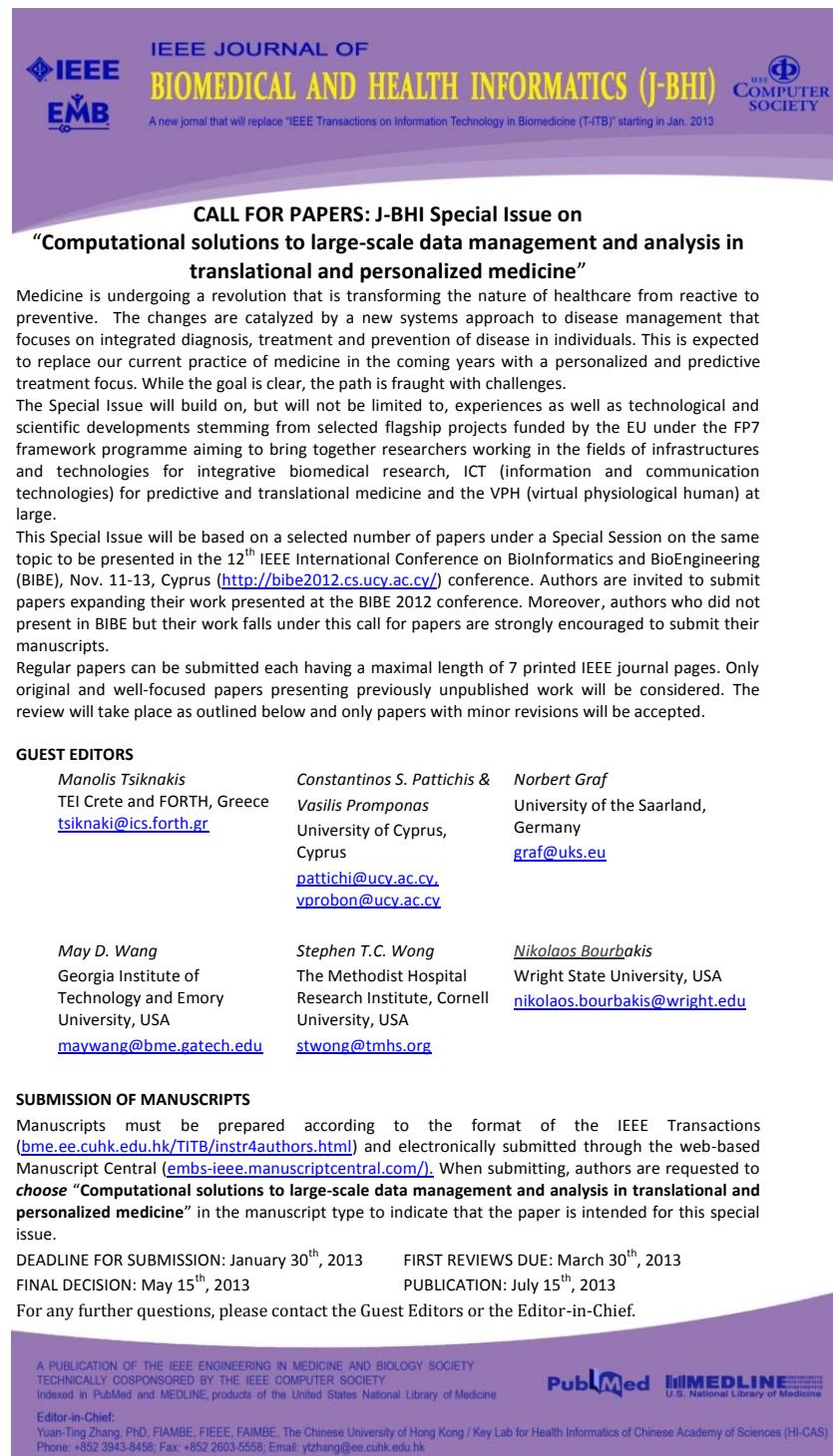
Nikolaus Forgo, Magdalena Goralczyk and Constantin Graf von Rex

*Institute for Legal Informatics, LUH Hannover, Germany***Tue. SS. 19.6** **15:45-16:00****The effects of applying cell-suppression and perturbation to aggregated genetic data**Athos Antoniades¹, John Keane², Aristos Aristodimou¹, Christa Philipou¹, Andreas Constantinou¹, Christos Georgousopoulos³, Federica Tozzi⁴, Kyriacos Kyriacou⁵, Andreas Hadjisavvas⁵, Maria Loizidou⁵, Christiana Demetrou⁵ and Constantinos Pattichis¹¹*University of Cyprus, Nicosia, Cyprus;* ²*University of Manchester, Manchester, United Kingdom;* ³*INTRASOFT International, Luxembourg, Brussels;* ⁴*School of Medicine, University of North Carolina, Chapel Hill, NC, USA;* ⁵*Cyprus Institute of Neurology and Genetics, Nicosia, Cyprus***Coffee Break** **16:00-16:30**

³ See Special Session description: Computational Solutions to Large-scale Data Management and Analysis in Translational and Personalized Medicine

1.1.2.Issue of the IEEE journal on Biomedical and Health Informatics

Following the success of the BIBE special session Prof. Norbert Graf and Dr. Manolis Tsiknakis are amongst the Guest Editors (with significant scientific participation from the US) of a dedicated issue of the IEEE Journal on Biomedical and Health Informatics (a replacement of the IEEE Transactions on Information Technology in Biomedicine), in which p-medicine architecture and technologies will be clearly presented.



The cover page features the IEEE EMB logo, the journal title "IEEE JOURNAL OF BIOMEDICAL AND HEALTH INFORMATICS (J-BHI)", and the IEEE Computer Society logo. A note states: "A new journal that will replace 'IEEE Transactions on Information Technology in Biomedicine (T-ITB)' starting in Jan. 2013".

CALL FOR PAPERS: J-BHI Special Issue on
"Computational solutions to large-scale data management and analysis in translational and personalized medicine"

Medicine is undergoing a revolution that is transforming the nature of healthcare from reactive to preventive. The changes are catalyzed by a new systems approach to disease management that focuses on integrated diagnosis, treatment and prevention of disease in individuals. This is expected to replace our current practice of medicine in the coming years with a personalized and predictive treatment focus. While the goal is clear, the path is fraught with challenges. The Special Issue will build on, but will not be limited to, experiences as well as technological and scientific developments stemming from selected flagship projects funded by the EU under the FP7 framework programme aiming to bring together researchers working in the fields of infrastructures and technologies for integrative biomedical research, ICT (information and communication technologies) for predictive and translational medicine and the VPH (virtual physiological human) at large.

This Special Issue will be based on a selected number of papers under a Special Session on the same topic to be presented in the 12th IEEE International Conference on BioInformatics and BioEngineering (BIBE), Nov. 11-13, Cyprus (<http://bibe2012.cs.ucy.ac.cy/>) conference. Authors are invited to submit papers expanding their work presented at the BIBE 2012 conference. Moreover, authors who did not present in BIBE but their work falls under this call for papers are strongly encouraged to submit their manuscripts.

Regular papers can be submitted each having a maximal length of 7 printed IEEE journal pages. Only original and well-focused papers presenting previously unpublished work will be considered. The review will take place as outlined below and only papers with minor revisions will be accepted.

GUEST EDITORS

<i>Manolis Tsiknakis</i> TEI Crete and FORTH, Greece tsiknaki@ics.forth.gr	<i>Constantinos S. Pattichis & Norbert Graf</i> University of the Saarland, Germany pattichi@ucy.ac.cy , vprobon@ucy.ac.cy
---	---

<i>May D. Wang</i> Georgia Institute of Technology and Emory University, USA maywang@bme.gatech.edu	<i>Stephen T.C. Wong</i> The Methodist Hospital Research Institute, Cornell University, USA stwong@tmhs.org	<i>Nikolaos Bourbakis</i> Wright State University, USA nikolaos.bourbakis@wright.edu
---	--	---

SUBMISSION OF MANUSCRIPTS

Manuscripts must be prepared according to the format of the IEEE Transactions (bme.ee.cuhk.edu.hk/TITB/instr4authors.html) and electronically submitted through the web-based Manuscript Central (embs-ieee.manuscriptcentral.com/). When submitting, authors are requested to choose "Computational solutions to large-scale data management and analysis in translational and personalized medicine" in the manuscript type to indicate that the paper is intended for this special issue.

DEADLINE FOR SUBMISSION: January 30th, 2013 FIRST REVIEWS DUE: March 30th, 2013
FINAL DECISION: May 15th, 2013 PUBLICATION: July 15th, 2013

For any further questions, please contact the Guest Editors or the Editor-in-Chief.

A PUBLICATION OF THE IEEE ENGINEERING IN MEDICINE AND BIOLOGY SOCIETY
TECHNICALLY COSPONSORED BY THE IEEE COMPUTER SOCIETY
Indexed in PubMed and MEDLINE, products of the United States National Library of Medicine

Editor-in-Chief:
Yuan-Ting Zhang, PhD, FIAMBE, FIEEE, FAIMBE, The Chinese University of Hong Kong / Key Lab for Health Informatics of Chinese Academy of Sciences (HI-CAS)
Phone: +852 3943-8458; Fax: +852 2603-5558; Email: ytzhang@ee.cuhk.edu.hk

PubMed  **MEDLINE**  U.S. National Library of Medicine

1.1.3. Special session proposal in 35th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC'13)

Following BIBE, Manolis Tsiknakis in cooperation with Norbert Graf have submitted a proposal for the organization of a relevant Special Session during the 35th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC'13), which will take place 3-7 July 2013 in Osaka, Japan⁸. A draft agenda of this session follows:



Special Session (90 min; EMBC2013_318)

Computational solutions to large-scale data management and analysis in translational, personalized and predictive medicine

Agenda (first draft)

5 min	Norbert Graf: Introduction to the topic
10 min + 4	Manolis Tsiknakis: A semantically aware architectural framework enabling knowledge driven discovery and orchestration of VPH models in support of personalized and predictive medicine
10 min + 4	Nikolaus Forgó, Magdalena Góralczyk: Legal frameworks for data sharing from a European data protection perspective
10 min + 4	Kostas Marias: Defining the interactions between computational models and imaging biomarker tools for improving personalized predictions Vangelis Sakkalis: Employing novel imaging modalities in developing modeling tools for enabling personalized cancer prediction and treatment response
10 min + 4	Georgios Stamatakos: The Oncosimulator as a tool for decision support
10 min + 4	Anca Bucur: EURECA and INTEGRATE: two European VPH projects
10 min + 4	Yuzuru Tanaka, Jonas Sjøberg: Trial Outline Builder (TOB) for visualizing clinical trials from data entry, patient follow-up to trial analysis.

⁸ <http://www.embc2013.embs.org/>

Conclusions

In the document we have presented a number of key activities and events for the open consultation process and the project's outreach to the relevant user and developer communities. In general these efforts have been very successful and have set the path for future collaborations, such as with the RICORDO and VPH-Share projects. The outcome of such collaborations and efforts will be documented in the related tasks of the project's technical plan.